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(71) Applicants (for all designated States except US): GALA-
PAGOS GENOMICS N.V. [BE/BE]; Generaal de
Wittelaan 11 A3, B-2800 MECHELEN (BE); VAN DER
SCHUEREN, Jan [BE/BE]; Spaarstraat 56, B-3010
KESSEL-LO (BE).

(72) Inventors; and

(75) Inventors/Applicants (for US only): ARTS, Gerardus,
Johannes, Franciscus [NL/NL]; Wikkestraat 46, NL-2403
ES ALPHEN AAN DE RIJN (NL); LAMBRECHT,
Mark, Jacques, Yvonne [BE/BE]; Bukenstraat 89,
B-1910 BUKEN (BE); DJOKIC, Kristina [NL/NL];
Joseph Haydnlaan 58, NL-2324 AT LEIDEN (NL).

CLASEN, Remko, Johannes [NL/NL]; Middelweg 15
H, NL-2312 KE LEIDEN (NL). MESIC, Emir [NL/NL];
Koningstraat 1, NL-2316 CA LEIDEN (NL). GRIF-
FJOEN, Sandra [NL/NL]; Maresingel 47A, NL-2316 HD
LEIDEN (NL). BERGS, Carolina, Johanna, Leonarda
[NL/NL]; Van Vollenhovenplein 102, NL-2313 EE LEI-
DEN (NL).

(74) Agent: VERNOUT, Robert; Arnold & Siedsma, Sweet-
inckplein 1, NL-2517 GK THE HAGUE (NL).

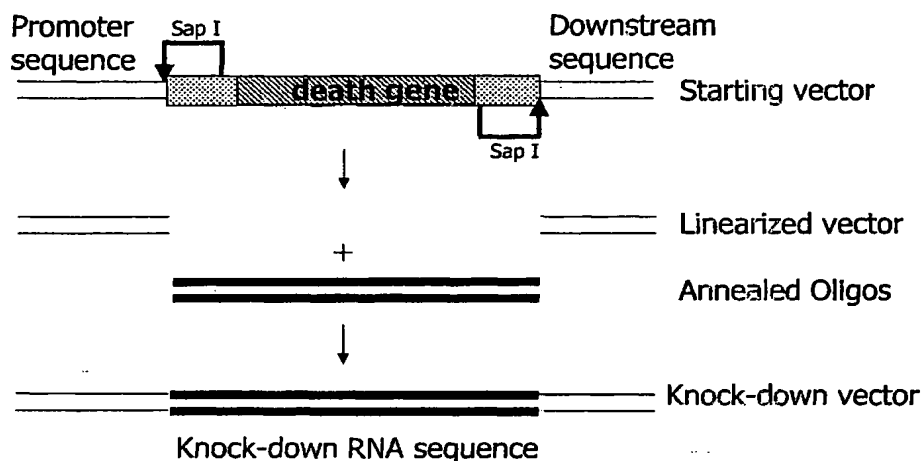
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(54) Title: EFFECTIVE SIRNA KNOCK-DOWN CONSTRUCTS

Vector development



(57) Abstract: The present invention provides polynucleotides comprising an RNA sequence comprising a first stretch of 21 consecutive nucleotides and a second stretch of 21 consecutive nucleotides, complementary to the first stretch of 21 consecutive nucleotides, wherein in first stretch of 21 consecutive nucleotides: in the 5' -> 3' direction, the first nucleotide is an A-nucleotide, the second nucleotide is a C-nucleotide and the last nucleotide is a C-nucleotide; and no stretches of four or more consecutive identical nucleotides are present; the total number of G- and C-nucleotides is between 33-71% of the total number of nucleotides and in the 5' -> 3' direction, consecutive nucleotides 3-21 are homologous to a RNA-molecule. Vectors encoding the polynucleotide of the present invention are also provided. Furthermore libraries of the polynucleotides and vectors encoding and methods to produce vectors and libraries are given.

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Effective siRNA knock-down constructs

The present invention relates to polynucleotide constructs, methods for their preparation, and preparations for their use in methods that lower the amount of RNA and/or protein production in cells based on the intracellular expression of small interfering polyribonucleic acid molecules.

Pharmaceutical companies are interested in reliable knockdown based technologies since their drug screens with small molecules are based on inhibiting the activity and effect of an expressed protein. Therefore, blocking expression or function of a potential target, either through screening in a cellular assay or through single gene validation will provide an important data set regarding drug-ability of the target early on in the drug development process. This data set forms a strong basis for the start of a drug development program, based on a compound, antibody or biological, with the aim to develop an effective therapy.

Various knockdown or knockout approaches are used to study gene function in mammalian cells (e.g. antisense, antibodies, ribozymes, aptamers, zinc finger proteins, chimeric RNA-DNA oligos, etc.). However, these technologies are not robust and efficient nor they can be generically applied to all genes and all cell types.

RNA interference (RNAi) is the post-transcriptional process of gene silencing mediated by double stranded RNA (dsRNA) that is homologous in sequence to the silenced RNA and is observed in animals and plants. The dsRNA is processed into 21-23 nucleotides (nts) molecules, called small interfering RNAs (siRNAs), which guide the sequence-specific degradation of the target RNA.

RNAi provides researchers with an additional genetic tool to study gene functions. In C. elegans, chromosomes I and III have now systematically been analyzed for phenotypic effects. The RNAi approach creates extra possibilities in developmental studies. Classical knockouts with lethal effects during development could never be analyzed in later developmental stages. With RNAi, the onset of the effect may be varied and roles in later stages of development may be studied.

The use of RNAi in mammalian cells has been problematic since introduction of long (>30 base pairs) dsRNA results in two major intracellular responses: activation of the double stranded RNA dependent protein kinase PKR, which results in a general block of protein synthesis. Long dsRNA is also known to activate the interferon-induced (2'-5') oligoadenylate synthetase. Upon activation, this enzyme polymerizes ATP into 2'-5'-linked nucleotide oligomers (also indicated by 2-5A). The 2-5A oligomers activate the ribonuclease RNase L that results in RNA degradation.

Recently, it has been demonstrated that RNAi can be used in a panel of mammalian cell lines. The approach is based on direct transfection of the 21-23 nts siRNA duplexes into the cells. This circumvents the intracellular responses mentioned above and results in sequence-specific silencing of endogenous and heterologous genes.

An important bottleneck in the siRNA transfection approach is its limited applicability to target different cell types, especially primary cells. Primary cells are closest to the in vivo situation and often have the highest physiological relevance. Non-viral DNA or siRNA transfection technologies have severe limitations with regard to these cells and are not efficient and reliable. Practical use of these approaches needs significant optimisation of

conditions, and in general lack the robustness necessary for large-scale applications. The gene transfer reagents used are often toxic, yielding lower levels of viable transduced cells. In essence, they do not allow a generic siRNA
5 application for a wide variety of cell types, including primary cell types such as T cells, B cells, mast cells, endothelial cells, synoviocytes and lung epithelial cells. Furthermore, transfection of the siRNA gives a short knock-down effect. For a prolonged knock-down effect in cells
10 several additional transfections are necessary.

Viral constructs encoding the siRNA molecule circumvent the problems described above. WO03020391 describes adenoviral vectors which express hairpin RNAs that are further processed to siRNAs. Infection of cell lines, or primary human cells,
15 with these viruses leads to an efficient, sequence-specific, and prolonged reduction of the corresponding target mRNA, resulting in a functional knock-down of the encoded protein.

However, not every siRNA can effectively downregulate a gene. siRNAs directed to different regions of a mRNA can
20 result in different levels of gene silencing. It is estimated that between 25% and 75% of siRNAs are effective. Some RNAi's have a 10-fold effect, some have seen a 50-fold effect, and some don't work at all. For example, a siRNA directed against vimentin (nt 346-368 from Genbank (NCBI): NM_003380
25 relative to start codon) did not give a silencing effect. Three other siRNAs against vimentin were designed and these all gave an effective gene silencing effect (nt 1145-1167, nt 863-885 and nt 1037-1059 from NM_003380 relative to start codon, (Elbashir et al 2001)). A procedure for designing
30 siRNAs for efficiently inducing RNAi in mammalian cells has been suggested (Elbashir et al 2002). However, a siRNA against c-myc, designed according to this protocol was ineffective in silencing. and did not show a reduction in

protein expression Jarvis and Ford (2002). This clearly demonstrates that target site selection is critical for the effective induction of RNAi by siRNAs.

The present invention provides polynucleotides that are
5 very effective in the silencing a RNA molecule.

The present invention provides polynucleotide comprising an RNA sequence comprising a first stretch of 21 consecutive nucleotides and a second stretch of 21 consecutive nucleotides, complementary to the first stretch of 21
10 consecutive nucleotides, wherein in first stretch of 21 consecutive nucleotides:

a. in the 5' -> 3' direction, the first nucleotide is an A-nucleotide , the second nucleotide is a C-nucleotide and the last nucleotide is a C-nucleotide; and

15 b. no stretches of four or more consecutive identical nucleotides are present;

c. the total number of G- and C-nucleotides is between 33-71% of the total number of nucleotides;

d. in the 5' -> 3' direction, consecutive nucleotides 3-
20 21 are homologous to a RNA-molecule.

The total number of G- and C-nucleotides can be 33, 35, 40, 45, 50, 55, 60, 65, 70, and 71 % of the total number of nucleotides. The consecutive nucleotides 3-21 in the 5' -> 3' direction of the first stretch of 21 consecutive nucleotides
25 are homologous to the RNA-molecule to be silenced.

"Homologous" to the RNA-molecule can mean that nucleotides 3-21 of the stretch of 21 consecutive nucleotide are identical to a stretch of 19 consecutive nucleotides present in the RNA-molecule to be silenced; or that 95%, 90%,
30 85% or 80% of the nucleotides 3-21 of the stretch of 21 consecutive nucleotide are identical to a stretch of 19 consecutive nucleotides present in the RNA-molecule to be silenced. A polynucleotide with all 21 nucleotides of the

stretch of 21 consecutive nucleotide identical to a stretch of 21 consecutive nucleotides present in the RNA-molecule to be silenced is also possible. In a suitable manner of the present invention the first and second stretch of 21
5 consecutive nucleotides form a double stranded RNA molecule.

In a preferred embodiment the invention provides polynucleotides wherein the RNA-molecule is a human RNA molecule. The RNA molecule will be silenced by the polynucleotides of the present invention. The RNA molecule to
10 be silenced can be a drugable gene. Drugable genes are genes with a pharmaceutical value, ie that can be used to discover and develop small molecule drugs. New drugable genes can be found on the bases on their similarity to proteins which have proven amenable to small molecule compound development in the
15 past. Known drugable genes include but are not limited to: G-protein coupled receptors (GPCRs), ion channels, nuclear hormone receptors, kinases, phosphatases, proteases and other enzymes.

In a preferred embodiment the invention provides
20 polynucleotides wherein in the first stretch of 21 consecutive nucleotides no stretches of three or more consecutive A- nucleotides are present.

In another preferred embodiment the invention provides polynucleotides wherein in the first stretch of 21
25 consecutive nucleotides no stretches of three or more consecutive U-nucleotides are present

In a preferred embodiment the invention provides polynucleotides, wherein, in the 5' -> 3' direction, consecutive nucleotides 3-21 of the first stretch of 21
30 consecutive nucleotides are unique. These unique oligonucleotides are homologous to a stretch of 21 consecutive nucleotides that is found only once in known sequences. Sequence databases can be searched to check if

these sequences occur only once. Known databases include the EST database, the EMBL nucleotide sequence database, GenBank, and the Entrez nucleotide database, but there are many more sequence databases and all of these can be used. The
5 polynucleotide with the unique consecutive nucleotides 3-21 in the 5' -> 3' direction, of the first stretch of 21 consecutive nucleotides will silence only one specific mRNA molecule. Alternatively, the consecutive nucleotides 3-21 in the 5' -> 3' direction, of the first stretch of 21
10 consecutive nucleotides are found more than once in sequence databases. These polynucleotides can silence alternative gene transcripts of the same sequence or alternative splicing variants. In addition, the stretch of 21 consecutive nucleotides can be designed in such a way that the sequence
15 is found in more than one member of a family of proteins. The polynucleotides containing this stretch of 21 consecutive nucleotides can silence more than one member of a family of proteins.

According to another preferred embodiment of the
20 invention polynucleotides are provided wherein, in the 5' -> 3' direction, consecutive nucleotides 3-21 of the first stretch of 21 consecutive nucleotides are homologous to a sequence positioned at least 75 nucleotides downstream of the translation initiation site of the transcribed RNA molecule
25 encoding a polypeptide.

According to a preferred embodiment of the invention polynucleotides are provided wherein, in the 5' -> 3' direction, consecutive nucleotides 3-21 the first stretch of 21 consecutive nucleotides homologous are to a sequence
30 positioned at least upstream of the translation termination site of the transcribed RNA molecule encoding a polypeptide.

According to a preferred embodiment of the invention polynucleotides are provided, wherein the RNA sequence also

comprises a linker sequence linking the first stretch of 21 consecutive nucleotides with the second stretch of 21 consecutive nucleotides.

Preferably the linker sequence is 4-30 nucleotides long, more preferably 5-15 nucleotides long and most preferably 8 nucleotides long.

In a most preferred embodiment the linker sequence is UUGCUAUA (SEQ ID NO: 1).

According to a preferred embodiment the invention provides polynucleotides, wherein the first stretch of 21 consecutive nucleotides is selected from a group consisting of SEQ ID NO: 2-11888.

According to another preferred embodiment the invention provides polynucleotides, wherein the first stretch of 21 consecutive nucleotides is selected from a group consisting of SEQ ID NO: 1342, 1338, 1343, 633, 635.

Another embodiment of the invention provides vector capable of transfecting a host cell and comprising a sequence encoding the polynucleotides of the present invention and a promoter sequence operatively linked to the sequence encoding the polynucleotide.

Preferably the promoter is a microRNA promoter, more preferably a let-7 promoter.

More preferably the promoter is a promoter recognized by RNA Polymerase III, more preferably U6 small nuclear RNA. A person skilled in the art can use other promoters recognized by Polymerase III for the vectors of the present invention such as, H1, tRNA, snRNA, VA RNA, 5S rRNA.

According to a preferred embodiment of the invention vectors are provided, wherein the vector is an adenoviral vector, preferably the adenoviral vector is replication defective. The replication defective adenoviral vectors are E1-deleted, and/or E1 and E2A deleted. The adenoviral vectors

include the E1-deleted adenoviral serotype 5 vectors. Vectors may also be prepared from other adenoviral serotypes and corresponding packaging cells that include sequences for viral proteins deleted from such vector backbones. A suitable approach of the present invention has an adenoviral vector/packaging cell wherein the packaging cell and vector do not include any overlapping adenoviral sequences, which overlap would provide the statistical possibility of the production of replication competent adenoviral particles.

Packaging cells useful in the production of such vectors include the 293 and 911 cells, with the most suitable cells being the PER.C6 cell line. The modified PER.C6/E2A cell line is especially suitable. It complements the E1, E2A deleted adenoviral vector constructs, with non-overlapping adenoviral E1, E2A sequences. Other viral vector systems can be used such as the retroviral vector systems. Retroviruses are integrating viruses that infect dividing cells, and their construction is known in the art. Retroviral vectors can be constructed from different types of retrovirus, such as, MoMuLV ("murine Moloney leukemia virus" MSV ("murine Moloney sarcoma virus"), HaSV ("Harvey sarcoma virus"); SNV ("spleen necrosis virus"); RSV ("Rous sarcoma virus") and Friend virus. Lentivirus vector systems such as human immunodeficiency virus (HIV) or equine lentivirus may also be used in the practice of the present invention. Another suitable viral vector system is the adeno-associated virus ("AAV"). The AAV viruses are DNA viruses of relatively small size that integrate, in a stable and site-specific manner, into the genome of the infected cells. They are able to infect a wide spectrum of cells without inducing any effects on cellular growth, morphology or differentiation, and they do not appear to be involved in human pathologies. It is also possible to introduce a DNA vector in vivo as a naked DNA

plasmid. Naked DNA vectors for gene therapy can be introduced into the desired host cells by methods known in the art, e.g., transfection, electroporation, microinjection, transduction, cell fusion, DEAE dextran, calcium phosphate precipitation, use of a gene gun, or use of a DNA vector transporter.

The invention further provides libraries of polynucleotide of the present invention.

Preferably the library of the present invention provides vectors according to the present invention. The vectors may comprise plasmids, naked RNA. Preferably, the vectors are viral vectors preferably selected from a group consisting of AAV, Lentivirus or Retrovirus. Alternatively, more than one vector thereby introducing more than one stretch of 21 consecutive nucleotides can be introduced into a single host cell.

More preferred vectors are adenoviral vectors, preferably the adenoviral vectors are replication defective. Replication deficient vectors may be multiplied in a packaging cell having complementary sequences to the sequence contained in the vector itself.

The present invention also provides means to prepare libraries of polynucleotides and vectors as described herein. These libraries may be prepared as single element, compartmentalized, or discrete elements. Alternatively, a library comprising pools of vectors may be prepared. Methods are described for making a vector comprising the synthesis a forward primer and a reverse primer.

- a. The forward primer is synthesized with the following sequence: in the 5' -> 3' direction:
 - i. the nucleotides ACC
 - ii. a DNA sequence corresponding to a sequence selected from the group consisting of SEQ ID NO: 2-11888

iii. the nucleotides TTGCTATA

iv. the antisense sequence corresponding to the DNA sequence from step a-ii

v. the nucleotides TTT

5 b. the reverse primer is synthesized with the following sequence in the 5' -> 3' direction

i. the nucleotides TAAAAA

ii. a DNA sequence corresponding to a sequence selected from the group consisting of SEQ ID NO: 2-11888

10 iii. the nucleotides TATAGCAA

iv. the antisense sequence corresponding to the DNA sequence from step b-ii

c. The primers are annealed and cloned in plasmid pKD122, thereby exchanging the ccdB sequences for the annealed primers.

15

The orientation of the sequence encoding the sequence selected from the group consisting of SEQ ID NO: 2-11888 can be reversed. The forward and reverse primers look then as follows:

20 a. forward primer with the following sequence in the 5' -> 3' direction:

i. the nucleotides ACC

ii. a DNA sequence corresponding to a sequence selected from the group consisting of SEQ ID NO: 2-11888

25 iii. the nucleotides TTGCTATA

iv. the antisense sequence corresponding to the DNA sequence from step a-ii

v. the nucleotides TTT

b. a reverse primer with the following sequence in the 5' -> 3' direction

30

i. the nucleotides TAAAAA

ii. a DNA sequence corresponding to a sequence selected from the group consisting of SEQ ID NO: 2-11888

iii. the nucleotides TATAGCAA

iv. the antisense sequence corresponding to the DNA sequence from step b-ii

The invention further provides methods of determining the function of a naturally occurring polynucleotide sequence comprising transfecting a host cell with a vector according to claims 12-15, the vector transcribing a polynucleotide sequence according to claims 1-11 and detecting a change in cellular phenotype.

According to a preferred embodiment of the present inventions methods of determining the function of a naturally occurring polynucleotide sequence in a high throughput setting are provided wherein,

- a. providing a library of vectors according to claims 16 - 19
- b. transducing a host cell with the vectors of step (a),
- c. expressing in the host cell the product(s) of the vectors of step (a),
- d. thereby altering a phenotype of the host,
- e. identifying the altered phenotype and,
- f. assigning a function to the naturally occurring polynucleotide sequence (s).

The libraries according to the invention may be used to assist in the elucidation of the functions of host cell RNA molecules including the polynucleotide of the present invention residing in each compartment of said library. In other words, determining the function of a naturally occurring polynucleotide sequence comprising transfecting a host cell with a vector according to the invention, the vector, encoding a RNA molecule including a stretch of 21 consecutive nucleotides homologous to a portion of the naturally occurring polynucleotide and detecting a change in cellular phenotype. Each vector in the library may be

introduced into one or more cells and changes in protein expression, or phenotype observed. Methods are described for infecting a host with the adenoviral vectors that express the RNA molecules including the stretch of 21 consecutive
5 nucleotides in the host, identifying an altered phenotype induced in the host by the knockdown of the expressed RNA molecules, and thereby assigning a function to the product(s) encoded by the expressed RNA molecules. The methods can be fully automated and performed in a multiwell format to allow
10 for convenient high throughput analysis of expressed RNA molecules.

The term "homologous" to a RNA molecule refers to a nucleic acid having a nucleotide sequence of which 95%, 90%, 85% or 80% of the nucleotides 3-21 of the stretch of 21
15 consecutive nucleotide are identical to a stretch of 19 consecutive nucleotides present in the RNA-molecule to be silenced. For example, with 95% homology the nucleotide sequence is identical to reference nucleotide, i.e. the RNA molecule, except that the nucleotide sequence may include up
20 to five point mutations per each 100 nucleotides of the reference nucleotide sequence. In other words, to obtain a nucleic acid having a nucleotide sequence of at least 95% homology to a reference nucleotide sequence, up to 5% of the nucleotides in the reference sequence may be deleted or
25 substituted with another nucleotide, or a number of nucleotides up to 5% of the total nucleotides in the reference sequence may be inserted into the reference sequence.

The term identical refers to two stretches of
30 nucleotides that have at each position of the stretch the same nucleotide, meaning that if one stretch has a A-nucleotide on position three, the other stretch of

nucleotides also has a A-nucleotide on position three. This is applicable for each nucleotide in both stretches.

The term polynucleotide refers to a nucleic acid sequence. A polynucleotide can be a DNA-, RNA-, peptide
5 nucleic acid sequence. It may have natural occurring nucleotides but also chemically modified nucleotides.

Brief Description of the Drawings

Figure 1 is a schematic representation of the cloning
10 strategy for vector construction showing utilization of SapI sites and an E. coli death gene.

Figure 2 is a schematic representation of the vector construction for cloning. Adenoviral vector development for 56 nt inserts. The schematic presentation of the oligos used
15 for the vector construction is also given.

Figure 3 is a schematic presentation of the knock-down vector pKD122.

Figure 4 is a graph showing the functional knock-down of GNAS. Adenoviral constructs encoding hairpin siRNA targeted
20 against GNAS give a specific knock-down of GNAS on the functional level.

Figure 5 is a graph showing the functional knock-down of SYK as measured by the released beta-hexosaminidase.

Figure 6 shows a graph demonstrating that adenoviral
25 mediated knock-down of IKK β leads to reduced levels of phosphorylated I κ B α , an I κ B kinase substrate, upon TNF α induction. Western detection of IKK β and β -tubulin in the samples derived from U2OS cells (no virus infection, lanes 1-3; infected with adenovirus Ad-IKK- β , lanes 4-6) harvested at
30 different time points after 50 ng/ml TNF α stimulation (0 minutes, lanes 1, 4, or 10 minutes, lanes 2, 5, or 30 minutes, lanes 3, 6). Detection of phosphorylated I κ B α by

Bio-Plex phosphoprotein analysis of the same samples as described. The phosphorylation state of I κ B α is given as Mean Fluorescent Intensity (M.F.I.) at the vertical axis.

Figure 7: shows a graph demonstrating the functional
5 knock-down of MMP2. The effect of adenoviral knock-down was determined by RT-PCR and at the level of protein activity. Gelatin-degrading activity of MMP2 was measured using 10% gelatin-zymogram gels. For reference, an adenoviral cDNA expression construct encoding the *MMP2* protein (Ad-MMP2) was
10 used and demonstrated the identity of the *MMP2* band. The inverted image of the zymogram is presented.

The various aspects of the present invention are further illustrated in the following non-limiting Examples.

15

Example 1: selecting target sequences:

The polynucleotides of the present invention are built from the stretches of 21 consecutive nucleotides as explained in example 2. The design for the 21 consecutive nucleotide
20 sequences that form part of the polynucleotides of the present invention is fully automated. A program has been developed that looks for candidate sequences of 21 consecutive nucleotides. These 21 nucleotide sequences are searched in a target cDNA sequence. The program searches 21
25 nucleotide sequences according to the following scheme:

1. The search for the 21 nucleotide sequences starts 75
nucleotides downstream from the startcodon of the cDNA.
If a startcodon is not known or available, the search
30 starts 75 nt downstream of the first ATG. If no ATG is present, the 21 nucleotide sequences are searched starting from the first nucleotide of the cDNA sequence.

2. The cDNA sequence is scanned from 5' to 3' direction and when a 21 nucleotide sequence is found that conforms to a NM(N¹⁸)C pattern, it is retained (N=any nucleotide, M=A,C). This procedure is stopped 21 nucleotides before the end of the cDNA sequence.
3. At this point, the 21 nucleotide sequences that are found are attributed a score of 1000.
4. Then, the candidate 21 nucleotide sequence is checked for the presence of 4 consecutive identical nucleotides. If this pattern is found, this candidate 21 nucleotide sequence is rejected and the program starts at step 2 again.
5. If the 21 nucleotide sequence is not rejected in step 4, the percentage of G and C nucleotides of the candidate 21 nucleotide sequence is determined. The percentage of G and C nucleotides should be between 30 and 70%. If it is not between 30 en 70%, the 21 nucleotide sequence is rejected and the procedure starts at step 2 again. If the percentage is between 30 and 70%, the score of the candidate 21 nucleotide sequence is decreased according to the following rule :
- $$[(G - 0.5) * 100]$$
- with G = the fraction of G and C nucleotides of the 21 nucleotide sequence . The absolute value is subtracted from the score of the 21 nucleotide sequence.
6. The candidate 21 nucleotide sequence is checked for the presence of 3 consecutive A- or T-nucleotides. If this pattern is found, the score of the 21 nucleotide sequence is decreased with 5 units.
7. The 21 nucleotide sequence is then searched against a number of public sequence databases. The blast algorithm, (the National Center for Biotechnology Information (NCBI)) is used to match the 21 nucleotide sequence against ;

- a. -a human cDNA database, consisting of the complete RefSeq collection. For every extra cDNA sequence, apart from the target cDNA sequence, that matches the 21 nucleotide sequence, the score of the 21 nucleotide sequence is decreased. The score is decreased with 10 units for the first additional matching cDNA sequence and with another 4 units for every additional matching cDNA sequence.
- b. -the mouse RefSeq database
- c. -the rat RefSeq database The score of the 21 nucleotide sequence is increased with 35 units for every matching mouse or rat cDNA sequence.
8. The 21 nucleotide sequence is then searched against the human 'Expressed Sequence Tag' (EST) database. If the 21 nucleotide sequence does not match any ESTs, its score is decreased by 10 units. If the 21 nucleotide sequence matches perfectly to an EST, the complete EST is matched against the target cDNA sequence. The program used for this pairwise sequence comparison is blast2seq, available from NCBI. From this pairwise sequence comparison, one can determine the sequence similarity of the EST and cDNA (p-value). If the p-value is e^{-100} or lower than the EST is similar to the cDNA target sequence, if the p-value is more than e^{-100} than the EST is dissimilar to the cDNA sequence. If the 21 nucleotide sequence does match ESTs, its score is decreased by 50 units for the first dissimilar EST and another 5 units for every extra dissimilar EST. The score of the 21 nucleotide sequence is increased with one unit for every EST sequence similar to the target cDNA sequence.
9. Procedure 2 until 8 is repeated until the end of the cDNA is reached or when 25 oligonucleotide sequences homologous to the target cDNA have been identified when the cDNA is

shorter than 2000 basepairs, or when the cDNA sequences is longer than 2000 basepairs, 50 nucleotide sequence are searched, and if the cDNA sequence is longer than 3000 basepairs, 60 nucleotide sequence are searched.

- 5 10. Each 21 nucleotide sequence has a score. All possible combinations of 4 of the designed 21 nucleotide sequence (so called 'sets') are made. For each set a combined score is calculated according to the following formula :

$$F(\text{oligo } 1\text{-}n) = T + ((\Delta_1 * \dots * \Delta_{n-1}) * W / S^{n-1}) \text{ with}$$

10 $T =$ sum of scores of all 21 nucleotide sequence in set
 $\Delta_n =$ difference of position on target cDNA of oligo $n+1$ and position on target cDNA of oligo n in set. Oligo 1 to n are sorted according to their position on the target cDNA sequence

15 $W =$ weighing factor to weigh importance of second term in above formula, W is set to 10000.

$S =$ scaling factor to normalize for size of cDNA (= size of open reading frame on target cDNA sequence: (position stopcodon - position startcodon)).

20 When sets are made of 5 or another number of 21 nucleotide sequence then the formula above can still be used to calculate the combined score.

11. For all computed sets and their attached function outcomes, the set with the highest function outcome is
25 kept and marked in the output report as the 'best' set. This 'best' set of four is suggested to the end-user on the generated output report (see point 12)

12. From this best set of 4 21 nucleotide sequences, obtained in step 10, the 3 highest scoring 21 nucleotide
30 sequences are used to design the oligos for the plasmid construction as described in example 2. The first and second nucleotide in the 21 nucleotide sequence are

exchanged for AC. These 21 nucleotide sequence are listed in Table 1.

13. Finally, an output report is generated. In this report, the cDNA sequence is graphically represented, together with all the designed 21 nucleotides sequence, and with the similar and dissimilar EST sequences. In a second part of the report, the designed 21 nucleotide sequences are listed with the characteristics mentioned in point 1 to 7. These include the matching human, mouse and rat transcript sequences, the number of ESTs, and the outcome of each of the pairwise comparisons to the target cDNA sequence.

The program performing the rules described above has been written in perl (practical extracting and reporting language). In our case extensive use has been made of the 'bioperl' bioinformatics toolkit (Perl, O'Reilly.com). However, a person skilled in the art can use another language to implement the rules set above in a program and use this program to design siRNA that give an effective knock-down effect.

Example 2: siRNA expression constructs:

Non viral siRNA expression constructs:

The construction of the siRNA expression constructs is depicted in figure 1. In short, oligos containing knock-down target sequences as depicted in table 1 (21 nt) are cloned in the knock-down vector, pKD122. This non-viral DNA expression plasmids can be used using DNA transfer methods known in the art, such as lipofectamine or PEI. The individual knockdown constructs for each gene can be pooled or can be used separately.

adenoviral siRNA expression constructs

The siRNA expression construct can also so be contained in viruses. The viruses can be made in an arrayed format, if

preferred. The arrayed viruses mediate expression of the siRNA constructs; each well contains a unique recombinant virus carrying a siRNA expression construct targeted against a gene, i.e. one target gene per well. Further details about
5 the concept of arrayed adenoviral vectors can be found in WO 9964582, US 6,340,595 and 6,413,776 (Arrayed adenoviral libraries for performing functional genomics).

In addition to the knock-down vector, pKD122 two other materials are needed for the generation of recombinant
10 adenovirus particles: a helper cosmid and a packaging cell line (see also WO9964582. US 6,340,595). The cosmid (pWE/Ad.AflIII-rITRAE2A) contains the main part of the adenovirus serotype 5 genome (bp 3534-35953) from which the E2A gene is deleted. The Per.C6/E2A packaging cell line
15 (Crucell NV) is derived from human embryonic retina cells (HER) transfected with plasmids mediating the expression of the E1 and E2A genes. The adenoviral genes that are integrated into the genome of the PER.C6/E2A cell line share no homology with the adenoviral sequences on the knock-down
20 plasmid and the cosmid. Consequently, vector stocks that are free of replication competent adenoviruses (RCAs) are prepared.

To obtain viruses, the knockdown plasmid is co-transfected with the helper cosmid into a packaging cell line
25 PER.C6/E2A. Once these plasmids are transfected into the PER.C6/E2A cell line, the complete Ad5 genome is reconstituted by homologous recombination. The helper and knock-down plasmids contain homologous sequences (bp 3535-6093), which are a substrate for this recombination event.

30 Design of oligos:

Oligonucleotides are designed to be targeted against specific mRNAs. The selected target sequences are listed in

Table 1 and are used for the construction of knock-down adenoviral expression clones. Specific pairs of forward (F) and reverse (R) oligonucleotides are annealed together forming a duplexed structure that is used for cloning into the knock-down vector (see figure 2). The 56 nt oligos containing knock-down target sequences have the following structure :

the Forward oligonucleotide:

5'-ACC- N21*- TTGCTATA -N21--TTT-3'

Reverse oligonucleotide:

3'-N21-AACGATA- N21* -AAAAAT-5'

N21 are DNA sequences corresponding to the sequences as depicted in Table 1, N21* is the antisense sequence of this sequence.

The single stranded oligonucleotide components are synthesized and annealed in 96 or 384 well plates to generate the double stranded oligonucleotides at a final concentration of 50 pmol/ μ l, 100 μ l total volume per well (Sigma).

2 μ l annealing buffer (NEBuffer 2, 10x concentrated, Biolabs) to a 96 well PCR plate was added to 18 μ l oligos, the plates are spun down briefly and subsequently sealed. The plates are incubated in the PCR machine for 5' at 95°C and slowly cooled. The annealed oligos are diluted 1000x.

Design of pKD122

The knock-down expression vector, pKD122 (figure 3) is based on the pIPspAdapt6 (WO 9964582). The pIPspAdApt6 plasmids contain the 5' part (bp 1-454 and bp 3511-6093 of the adenovirus serotype 5 genome in which the E1 gene is deleted and a promoter is introduced. In contrast, to the plasmid pIPspAdApt6, the siRNA expression vectors of pIPspAdapt lack the CMV promoter and the SV40 polyadenylation site and the larger part of the polylinker, pKD122 further

contains U6 promoter, Sap I recognition sites and the *E. coli* lethal gene, *ccdB*.

Sap I cuts adjacent to its recognition sites (GCTCTTC(N)_{1/4}) creating a 3' overhang (see figure 2). This
5 has the advantage that it cuts any sequence containing the recognition sequence but the recognition sequence will not be present in the final construct since as it will be present on the excised fragment. For these reasons SapI is used for the construction of expression plasmids. The *ccdB*, is included in
10 the fragment to be excised. When the restriction fragment is not correctly excised and the *ccdB* gene remains in the plasmid, after transfection no *E. coli* colonies are formed. Only *E. coli* containing correct expression plasmids with the two unique SapI overhangs and without the *ccdB* gene will form
15 colonies.

pIPspAdapt6 was grown in the methylase negative *E. coli* strain DM1 to prevent methylation of the second Xba-site. The DNA was isolated and digested with Xba I, thereby excising a 142 bp fragment containing the poly A signal. The
20 religated vector is called pIPspAdapt6-deltaPolyA. The polylinker was removed from pIPspAdapt6-deltaPolyA by digestion with EcoRI and BamHI, blunted with Klenow, religated and digested with AscI to reduce background. This religated vector is called pIPspAdapt6-deltaPolyA delta-
25 polylinker.

pIPspAdapt6-deltaPolyA-delta polylinker was digested with AvrII and HindIII to remove the CMV promoter and purified on a 1% agarose TAE gel and isolated using the Qiaquick gel extraction kit (Qiagen).

30 The *ccdB* gene is cut from pIPspAdapt10ZeoDestA (WO9964582) with BamHI and Sal I. The 676 bp *ccdB* fragment is purified on a 0.8% agarose TAE gel and isolated using the Qiaquick gel extraction kit (Qiagen).

The genomic human U6 gene (Accession number M14486 (GenBank, NCBI)) is cloned by a PCR based strategy using human genomic DNA. The region to be cloned starts at nucleotide -265 upstream of the transcription start site
5 until nucleotide +198 downstream of the transcription start site. The primers used are:

5'-GcacgTTCTAGAAGGTCGGGCAGGAAGAGGGCCT-3' (SEQ ID NO: 11889)

10 5'-ccgtgcAAGCTTTGGTAAACCGTGCACCGGCGTA-3' (SEQ ID NO: 11890)

The PCR product is cloned into the Xba I and Hind III sites of pIPspAdapt6-deltaPolyA, the resulting vector is hU6(+1)pIPspAdapt6-dpA.

Two U6 Sap I PCR fragments (a left, L, and a right R) containing the U6 promoter sequences together with the SapI recognition sequences are made with the following primers:

5'-CGACCATGCGCGGATCCGCTCTTCTGGTGTTCGTCCTT-3' (SEQ ID NO: 11891)

20 5'-CGGATCCGCGCATGGTCGACGCTCTTCATTACATCAGGTTGTTT-3' (SEQ ID NO: 11892).

(SEQ ID NO: 11891) with (SEQ ID NO: 11889) gives the L fragment and (SEQ ID NO: 11892) with (SEQ ID NO: 11890) gives the R fragment with the hU6(+1) pIPspAdapt6-dpA delta polylinker as template.

25 The PCR fragments are purified on a 1% agarose TAE gel and isolated using the Qiaquick gel extraction kit (Qiagen).

The R-fragment is digested with XbaI and BamHI, and the L-fragment is digested with SalI and HindIII. pIPspAdapt6-deltaPolyA-delta polylinker was digested with AvrII and
30 HindIII. The digested R- and L-fragments together with the digested pIPspAdapt6-deltaPolyA delta polylinker and the ccdB fragment are ligated with T4 in ligase buffer (about 30 ng of

each fragment in the ligation) and transformed in DB3.1 cells (wherein the ccdB is not toxic, Invitrogen)

A colony PCR is performed to check sequences with primers SEQ ID NO: 11889 and 11890 this should generate a 1000 bp fragment. Positive clones are digested with HincII and BglII, the correct clones give fragments of 3800, 1400, 538, 402 and 134 bp in size. Clones that give these fragments are sequenced. The resulting vector is pKD122 (figure 3)

Cloning of the oligos

The knockdown vector pKD122 (figure 3) is digested by Sap I and gel purified. Digestion mix: 30 µl Neb 4, 10 µl Sap I in 300 µl total volume for 9 µg of knock-down vector, and incubated at 37 °C over night. Gel: 1 % agarose in 1x TAE, 2 µl 10x loading buffer to 5 µl of digestion mix; the digested vector is isolated from gel with QIAquick gel extraction kit (Qiagen).

Ligation of the annealed oligos in the knock-down vector: 0.5 µl digested knock-down vector (40 ng/µl), 1 µl T4 DNA ligase buffer (10x concentrated, Biolabs) 0.5 µl T4 DNA ligase (Biolabs) and 7 µl milliQ are added per well. Added to this is 1 µl of the diluted annealed oligos. The plates are incubated over night at RT.

Transformation:

5 µl of each ligation mix is put into a new PCR plate and put on ice 25 µl competent DH5α-cells (Subcloning efficiency, Invitrogen) is added and incubated on ice for 30 minutes. The bacteria are heat shocked for 40 seconds at 37°C and put on ice for 2 minutes. 170 µl RT SOC-medium (Invitrogen) is added to each well. The bacteria are recovered by shaking for 1 hour at 37°C and 100-150 rpm. Cells are spun down at 1700 g for 1 min. 100 µl supernatant is taken and the bacteria are resuspended in the remainder of

the supernatant (100 µl). 50 µl of the cell suspension (50%) is plated out in 1 well of a 6-wells plate (filled with 3 ml LB agar+100 µg/ml ampicillin /well). The plates are incubated overnight at 37°C.

5 **Colony picking:**

3 colonies of each construct are picked and inoculated as agar-stab (LB agar with 100 µg/ml ampicillin) and liquid culture (LB medium with 100 µg/ml ampicillin). The clones in the agar-stab are sequenced. Clones with the correct sequence
10 are transfered to a new 96 well plate. The knock-down vector with the annealed oligos is digested with PI-PspI.

PI-PspI digestion mix (1x) contains 0.5 µg annealed knock-down vector 2.5 µl PI-PspI enzyme, (1U/µl, Biolabs), 2.5 µl PI-PspI NEBuffer, (10x concentrated Biolabs), 0.25 µl
15 BSA (100x concentrated Biolabs) in a total volume of 25 µl (end concentration = ± 20 ng/µl). The mixture is incubated over night at 65°C in a humified box. The digestion is checked on gel: 10 µl PI-PspI digestion mix, added to this is 2 µl loading buffer (10x concentrated), and put on gel (1%
20 agarose in 1x TAE buffer + etidium bromide).

Transfection

Co-transfect each clone to PER.C6/E2A cells together with the cosmid pWE/Ad.AflIII-rITRAE2A (WO9964582. US 6,340,595. Score CPE 14 days after transfection. After the
25 final scoring store the plates at -80°C until further propagation of the viruses.

Virus propagation

The final virus propagation step is aimed at obtaining a higher percentage of wells showing CPE and more homogenous
30 virus titers. Viruses are propagated according to the following procedure. The transfection plates stored at -80°C

are thawed at room temperature for about 1 hour. By means of a 96 channel Hydra dispenser (Robbins), 20 μ l of the supernatant is transferred onto PER.C6/E2A cells seeded in 96 well plates at a density of 2.25×10^4 cells/well in 180 μ l of DMEM + 10% FBS. Cells are incubated at 34°C, 10% CO₂ for approximately 10 days and the number of wells showing CPE is scored. In general, the number of wells showing CPE is increased after propagation. The plates are then stored at -80°C.

10 In addition, modifications to the viral coat proteins can be introduced to obtain a different or improved tropism (EP 1191105).

The individual knockdown adenoviruses can be used as arrays but also can be pooled to various degrees i.e. sets of 15 pools or one large pool.

Example 3: Knock-down effects with the selected knock-down target sequences:

Knock-down of GNAS:

20 GNAS encodes the G α subunit of G_s, a heterotrimeric G-protein (α , β , γ). G proteins interact with 7 transmembrane receptors, the so-called G-protein coupled receptor (GPCR). Binding of a ligand to the GPCR induces a conformational change of the receptor that results in activation of the G-protein. The activated G protein will dissociate into its α subunit and the $\beta\gamma$ subunit. In the case of G α_s the α subunit will interact with adenylate cyclase and in turn activate this enzyme. - Adenylate cyclase converts ATP into cAMP. Activation of GPCRs that are coupled to G_s will therefore 25 upon activation elevate the cellular cAMP levels. Variation in cAMP levels in the cell can be measured by cAMP responsive elements (CRE). cAMP responsive element activates 30

transcription when bound by activated cAMP responsive element binding protein (CREBP). CREBP is activated by Protein Kinase A (PKA) that in turn is activated by cAMP. When the CRE is coupled to a luciferase gene, variations in cAMP levels in a cell can be visualized. An increase in cellular cAMP will result in an increase in the amount of luciferase and a decrease of cAMP results in a decrease of luciferase content.

The following assay is designed to measure the knock-down of GNAS at a functional level.

U2OS cells are infected with an adenoviral construct encoding a GPCR ($\beta 2$ adrenergic receptor) that couples to G_s (MOI 500) together with an adenoviral reporter construct carrying CRE elements upstream of a luciferase gene (MOI 750). The infected cells are co-infected with either an adenoviral construct encoding a RNA molecule (SEQ ID NO:1342) targeted against GNAS or an empty virus (MOI 1500).

Two days post infection, the $\beta 2$ adrenergic receptor is activated with isoproterenol, which is an agonist for the $\beta 2$ adrenergic receptor. Six hours later the luciferase activity is measured. After activation of the receptor, successful knock-down of GNAS results in a much lower cAMP levels compared with cAMP levels observed in the control cells transfected with empty virus. To ensure that the decreased cAMP levels are due to the knock-down of GNAS and not due to a non-specific effect on cAMP levels, forskolin is added to the triply infected cells. Forskolin increases intracellular cAMP levels by direct activation of adenylate cyclase and therefore is independent of G-protein (GNAS).

Figure 4 shows the results of the functional knock-down measurements of GNAS. The luciferase activity in cells infected with the adenoviral GNAS knock-down construct are much lower than the luciferase levels of the cells that are

not infected with the GNAS knock-down construct. The forskolin results show that the cAMP reduction is due to the knock-down of GNAS rather than a general down-stream effect on the signal transduction route leading to the activation of CREBP.

Knock-down of SYK

Syk (NM_003177) is a tyrosine kinase that is essential for mast cell degranulation mediated by IgE. In a paper by Moriya et al (1997), it is shown that a specific inhibitor abolished IgE-mediated mast cell degranulation. If a knock-down construct against Syk is successful then mast cells are unable to degranulate.

Mast cell degranulation can be determined by measuring the release of β -hexosaminidase. Total hexosaminidase is measured from the hydrolysis of the synthetic substrate 4-methylumbelliferyl N-acetyl- β -D-glucosaminide by hexosaminidase, which releases fluorescent 4-methylumbelliferone.

Experimental:

Culture of human Mast cells (hMC's)

Human mast cells are derived from cord blood mononuclear cells (#2C-150A; 10^8 cells/vial, Cambrex). Cells are cultured in RPMI 1640 (#52400-025, Gibco BRL) supplemented with 10% FBSHI (Gibco BRL), 1% MEM non essential amino acids (#11140-35, Gibco BRL), 1% L-Glutamin (200mM, 100x) (#25030-024, Gibco BRL), 1% Pen/Strep (10000U:µg/ml) (#15140-122, Gibco BRL), 0.1% Gentamicin (10mg/ml) (#15710-049, Gibco BRL) and 0.1% 2-Mercaptoethanol (#31350-010, Gibco BRL) in the presence of 100 ng/ml SCF (#300-07, Peprotech), 50 ng/ml hIL-6 (#200-06, Peprotech) and 10 ng/ml hIL-10 (#200-10, Peprotech). The cell suspensions are seeded at a density of 10^6 cells/ml and the entire volume of cytokine supplemented medium is replaced on a weekly basis. The adherent fraction

of cells is discarded weekly by the transfer of the non-adherent cells to fresh culture flasks. Cells are cultured for 9-11 weeks before use as described by Ochi et al (1999)

Two weeks prior to the experiment cells are cultured
5 with addition of 10 ng/ml hIL-4 and 5 µg/ml human myeloma IgE (Biodesign) to enhance FcγRI expression as described by Ochi et al (2000). Cells are checked by toluidine blue staining and Flow cytometric analysis. Toluidine blue staining is performed on a weekly basis starting 6th week of culture.
10 Cells are stained for C-kit and FcεRI expression and analyzed by FACS.

Degranulation assay

Cells are seeded at a density of 1E+05 cells/well in a 96 well V-bottom plate (Greiner) and transduced with an
15 Adenovirus at a MOI of 1000. Three days past infection the culture medium containing virus is removed from the cells and replaced by 200 µl of 1500 ng/ml anti-IgE (#501, DAKO) in culture medium. After one-hour of stimulation, at 37°C, 100 µl supernatant is transferred to a (black) flat-bottom 96
20 well plate (Greiner). The remaining supernatant is discarded and the cells are lysed (to determine β-hexosaminidase present in cells) using 200 µl 0.2% Triton X-100 (#B32844, Calbiochem) in culture medium. After cell lysis 100 µl supernatant is transferred to a (black) flat-bottom 96 well
25 plate. For fluorimetric (Excitation at 360nm/Emission at 450nm) determination, 50 µl of 4mM 4-methylumbelliferyl N-acetyl-β-D-glucosaminide (4-MUG) (Sigma) is added to the supernatant on both plates. The plates are incubated for 1 hour at 37°C after which 100 µl of 0.4 M glycine buffer (pH
30 10.7) is added to stop the reaction. The hydrolysis of 4-MUG is measured with excitation at 360nm and emission measured at: 450nm. The degranulation is represented as the percentage of

β -hexosaminidase released from the total amount of β hexosaminidase present in the cells before stimulation.

Experimental setup

SyKT402 a dominant negative form of Syk, which is a key
5 player in the degranulation pathway, as shown by Moriya et al
(1997). SyKT402 is a truncated form of WT Syk at amino acid
402. Cells with the SyKT402 mutant are unable to degranulate.

In this experiment, cells are transduced, at a MOI of
1000.

10 Cells are transduced either with the SyKT402 mutant, a
Syk knock-down virus construct (SEQ ID NO: 1338 and see
example 2) or empty virus as a negative control. Knock-down
virus directed against GL2 is taken along to check for
specific knock-down. Three days past transduction, cells are
15 stimulated with 1500 ng/ml anti-IgE as described in
'degranulation assay'. Without stimulation the mast cells
have already a β -hexosaminidase release of ~7%, this
background is subtracted from all values measured. When
comparing anti-IgE only (no viral infection) to empty (virus)
20 one can see that viral infection has little to no effect on
degranulation.

Results:

The results are summarized in figure 5. As expected, the
truncated form of Syk (SyKT402) shows a low level of β -
25 hexosaminidase release (about 20% of normal levels). The
control virus for knockdown, GL2, shows a comparable β -
hexosaminidase release level as the empty virus,
demonstrating that there is no non-specific knock-down
effect. The knockdown virus g-SYK (63) displays a level of β -
30 hexosaminidase release similar to the dominant negative
mutant of Syk (SyKT402), demonstrating the effectiveness of
our knock-down constructs.

Knock-down of IKK- β

The functional effect of an adenoviral knock-down was studied using the well-known NF κ B pathway by measuring the phosphorylation of I κ B α , one of the inhibitory proteins which normally associate with and hold NF- κ B inactive in the cytoplasm. Activation of the IKK kinase complex by TNF α stimulation results in phosphorylation of I κ B β , followed by its ubiquitination and degradation by the 26S proteasome. Phosphorylation and degradation of I κ B α releases NF- κ B, allowing it to translocate into the nucleus to activate target genes.

In the following experiment, U2OS cells were infected with IKK β knock-down virus (SEQ ID NO:1343), GL2 control knock-down virus, or the cells were not infected at all. Figure 6 clearly shows that the adenoviral siRNA expression gives a specific reduction of the IKK β protein, but leaves β -tubulin unaffected (6 days post infection). At 6 days post-infection, the cells were stimulated with 50 ng/ml TNF α for 0 minute, 10 minutes, or 30 minutes. The phosphorylation state of I κ B α was determined by Bio-Plex phosphoprotein analysis using phospho-specific I κ B α antibodies. U2OS cells stimulated with TNF α show strong induction of phosphorylated I κ B α peaking around 10 minutes and fading by 30 minutes. The peak level of induction of phosphorylated I κ B α was reduced in cells that were infected with adenoviral knock-down constructs directed against IKK β . Altogether these data demonstrate that our adenoviral knock-down system results in specific reduction of the target at the levels of mRNA, protein, and function of the protein.

30 Phosphoprotein assay for I κ B α

The phosphorylation state of I κ B α was determined by using the Bio-Plex phospho-I κ B α kit (Bio-Rad), an assay that

is similar to a capture sandwich ELISA but utilizes antibodies covalently coupled to dyed polystyrene beads. U2OS cells were infected with adenoviral knock-downs as indicated. Six days post infection, cell lysates were
5 prepared after either treatment with 50 ng/mL of TNF α (Sigma) for 10 or 30 minutes, or non-treated (0 minute). The Bio-Plex phospho-I κ B α assays were performed according to the manufacturer's instruction. Briefly, equal amount of cellular proteins were incubated overnight with the dyed beads
10 conjugated with the I κ B α capture antibodies. After a series of washes to remove unbound protein, a biotinylated detection antibody specific for Phospho-I κ B α (Ser32) was added to the reaction. Streptavidin-phycoerythrin (PE) was added to detect the formation of a sandwich of antibodies around the
15 phosphoraylated I κ B α . The Luminex IS100 system was used to read each individual bead in the reaction mixture (Luminex, Austin).

Knock-down of MMP2

In another experiment, the constitutively expressed
20 matrix metalloproteinase *MMP2* (gelatinase A) was targeted for knock-down with 2 different adenoviral constructs (Ad-siRNA-MMP2-1 (SEQ ID NO: 633 or Ad-siRNA-MMP2-3 SEQ ID NO: 635) in primary human synoviocytes. Supernatants of primary synoviocytes were analysed 6 days after infection at MOI 7500
25 with Ad-siRNA-MMP2-1 and Ad-siRNA-MMP2-3, and compared to Ad-siRNA-control, a virus containing a target sequence against *M6PR*. Both constructs resulted in very efficient reduction (>95% knock-down) of *MMP2* mRNA determined by real time PCR analysis (figure 7), as well as the *MMP2* protein activity as
30 determined by its gelatin-degrading activity using zymogram gels (figure 7). Adenoviral overexpression of the *MMP2* protein (Ad-MMP2) demonstrates the identity of the band

visualised in this assay. Altogether, this clearly shows that adenoviral vectors can efficiently introduce and express siRNAs to levels that result in a specific functional knock-down of the targeted transcript and the encoded protein in
5 primary human cells.

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Table 1: Knock-down target sequences, 21 consecutive nucleotides. The target gene is given in column 1 and 2. Accession numbers starting with SK: are from the kinase database (Manning et al, 2002), ENS from ENSEMBL database and other from GenBank.

ACCESSION	Gene	SEQ ID NO:	KD construct sequence
NM_003961	RHBDL	2	ACATGTTTCATGCACGTTGGGC
Y17108	HSY17108	2	ACATGTTTCATGCACGTTGGGC
NM_003961	RHBDL	3	ACAAGTTGCTGAGGATGGTGC
Y17108	HSY17108	3	ACAAGTTGCTGAGGATGGTGC
AK000442	AK000442	4	ACTCAGATATCTTGTGGGAGC
NM_017821	FLJ20435	4	ACTCAGATATCTTGTGGGAGC
NM_003293	TPS1	5	ACCTCTACTACCAGGACCAGC
NM_003294	TPSB1	5	ACCTCTACTACCAGGACCAGC
NM_012217	TPSD1	5	ACCTCTACTACCAGGACCAGC
NM_024164	TPSB2	5	ACCTCTACTACCAGGACCAGC
NM_003293	TPS1	6	ACCCACAGTTCTACATCATCC
NM_012217	TPSD1	6	ACCCACAGTTCTACATCATCC
NM_000076	CDKN1C	7	ACCGCTGGGATTACGACTTCC
NM_000076	CDKN1C	8	ACTGGTCCCAAAGTGTAAGC
NM_000476	AK1	9	ACACTGCTGCTGTATGTGGAC
NM_000858	GUK1	10	ACATCAAGGCCACCGATCTGC
NM_000858	GUK1	11	ACATGGAGAGCAGCAAGGAGC
NM_001320	CSNK2B	12	ACTGGTTTCCCTCACATGCTC
NM_001625	AK2	13	ACCACGAGGAGTTCAACCCTC
NM_013411	AK2	13	ACCACGAGGAGTTCAACCCTC
XM_086211	LOC148505	13	ACCACGAGGAGTTCAACCCTC
NM_001744	CAMK4	14	ACATCCATTGTGTACAGATGC
SK061	CaMK4	14	ACATCCATTGTGTACAGATGC
NM_001744	CAMK4	15	ACATCAAGTGCTCATGAAGAC
SK061	CaMK4	15	ACATCAAGTGCTCATGAAGAC
NM_001827	CKS2	16	ACATGATTCATGAGCCAGAAC
XM_095990	LOC169874	16	ACATGATTCATGAGCCAGAAC
NM_001892	CSNK1A1	17	ACTTAAACTATTGTCTGTTGGC
SK082	CK1a	17	ACTTAAACTATTGTCTGTTGGC
XM_046996	CSNK1A1	17	ACTTAAACTATTGTCTGTTGGC
NM_005793	NM23-H6	18	ACTTCTCCTAGACATCTAGTC
NM_012474	UMPK	19	ACAGCTAGCGGCAAGTCTTCC
AF091486	AF091486	20	ACAGCATCTCAGAGGAGGGAC
AF145710	AF145710	20	ACAGCATCTCAGAGGAGGGAC
NM_015981	CAMK2A	20	ACAGCATCTCAGAGGAGGGAC
SK057	CaMK2a	20	ACAGCATCTCAGAGGAGGGAC
XM_042551	CAMK2A	20	ACAGCATCTCAGAGGAGGGAC
AF091486	AF091486	21	ACCATTAACCCATCCAAACGC
AF145710	AF145710	21	ACCATTAACCCATCCAAACGC
NM_015981	CAMK2A	21	ACCATTAACCCATCCAAACGC
SK057	CaMK2a	21	ACCATTAACCCATCCAAACGC
XM_042551	CAMK2A	21	ACCATTAACCCATCCAAACGC

NM_020126	SPHK2	22	ACGCTTTGCCCTCACCCTTAC
NM_020126	SPHK2	23	ACTTCTGCATCTACACCTACC
NM_030662	MAP2K2	24	ACTTCGAAAGGATCTCAGAGC
SK218	MAP2K2	24	ACTTCGAAAGGATCTCAGAGC
NM_002963	S100A7	25	ACAGACTACCACAAGCAGAGC
NM_012467	TPSG1	28	ACTCATCCGACTACCAGGTGC
NM_012467	TPSG1	29	ACCCATCTGCGGATGGTACTC
NM_145699	APOBEC3A	30	ACCTGTGCTACGAAGTGGAGC
NM_145699	APOBEC3A	31	ACTAGATGAGCACAGCCAAGC
NM_003955	SOCS3	32	ACCTTTCTGATCCGCGACAGC
NM_003955	SOCS3	33	ACCCAGTCTGGGACCAAGAAC
NM_003955	SOCS3	34	ACGTGGCCACTCTTCAGCATC
NM_003955	SOCS3	35	ACTCCTATGAGAAAGTCACCC
NM_002009	FGF7	36	ACACAGTGGTACCTGAGGATC
NM_002009	FGF7	37	ACACTAAGTCTAGCACACAGC
NM_002009	FGF7	38	ACTAGAAAGAACTGCCCTTCC
NM_004465	FGF10	39	ACCAACTCTTCTTCTCCTCC
NM_001565	SCYB10	40	ACCGTACGCTGTACCTGCATC
NM_001565	SCYB10	41	ACATGGAGTATATGTCAAGCC
NM_001565	SCYB10	42	ACTTCATGGACTTCCACTGCC
NM_000584	IL8	43	ACATACTCCAAACCTTTCCAC
NM_000584	IL8	44	ACTTCATGTATTGTGTGGGTC
NM_001323	CST6	45	ACATCATCAAGGCGCAGAGCC
NM_001323	CST6	46	ACTTTGAGGTCCTTGTGGTTC
NM_001323	CST6	47	ACTCCTCTCAGCTCCTAAAGC
NM_000396	CTSK	48	ACAAGGTGGATGAAATCTCTC
NM_000396	CTSK	49	ACAGGCAAGGCAGCTAAATGC
NM_000396	CTSK	49	ACAGGCAAGGCAGCTAAATGC
NM_000396	CTSK	50	ACTGTGGCCATCAGGACTTTC
NM_000594	TNF	51	ACCTCTCTCTAATCAGCCCTC
NM_000594	TNF	52	ACCTCATCTACTCCCAGGTCC
NM_000594	TNF	53	ACCAGACCAAGGTCAACCTCC
NM_005409	SCYB11	54	ACGCTGTCTTTGCATAGGCCC
NM_005409	SCYB11	55	ACAATCAGAATTCCACTGCCC
NM_005409	SCYB11	56	ACCTTAAGAAAGGCTGGTTAC
NM_006664	SCYA27	57	ACTGCCTGCTGTACTCAGCTC
NM_006664	SCYA27	58	ACCTCCAGGCTTTCGTGCTTC
NM_015926	ZSIG11	59	ACTGTGGCCTACAAGTTCAC
NM_015926	ZSIG11	60	ACCAGATCCATTTTCATGTGCC
NM_005978	S100A2	61	ACTGTCATGTGCAATGACTTC
NM_003745	SSI-1	62	ACACGCACTTCCGCACATTCC
NM_003745	SSI-1	63	ACGCAGCATTAAGTGGGATGC
NM_003745	SSI-1	64	ACTGTATCTGGAGCCAGGACC
NM_003745	SSI-1	65	ACCTGAACTCGCACCTCCTAC
NM_004591	SCYA20	66	ACACAGACCGTATTCTTCATC
NM_004591	SCYA20	67	ACATCATGGAGGGTTTAGTGC

NM_004591	SCYA20	68	ACTTTCTTGCAAGCAACAAGC
NM_005547	IVL	69	ACCTGAAGCACCTAGAGCAGC
NM_005547	IVL	70	ACCTGGATCAGCAGGAGAAGC
NM_024628	SLC12A8	71	ACCTGCTCTTAGAGAAAGCTC
NM_024628	SLC12A8	72	ACCAAGGACATGGATCAGCTC
NM_024628	SLC12A8	73	ACCCAGGAGAATGCAGACTTC
NM_024628	SLC12A8	74	ACTAGATGCAGTGTGGGACC
AB083587	AB083587	75	ACATGCCTGGCTGTGTACTAC
AB083589	AB083589	76	ACACCTCCATTCTGTGCGTTC
XM_115681	LOC200379	76	ACACCTCCATTCTGTGCGTTC
AB083589	AB083589	77	ACAGTGAGGTACTCATGATGC
XM_115681	LOC200379	77	ACAGTGAGGTACTCATGATGC
AB083593	AB083593	78	ACTGTCCTCAACGTCTATGCC
XM_060898	LOC128227	78	ACTGTCCTCAACGTCTATGCC
AB083601	AB083601	79	ACATTGCCAGGGCTGTGGAAC
AB083601	AB083601	80	ACACTGTTGTCCCTCCTCTCC
AB083605	AB083605	81	ACTGCTACTCTTCACTCAGGC
ENSG00000175180	ENSG00000175180	81	ACTGCTACTCTTCACTCAGGC
AB083605	AB083605	82	ACCTTAGGCTTCATCCTCTTC
ENSG00000175180	ENSG00000175180	82	ACCTTAGGCTTCATCCTCTTC
AB083607	AB083607	83	ACCTGCCTCTTGAGTGTCTTC
AB083609	AB083609	83	ACCTGCCTCTTGAGTGTCTTC
AB083607	AB083607	84	ACTGCTGCACTAATCATTGCC
XM_064908	LOC126022	84	ACTGCTGCACTAATCATTGCC
AB083608	AB083608	85	ACCTGTCTCTCATCCACATAC
AB083610	AB083610	86	ACAGCTGTGTATGTGATACAC
ENSG00000174930	ENSG00000174930	86	ACAGCTGTGTATGTGATACAC
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ENSG00000174930	ENSG00000174930	87	ACTCAACTTACATCCATGCAC
AB083614	AB083614	88	ACAAGCGGCATGCTCATCAGC
AB083614	AB083614	89	ACCGCTAAACGAGACAGACAC
AB083617	AB083617	90	ACTGTCATCGATGACAGATCC
XM_167214	LOC222611	90	ACTGTCATCGATGACAGATCC
AB083620	AB083620	91	ACGTCTACTCTGGCTACCTGC
ENSG00000175514	ENSG00000175514	91	ACGTCTACTCTGGCTACCTGC
AB083620	AB083620	92	ACTCCGACTACCTGATCCTAC
ENSG00000175514	ENSG00000175514	92	ACTCCGACTACCTGATCCTAC
AB083620	AB083620	93	ACAGCTCAGCCACAGCTGAAC
ENSG00000175514	ENSG00000175514	93	ACAGCTCAGCCACAGCTGAAC
AF380189	TA3	94	ACTTCAAACAACATGCACACAC
AF380189	TA3	95	ACAGTGAGGTCTGTGGAGAGC
NM_000025	ADRB3	96	ACCTTCCTCTTCTCGTGATGC
XM_165515	LOC220846	96	ACCTTCCTCTTCTCGTGATGC
NM_000025	ADRB3	97	ACTCTCTGCTGGTTGCCCTTC
NM_000054	AVPR2	98	ACCTATGTACCTGGATTGCC
NM_000054	AVPR2	99	ACGCTAGTGATTGTGGTTCGTC

NM_000115	EDNRB	100	ACCTTATGGCCCAAGGGTTCC
NM_003991	EDNRB	100	ACCTTATGGCCCAAGGGTTCC
NM_000115	EDNRB	101	ACCCATCGAGATCAAGGAGAC
NM_003991	EDNRB	101	ACCCATCGAGATCAAGGAGAC
NM_000273	OA1	102	ACTATGTCACCATGTACCTGC
NM_000529	MC2R	103	ACCGCTACATCACCATCTTCC
NM_000634	IL8RA	104	ACTCTTTGCCCTGACCTTGCC
NM_001557	IL8RB	104	ACTCTTTGCCCTGACCTTGCC
NM_000648	CCR2	105	ACTTCAACAAACACGCCTTCC
NM_000677	ADORA3	106	ACATGGTATACTTCAGCTTCC
NM_000678	ADRA1D	107	ACCATGGAGGTTCTGGGCTTC
NM_000678	ADRA1D	108	ACTTCAACAGCTGCGTGAACC
NM_000682	ADRA2B	109	ACTGAACCCTGTTATCTACAC
NM_000682	ADRA2B	110	ACCATCTTCAACCAGGACTTC
NM_000707	AVPR1B	111	ACATGGGCTTCAACAGCCACC
NM_000752	LTB4R	112	ACTGCCCTGATGGTGCTGAAC
NM_000752	LTB4R	113	ACGAACATGAGCCTGTGCTTC
NM_000797	DRD4	114	ACGCCCACCAACTCCTTCATC
NM_000797	DRD4	115	ACCAACTCCTTCATCGTGAGC
NM_000797	DRD4	116	ACTGTCTTCAACGCCGAGTTC
NM_000865	HTR1E	117	ACGTCAGCAGATCTCTAGCAC
NM_000871	HTR6	118	ACTGTAACAGCACCATGAACC
NM_000913	OPRL1	119	ACGTCAACAGCTGCCTCAACC
NM_005161	AGTRL1	119	ACGTCAACAGCTGCCTCAACC
NM_000916	OXTR	120	ACCTCTTCCACGAACCTCGTGC
NM_000955	PTGER1	121	ACCCTTGGGTGTACATCCTAC
NM_000956	PTGER2	122	ACGATGCTCATGCTCTTCGCC
NM_000956	PTGER2	123	ACCCTTGGGTCTTTGCCATCC
NM_000957	PTGER3	124	ACGTGGTGCTTCATCAGCACC
NM_000960	PTGIR	125	ACGTGCTCCAAAGCAGAAGCC
NM_000960	PTGIR	126	ACAGTCAGGTCTGCTCTGGTC
NM_001051	SSTR3	127	ACATCGTCAACGTGGTGTGCC
NM_001052	SSTR4	128	ACACTTTCTGCTGGGCTTCC
NM_001053	SSTR5	129	ACAACTTCCGCCAGAGCTTCC
NM_001058	TACR1	130	ACCACATCTGTGTGACTGTGC
NM_015727	TACR1	130	ACCACATCTGTGTGACTGTGC
NM_001058	TACR1	131	ACATCAACCCAGATCTCTACC
NM_015727	TACR1	131	ACATCAACCCAGATCTCTACC
NM_001060	TBXA2R	132	ACGGAGAAGGAGCTGCTCATC
NM_000955	PTGER1	133	ACCTGGAACCAGATCCTGGAC
NM_001060	TBXA2R	133	ACCTGGAACCAGATCCTGGAC
NM_001462	FPRL1	134	ACAGTCAACCACCATCTGTTAC
NM_001462	FPRL1	135	ACTTCCGAGAGAGACTGATCC
NM_001480	GALR1	136	ACTTCTTACCGTGTCCATGC
NM_001504	GPR9	137	ACTTCAGCCTGAACTTCGACC
NM_001505	GPR30	138	ACGGGCCACATTGTCAACCTC

NM_001506	GPR32	139	ACGTGGTGCTGTTGGTCCATC
NM_001507	GPR38	140	ACCAACTTGTTACCTGGGCAGC
NM_001507	GPR38	141	ACTGCTGCTCGCAAGGAAGTC
NM_001508	GPR39	142	ACCGTGTTCCAGTCCAGCATC
NM_001526	HCRT2	143	ACTATGACGACGAGGAATTCC
NM_001784	CD97	144	ACGCATGAAGCTGAATTGGGC
NM_078481	CD97	144	ACGCATGAAGCTGAATTGGGC
NM_001841	CNR2	145	ACAGCTGTTGCTGTGTTGTGC
NM_002029	FPR1	146	ACAAGTGCCCTGGCCTTCTTC
NM_002036	FY	147	ACTGGATTTCCTGGTGAGGTC
NM_002386	MC1R	148	ACATCTCCATCTTCTACGCAC
NM_002548	OR1D2	149	ACGGTGGTGGGAAATGTGCTC
NM_002548	OR1D2	150	ACGCAGCTCTACTTCCTGGTC
NM_002564	P2RY2	151	ACCAACCTTTACTGCAGCATC
NM_002565	P2RY4	152	ACCCTATGGCTCTTCATCTTC
NM_002566	P2RY11	153	ACAGAGCGTATAGCCTGGTGC
NM_002921	RGR	154	ACCCTGACCATCTTCTCTTTC
NM_002921	RGR	155	ACGATCACTTCCTACAGTCTC
NM_003382	VIPR2	156	ACCAGTCTCAGTACAAGAGGC
NM_003468	FZD5	157	ACCTACCACAAGCAGGTGTCC
NM_003505	FZD1	158	ACCATCGTCATCGCCTGCTAC
NM_003507	FZD7	159	ACGCTCTTTACCGTTCTCACC
NM_003508	FZD9	160	ACGCTGGTCTTCCTACTGCTC
NM_003552	OR1D4	161	ACGGTGCTGGGAAATGTGCTC
NM_014566	OR1D5	161	ACGGTGCTGGGAAATGTGCTC
XM_064470	LOC125182	161	ACGGTGCTGGGAAATGTGCTC
NM_003552	OR1D4	162	ACAGCATTGATTGCCACTGGC
NM_003552	OR1D4	163	ACACCTATGATGAACCCTTTC
NM_014566	OR1D5	163	ACACCTATGATGAACCCTTTC
NM_003553	OR1E1	164	ACTGGATTCCCATCTCCACAC
NM_003553	OR1E1	165	ACCTTCCATGCCATGTTACAC
NM_003554	OR1E2	165	ACCTTCCATGCCATGTTACAC
NM_003554	OR1E2	166	ACTACACCGCCATCTGCTTCC
NM_003614	GALR3	167	ACGGACCTGTTCATCCTCAAC
NM_003614	GALR3	168	ACCATCTACACGCTGGATGCC
NM_003775	EDG6	169	ACATCACGCTGAGTGACCTGC
NM_003857	GALR2	170	ACCAACCTGTTTCATCCTTAAC
NM_003950	F2RL3	171	ACCATGCTGCTGATGAACCTC
NM_003950	F2RL3	172	ACATGTATGGCTCAGTGCTGC
NM_003967	PNR	173	ACAGTACATACTCTGGGCATC
NM_003967	PNR	174	ACACTGAGCCAGAAGGTCTTC
NM_003979	RAI3	175	ACCATGAATAGGACCAACGTC
NM_004122	GHSR	176	ACCACCAACCTCTACCTGTCC
NM_004154	P2RY6	177	ACCTGCTATATGCCTGCTCCC
NM_004154	P2RY6	178	ACTTCACCCAGAAGAAGTTCC
NM_004230	EDG5	179	ACAAGAGCTGCCGCATGCTTC

NM_004230	EDG5	180	ACCCTGAATTCCCTGCTCAAC
NM_004248	GPR10	181	ACCGTCTATGTGTCGGTGTTT
NM_004720	EDG4	182	ACCAGCCCATCTACTACCTGC
NM_004778	GPR44	183	ACAATGTGCTGCTCCTGAACC
NM_004778	GPR44	184	ACCAGCCTGGCCTTCTTCAAC
NM_004885	NPGPR	185	ACAGAACCTGTTGCTGCAGAC
NM_004885	NPGPR	186	ACTACTATCTTCACCAGCCTC
NM_053036	GPR74	186	ACTACTATCTTCACCAGCCTC
NM_005161	AGTRL1	187	ACCACTAAGGTGCAGTGCTAC
NM_005161	AGTRL1	188	ACCATCATGCTGACCTGTTAC
NM_005226	EDG3	189	ACCGTGCTCTTCTTGCTCATC
NM_005281	GPR3	190	ACGGACCTATGTGATGCTGGC
NM_005281	GPR3	191	ACACCTATCTTACCTTGCTCC
NM_005282	GPR4	192	ACCAGGTGCAGCTGAAGATGC
NM_005283	CCXCR1	193	ACCATCATGACCATCCACCGC
NM_005285	GPR7	194	ACCATCTGTGTCCTCTATACC
NM_005285	GPR7	195	ACCTTCCTGGTGGTGGCAATC
NM_005291	GPR17	196	ACCTGCTACCTGCTGATCATC
NM_005291	GPR17	197	ACTGTTTAGGACTCAGCAGAC
NM_005293	GPR20	198	ACACCCCTCAGTCATCTACACC
NM_005293	GPR20	199	ACGGTGCTCATCATCTTCTC
NM_005294	GPR21	200	ACTGTGCACCTTTGTTGAACC
NM_005294	GPR21	201	ACATCTTCCGCATCTGCCAAC
NM_005298	GPR25	202	ACAGTTCCGTGTTCCGTTGCC
NM_005299	GPR31	203	ACGCTGTCTACCTGCTCAACC
NM_005299	GPR31	204	ACCAGGTGCCACAGTTTCTAC
NM_005299	GPR31	205	ACCTGCACAGTGTCGTCAACC
NM_005303	GPR40	206	ACCTGCTGCTGACAGTCTCTC
NM_005304	GPR41	207	ACCACCATCTATCTCACC GCC
NM_005305	GPR42	207	ACCACCATCTATCTCACC GCC
NM_005306	GPR43	208	ACCTGCTACGAGAACTTCACC
NM_005683	GPR55	209	ACCGGAAGCATCCCTATCTAC
NM_005684	GPR52	210	ACTCTGTCACTTCTCCACTAC
NM_005684	GPR52	211	ACTCTGTCCTTCTTAACAACC
NM_005767	P2Y5	212	ACTTGGCAATGTCAGACTTGC
NM_005767	P2Y5	213	ACTTCACAACACGGAATTGGC
NM_005913	MC5R	214	ACCTACGTCACTCTGTGCCTC
NM_005959	MTNR1B	215	ACTGCCATCGCCATTAACCGC
NM_005959	MTNR1B	216	ACGGCACTGCATTCAAGATGC
NM_006018	HM74	217	ACCTGGCAGTAGCTGACTTTC
NM_006018	HM74	218	ACTTTCTACTGATCATCTGCC
XM_090326	LOC160484	218	ACTTTCTACTGATCATCTGCC
NM_006018	HM74	219	ACTGTTGGCCTAACAGTCCAC
NM_006056	GPR66	220	ACGCTACTGTTTGAGATGGTC
NM_006174	NPY5R	221	ACGGTAAACTTCCTCATAGGC
NM_006583	RRH	222	ACTTCGGACACCCACAAATGC

NM_007197	FZD10	223	ACCGTGCTCACCTTCCTCATC
NM_007197	FZD10	224	ACCTCCAAGACTCTGCAGTCC
NM_007264	ADMR	225	ACCTGGGCATTGTCCTGTCTC
NM_012152	EDG7	226	ACAGTCCTCAGCAGGAGTGAC
NM_012344	NTSR2	227	ACCGCGCTCCAAGTCTTTATC
NM_014373	GPCR150	228	ACCACATCTGCCTATTTACTC
NM_014449	GRCA	229	ACTTCCTTTGGGACTAAGCGC
NM_019858	GRCA	229	ACTTCCTTTGGGACTAAGCGC
NM_014499	P2Y10	230	ACAGTGCAGCCTTGTTGGGTTT
NM_014626	GPR58	231	ACTTCTATGTTGGTCGGTCCC
NM_014626	GPR58	232	ACCTTGTTTATGGCAGGTTTC
NM_014627	GPR57	233	ACTGGAGCCATGATTATCCAC
NM_014627	GPR57	234	ACTTCAACTCTACTTGCAACC
NM_016235	GPRC5B	235	ACACTGCTCCTGATGCTCATC
NM_016235	GPRC5B	236	ACCTCTTCGGCAATGTCAAGC
NM_016557	CCRL1	237	ACTCCTTCTATTCACTCTGCC
NM_000795	DRD2	238	ACACTGTGACTGCAACATCCC
NM_016574	DRD2	238	ACACTGTGACTGCAACATCCC
NM_017986	FLJ10060	239	ACCTGCCACCTCCTTTCTTAC
NM_017986	FLJ10060	240	ACCTGATGGCACTGGCAATCC
NM_018485	GPR77	241	ACAGCTGCCTCAATCCCATGC
NM_018654	GPRC5D	242	ACTGCAGCCAGTGGAATGTCC
NM_018949	GPR14	243	ACGCTGCTCACCAGGAACACT
NM_018970	GPR85	244	ACCGCTTCTATACAAAGAGGC
NM_014430	CIDEB	245	ACCGCTTTTCGTGCTTCCTTTC
NM_019839	BLTR2	245	ACCGCTTTTCGTGCTTCCTTTC
NM_019839	BLTR2	246	ACTACGGCCTTGGCCTTCTTC
NM_020400	GPR92	247	ACTCTCTGTCTTCCCTTCACAC
NM_020400	GPR92	248	ACAAAGTGTGGAAGCCAGGGC
NM_020633	V1RL1	249	ACTGGACACAAGCTGAGACCC
NM_020633	V1RL1	250	ACAAGAGTTTCCCTCAGCACC
NM_020633	V1RL1	251	ACTGTAGTTGCAAACCCAGGC
NM_020960	GPR107	252	ACCAAGAAGGCCTTTACAGTC
NM_021624	HRH4	253	ACCATCACAAACAGTCGGTC
NM_022049	GPR88	254	ACGTGGAGGAACGAGGAGTTC
NM_022571	HUMNPIIY20	255	ACCACATCTGCAAGACGGTGC
NM_022788	P2RY12	256	ACTTATCACAAATGGCCTGGC
NM_023915	GPR87	257	ACACAATTGTCTTGCCGGTGC
NM_023915	GPR87	258	ACATCCACAAATCCAGCAGGC
NM_023915	GPR87	259	ACCTGCTTTCTACCATATCAC
NM_030760	EDG8	260	ACGCTTGCTCCACTGTCTTGC
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NM_031866	FZD8	262	ACCGTGGTCTTCTTGCTGGTC
NM_031936	GPR61	263	ACCCTTTCTTCTATGGATGTC
NM_031940	BLP1	264	ACCATGGCAGAAGTAGAATCC
NM_031940	BLP1	265	ACGTGGAACACACTTCAGTCC

NM_078473	BLP1	265	ACGTGGAACACACTTCAGTCC
NM_032027	BBP	266	ACTGTACAAACTACACAGCTC
NM_032551	GPR54	267	ACCGTGACCAACTTCTACATC
NM_032551	GPR54	268	ACCAACTTCTACATCGCCAAC
NM_000796	DRD3	269	ACTGTCTGCTCCATCTCCAAC
NM_033659	DRD3	269	ACTGTCTGCTCCATCTCCAAC
NM_033663	DRD3	269	ACTGTCTGCTCCATCTCCAAC
AF380192	TA4	270	ACGTACAGCGGTGCTGTGTTT
ENSG00000146383	ENSG00000146383	270	ACGTACAGCGGTGCTGTGTTT
NM_053278	GPR102	270	ACGTACAGCGGTGCTGTGTTT
NM_054030	MRGX2	271	ACTGTGATGACCTGTGCCTAC
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NM_054030	MRGX2	273	ACAGTGAAGGATGCTTCCGTC
NM_054031	MRGX3	274	ACAGGAAACGCGGTTGTGCTC
NM_054031	MRGX3	275	ACTTCCTCTTCCCTTAGCGGCC
NM_054031	MRGX3	276	ACAGTGCTGGTCTTCCCTCCTC
NM_054032	MRGX4	276	ACAGTGCTGGTCTTCCCTCCTC
NM_054032	MRGX4	277	ACGTGCATCATTTCCCTTGTC
NM_054032	MRGX4	278	ACGTCAGATTTTCATCCCAGTC
NM_001401	EDG2	279	ACATCTTTGGCTATGTTGCGCC
NM_057159	EDG2	279	ACATCTTTGGCTATGTTGCGCC
NM_001401	EDG2	280	ACTTCTAGACGTGTGCTGTCC
NM_057159	EDG2	280	ACTTCTAGACGTGTGCTGTCC
NM_080819	GPR78	281	ACCTTCCTCATCTGCTTTGCC
NM_080819	GPR78	282	ACCCGTTACGTA CTCTCTGC
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NM_145015	MGC21621	284	ACATCTTCCTGCTCCTCTGCC
NM_145015	MGC21621	285	ACCTGCCTGCACAACTACTTC
NM_145015	MGC21621	286	ACACAGTCACCATGGAGATGC
NM_147199	MRGX1	287	ACAGGAAACGCGAGTTGTGCTC
NM_147199	MRGX1	288	ACTTTGCAGGCCTGAGCTTTC
NM_147199	MRGX1	289	ACAGTACTGGTCTTCCCTCCTC
NM_148962	TG1019	290	ACTTCATAACCTGAGCTCTCC
NM_148962	TG1019	291	ACTTCCTCCTGATCAGCAACC
XM_092406	LOC165140	291	ACTTCCTCCTGATCAGCAACC
AF280399	AF280399	292	ACAGAACCTCTTCCCTGGTGTC
AF280400	AF280400	292	ACAGAACCTCTTCCCTGGTGTC
D13538	HUMA2CIIA	292	ACAGAACCTCTTCCCTGGTGTC
J03853	HUMADRA2C	292	ACAGAACCTCTTCCCTGGTGTC
NM_000683	ADRA2C	292	ACAGAACCTCTTCCCTGGTGTC
U72648	HSU72648	292	ACAGAACCTCTTCCCTGGTGTC
AF280399	AF280399	293	ACAACCTGAAGCGCACACCAC
AF280400	AF280400	293	ACAACCTGAAGCGCACACCAC
D13538	HUMA2CIIA	293	ACAACCTGAAGCGCACACCAC
J03853	HUMADRA2C	293	ACAACCTGAAGCGCACACCAC
NM_000683	ADRA2C	293	ACAACCTGAAGCGCACACCAC

U72648	HSU72648	293	ACAACCTGAAGCGCACACCAC
XM_044591	GPR108	294	ACCAAGAGCATCTCTCTCCTC
XM_061555	LOC119586	295	ACTCTCACAGCCAGAACATTC
XM_066605	LOC139271	296	ACCTGGCCAACACATCAGGTC
XM_066605	LOC139271	297	ACCCAGTTTCCCGTATACTTC
XM_066605	LOC139271	298	ACACAATCAGCTGGCTCCCTC
XM_089954	LOC159954	299	ACTTCATCCTTTCCAACCTGC
XM_089954	LOC159954	300	ACCCAGTCATTGTGAATCCTC
XM_115412	LOC204496	301	ACTCTGCAAAGTCTGGGAAAC
XM_115412	LOC204496	302	ACCCAACCTCTTTGGTCATTCC
XM_115412	LOC204496	303	ACATTCATAGGACCCACTGGC
XM_115784	LOC205316	304	ACTGTGATGGCCTATGACAGC
XM_172703	LOC256774	305	ACCATGATTCCATATCCAGTC
AB012305	AB012305	306	ACCTTAAACCTCAGAATCTGC
NM_001798	CDK2	306	ACCTTAAACCTCAGAATCTGC
NM_052827	CDK2	306	ACCTTAAACCTCAGAATCTGC
BC005169	BC005169	307	ACCATGCTGTATGGCCAGTTC
BC007835	BC007835	307	ACCATGCTGTATGGCCAGTTC
BC008344	BC008344	307	ACCATGCTGTATGGCCAGTTC
SK492	SgK495	307	ACCATGCTGTATGGCCAGTTC
XM_029031	MGC4796	307	ACCATGCTGTATGGCCAGTTC
BC005169	BC005169	308	ACGAGTTTGAGAACTACATGC
BC007835	BC007835	308	ACGAGTTTGAGAACTACATGC
BC008344	BC008344	308	ACGAGTTTGAGAACTACATGC
SK492	SgK495	308	ACGAGTTTGAGAACTACATGC
XM_029031	MGC4796	308	ACGAGTTTGAGAACTACATGC
NM_001394	DUSP4	309	ACGGCTCTGTTGAATGTCTCC
NM_057158	DUSP4	309	ACGGCTCTGTTGAATGTCTCC
NM_001394	DUSP4	310	ACCTCGCAGTTCGTCTTCAGC
NM_057158	DUSP4	310	ACCTCGCAGTTCGTCTTCAGC
NG_000874	NG_000874	311	ACAACAAGACCAATAAGAGGC
NM_002138	HNRPD	311	ACAACAAGACCAATAAGAGGC
NM_031369	HNRPD	311	ACAACAAGACCAATAAGAGGC
NM_031370	HNRPD	311	ACAACAAGACCAATAAGAGGC
NM_002138	HNRPD	312	ACCAATAAGAGGCGTGGGTTC
NM_031369	HNRPD	312	ACCAATAAGAGGCGTGGGTTC
NM_031370	HNRPD	312	ACCAATAAGAGGCGTGGGTTC
NM_003690	PRKRA	313	ACACCGATTACAGGTATTACAC
NM_003690	PRKRA	314	ACTTTCACCTTCAGAGTAACC
NM_004853	STX8	315	ACAGGATGCAGGCCTTGATGC
NM_005394	PMS2L8	316	ACACCAAGGCTCGGAATCCAC
NM_005394	PMS2L8	317	ACAGCCTGTAGAACTGACTCC
NM_005399	PRKAB2	318	ACAGTGGGTTCATGATCCATC
NM_005399	PRKAB2	319	ACATCTTGTAGAGACCTTTCC
NM_006176	NRGN	320	ACCATGCGCTCCCAATCTTCC
NM_006176	NRGN	321	ACGAGTTCCTTTCGTTCTGTGC

NM_006176	NRGN	322	ACCGGAAGAGAAGTCCCTATC
NM_006197	PCM1	323	ACGTTCCCACACAGTAGATAC
NM_006197	PCM1	324	ACCGGTTGTCAATGGAGAATC
NM_006197	PCM1	325	ACAATCTTGTGCCAAAGAGGC
NM_006253	PRKAB1	326	ACTCCGAGGAAATCAAGGCAC
NM_006712	FASTK	327	ACTTGAGTCAGCTCATCATCC
NM_025096	FASTK	327	ACTTGAGTCAGCTCATCATCC
NM_033015	FASTK	327	ACTTGAGTCAGCTCATCATCC
SK139	FASTK	327	ACTTGAGTCAGCTCATCATCC
NM_006712	FASTK	328	ACATCTTGATGTCACTGTGCC
NM_025096	FASTK	328	ACATCTTGATGTCACTGTGCC
NM_033015	FASTK	328	ACATCTTGATGTCACTGTGCC
SK139	FASTK	328	ACATCTTGATGTCACTGTGCC
NM_014365	H11	329	ACAGTATTTGCCTCACTTTCC
NM_014365	H11	330	ACATTTGGAGAGAGCAGTTTC
NM_014365	H11	331	ACCCTAGGGCTTCTCTGATTC
NM_014446	MIBP	332	ACGGTGTGGAAGTGGTCTACC
NM_030974	DKFZP434N1923	333	ACCGTGGAAGGACAGAATGGC
NM_030974	DKFZP434N1923	334	ACTTGACGGAGAGAGAAGAGC
NM_030974	DKFZP434N1923	335	ACTGCACTGTTGCAGCTCTCC
NM_004178	TARBP2	336	ACGCCTGTGTACGACCTTCTC
NM_134323	TARBP2	336	ACGCCTGTGTACGACCTTCTC
NM_134324	TARBP2	336	ACGCCTGTGTACGACCTTCTC
NM_003559	PIP5K2B	337	ACCAGTTTATAGTGGAGTGTC
NM_138687	PIP5K2B	337	ACCAGTTTATAGTGGAGTGTC
NM_001315	MAPK14	338	ACAGATGACCATGTTTCAGTTC
NM_139012	MAPK14	338	ACAGATGACCATGTTTCAGTTC
NM_139013	MAPK14	338	ACAGATGACCATGTTTCAGTTC
NM_139014	MAPK14	338	ACAGATGACCATGTTTCAGTTC
NM_001315	MAPK14	339	ACATTGTTTCCTGGTACAGAC
NM_139012	MAPK14	339	ACATTGTTTCCTGGTACAGAC
NM_139013	MAPK14	339	ACATTGTTTCCTGGTACAGAC
NM_139014	MAPK14	339	ACATTGTTTCCTGGTACAGAC
NM_139021	ERK8	340	ACAGATGCCCAGAGAACATTC
NM_139021	ERK8	341	ACCCTCTCTGCAGACACTGAC
NM_144610	FLJ25006	342	ACTATCTGCACCAGGAATCCC
SK491	SgK494	342	ACTATCTGCACCAGGAATCCC
NM_144624	KIS	343	ACTCCTGGATGTCAGTGTTTC
SK661	KIS	343	ACTCCTGGATGTCAGTGTTTC
NM_144624	KIS	344	ACGTAACATATTGTGGAGTGTC
SK661	KIS	344	ACGTAACATATTGTGGAGTGTC
NM_145001	MGC22688	345	ACCTGCGTTATCACCTGCAAC
SK624	YANK1	345	ACCTGCGTTATCACCTGCAAC
NM_007194	CHEK2	346	ACAGTGTCCTCAGGAAGTTC
NM_145862	CHEK2	346	ACAGTGTCCTCAGGAAGTTC
NM_001553	IGFBP7	347	ACACCTGTCTCATCTGGAAC

NM_001553	IGFBP7	348	ACAACCTGGCCATTCAGACCC
NM_001150	ANPEP	349	ACGCTGAAACCCGATTCTTAC
NM_001150	ANPEP	350	ACCTTTGCCTACCAGAACACC
NM_001150	ANPEP	351	ACCTGAAGAAGCAGGTACACAC
NM_000065	C6	352	ACGGAAGTATAATCCCATCCC
NM_000065	C6	353	ACCGAGGAAGAAGCCAAACAC
NM_000065	C6	354	ACAAAGAAAGAATCCTGTGGC
NM_000070	CAPN3	355	ACGTGGTTATAGATGACTGCC
NM_000070	CAPN3	356	ACAAAGATGAGAAGGCCCGTC
NM_000070	CAPN3	357	ACGAGGTTCCCAAAGAGATGC
NM_001334	CTSO	358	ACCTTTGGCCCTTTGGTAGTC
NM_000119	EPB42	359	ACCATCATCTGTACTTCCGC
NM_000119	EPB42	360	ACACTGGAGTTGACTGACTCC
NM_000119	EPB42	361	ACTGTGGAAGTGGACTGCAAC
NM_000120	EPHX1	362	ACTTCTCTACCCTGACCCTCC
NM_000120	EPHX1	363	ACCTGCTGACCAACGTCATGC
NM_000120	EPHX1	364	ACAACAGGCACCATCATCTCC
NM_000505	F12	365	ACAAATGTACCCACAAGGGCC
NM_000505	F12	366	ACTGTCTCTGTCCACAACACC
NM_000505	F12	367	ACCCTGCAAGGCATCATCAGC
NM_000129	F13A1	368	ACACTAACAAGGTGGACCACC
NM_000129	F13A1	369	ACCAAGGATTTCAGTGTGGAAC
NM_000129	F13A1	370	ACTCAGGTAGTTGGTTCTGAC
NM_000133	F9	371	ACAACCATGACATTGCCCTTC
NM_000133	F9	372	ACATGTTCTGTGCTGGCTTCC
NM_000133	F9	373	ACCAAGGTATCCCGGTATGTC
NM_000308	PPGB	374	ACTAATGACACTGAGGTGCGC
NM_000308	PPGB	375	ACTTTGCCTACTACCATGGCC
NM_000308	PPGB	376	ACCAGAAGATGGAGGTGCAGC
NM_001807	CEL	377	ACTATGGCCTTCGGGATCAGC
NM_001807	CEL	378	ACAGTCTCTAAGGCCATGATC
NM_001908	CTSB	379	ACATGAGCTACTTGAAGAGGC
NM_001908	CTSB	380	ACGGCTGTAATGGTGGCTATC
NM_001908	CTSB	381	ACAAGTCAGGAGTGTACCAAC
NM_001814	CTSC	382	ACAGCATATGATGACCTTGGC
NM_001814	CTSC	383	ACCACACTGGTCTAAGAGACC
NM_001814	CTSC	384	ACTGGTCTAAGAGACCCTTTC
NM_001910	CTSE	385	ACCGAGTCCTGCTCAATGGAC
NM_001910	CTSE	386	ACCAAGTCTCTGTGGAAGGAC
NM_001910	CTSE	387	ACTGCCTACACCCTACTGGAC
NM_001911	CTSG	388	ACATGGCGTATCTTCAGATCC
NM_001911	CTSG	389	ACGGAATCGAAACGTGAACCC
NM_001911	CTSG	390	ACTGCTGGATCAGATGGAGAC
NM_001972	ELA2	391	ACCCTGATTGCGCCCAACTTC
NM_001972	ELA2	392	ACGACATCGTGATTCTCCAGC
NM_001972	ELA2	393	ACGGAATTGCCTCCTTCGTCC

NM_001977	ENPEP	394	ACGAGTCAAGAGCATAGCGGC
NM_001977	ENPEP	395	ACCCAAGAGCTAACCCCTTCTC
NM_001977	ENPEP	396	ACTTCCAAGGTCAAGTGAAGC
NM_002525	NRD1	397	ACTTGCAAGGCCTTCTGATGC
NM_002525	NRD1	398	ACATGTGTGAGAACATGCAGC
NM_002525	NRD1	399	ACTGAAGAGGCATTCAACACC
NM_002786	PSMA1	400	ACAACGATATGGCCGGAGACC
NM_002786	PSMA1	401	ACGCTTCCTGCAGAACAGGAC
NM_002786	PSMA1	402	ACAGAGAAAGGCACAGCCTGC
NM_002790	PSMA5	403	ACACAGAACCCTGGTTCACC
NM_002790	PSMA5	404	ACCCATCTGGGACCTTTGTAC
NM_002790	PSMA5	405	ACATTGAGCTAGCCACAGTGC
NM_002793	PSMB1	406	ACAATCCTGTATTCAAGGCGC
NM_002795	PSMB3	407	ACGGTTTGGCCCTTACTACAC
NM_002795	PSMB3	408	ACCTTTAAGCCCTTCATTTGC
NM_002795	PSMB3	409	ACCTGCGCCGAACAAATGTAC
NM_002796	PSMB4	410	ACTTTACAGAGGTCCAATCAC
NM_002796	PSMB4	411	ACACAGCTATAGTCCTAGAGC
NM_002796	PSMB4	412	ACTTAGTAGAACGCTGCATGC
NM_002797	PSMB5	413	ACAGCGGGTGCTTACATTGCC
NM_002797	PSMB5	414	ACGCATCTCTGTAGCAGCTGC
NM_002797	PSMB5	415	ACCTTCTCTGTAGGTTCTGGC
NM_002799	PSMB7	416	ACACAGACATGACAACCCAGC
NM_002799	PSMB7	417	ACAACCCAGCTCATTTCTTCC
NM_002799	PSMB7	418	ACCTCTACAGCATCTATCCTC
NM_002801	PSMB10	419	ACAAGAGCTGCGAGAAGATCC
NM_003119	SPG7	420	ACGACTTTGTCCACGAGATGC
NM_003119	SPG7	421	ACTGGAAGGGAAGGTGGATTC
NM_003119	SPG7	422	ACAGACACACCGAGAAGGTGC
NM_005200	CMAR	422	ACAGACACACCGAGAAGGTGC
NM_003227	TFR2	423	ACACCATCAGGCAAACCAGCC
NM_003227	TFR2	424	ACACCTGGCTTCCCTTCCTTC
NM_003227	TFR2	425	ACAGGTGGTGTTCACCAATCC
NM_003234	TFRC	426	ACAGTCATGTGGAGATGAAAC
NM_003234	TFRC	427	ACCCTTACACACCTGGATTCC
NM_003234	TFRC	428	ACTGAATGGCTAGAGGGATAC
NM_003249	THOP1	429	ACACAGTTTCAGAGGAATATCC
NM_003249	THOP1	430	ACGAGGTGGAGACCTACTTCC
NM_003249	THOP1	431	ACCAACATGCCTGCAACCTTC
NM_002630	PGC	432	ACCAGTCACTCCCCTTCAAC
NM_002630	PGC	433	ACCCTGACTGTCCAGAGCATC
NM_002630	PGC	434	ACCTCTCTGCTAACTGTGCCC
NM_002788	PSMA3	435	ACAGCTATTGGAATCAGATGC
NM_002788	PSMA3	436	ACATCTTGCAGACAGAGTGGC
NM_002788	PSMA3	437	ACAGAGTGGCCATGTATGTGC
NM_003118	SPARC	438	ACCTTCGACTCTTCTGCCAC

NM_003118	SPARC	439	ACAACCTTCTGACTGAGAAGC
NM_003118	SPARC	440	ACATCTTCCCTGTACACTGGC
NM_003245	TGM3	441	ACTGGAGTTCATTGACACCAC
NM_003245	TGM3	442	ACAGCCTGGACCATCATCTAC
NM_003245	TGM3	443	ACTTCTCCTGCAACAAGTTCC
NM_003241	TGM4	444	ACATGGGAGTTCCAAACGAGC
NM_003241	TGM4	445	ACGACTCTGTCTGGAATTTCC
NM_003241	TGM4	446	ACCTTGGACTCCAAGACCTAC
NM_002777	PRTN3	447	ACGACATTCTCCTCATCCAGC
NM_002777	PRTN3	448	ACATTTGCACTTTCGTCCCTC
NM_002777	PRTN3	449	ACTGGATCCGTTCTACGCTGC
NM_000386	BLMH	450	ACCCTGCAAATGATGGTGGCC
NM_000386	BLMH	451	ACTCTATACAACAACCAGCCC
NM_000386	BLMH	452	ACCATGGCCACAAAGGTTACC
NM_001868	CPA1	453	ACCCTGGAGGAGATCTATGAC
NM_001868	CPA1	454	ACTCCCAGCTCCTCATGTATC
NM_001868	CPA1	455	ACTATTGACTGGACCTACAGC
NM_001869	CPA2	456	ACAAGCTACGGCACTTTGGAC
NM_001869	CPA2	457	ACCCATCCATCACTTCCATT
NM_001869	CPA2	458	ACCCTTGCTCTGATTCTATACC
NM_001870	CPA3	459	ACCAGAGTCCGAGAAAGAGAC
NM_001870	CPA3	460	ACCTAACCATGAGGACTTGGC
NM_001870	CPA3	461	ACACATTTGCCTTTGAGCTCC
NM_001871	CPB1	462	ACCAAGGCCCTGGCTGATTT
NM_001871	CPB1	463	ACTCCCAAATGATGATCTACC
NM_001871	CPB1	464	ACAATGCTGAGTTGAATGCCC
NM_001874	CPM	465	ACAGTTCTGTCACTCACTTAC
NM_001874	CPM	466	ACCTATGCTTCAAGAAATCCC
NM_001874	CPM	467	ACCACTCAGCTGCAACAAAGC
NM_001993	F3	468	ACAACAGACACAGAGTGTGAC
NM_001993	F3	469	ACCTCGGACAGCCAACAATTC
NM_001993	F3	470	ACCGGAAGAGTACAGACAGCC
NM_002104	GZMK	471	ACCTCTCTTAGATCTGGAACC
NM_002104	GZMK	472	ACGCTATAGTCTCTGGAGGTC
NM_002104	GZMK	473	ACAAAGCCTGGAATCTACACC
NM_003363	USP4	474	ACATAACCTATTTCTGGCCC
NM_003363	USP4	475	ACTGCACCACTGACTGACTAC
NM_003363	USP4	476	ACAGATACTGGAGGGATAAGC
NM_003470	USP7	477	ACCAAGAATTACTCAGAACCC
NM_003470	USP7	478	ACGATGACGACCTGTCTGTTC
NM_003470	USP7	479	ACTGTGGGCATATCTACACAC
NM_003481	USP5	480	ACAGACCCTACCCAGGATTTTC
NM_003481	USP5	481	ACATGGTGGAGAGGAATTGCC
U47927	HSU47927	481	ACATGGTGGAGAGGAATTGCC
NM_003481	USP5	482	ACCTAAAGTCCGGGATGGTCC
U47927	HSU47927	482	ACCTAAAGTCCGGGATGGTCC

NM_003692	TMEFF1	483	ACCTCAATGGTTACTGCATCC
NM_003692	TMEFF1	484	ACAGATTGCCATCATAGTAGC
NM_003692	TMEFF1	485	ACACTGACCATGTGTATGTAC
NM_003891	PROZ	486	ACGTTCTGGTGAGGTGGAAGC
NM_003891	PROZ	487	ACTGATGGGTGTCAACACTTC
NM_003891	PROZ	488	ACTAACTGAAACTCAGCTAGC
NM_003940	USP13	489	ACCAGCCCTGGTAACAATTGC
NM_003940	USP13	490	ACTGAAGCCAATGTATGGTCC
NM_003940	USP13	491	ACCTAGAGTCAAGGATGGATC
NM_003365	UQCRC1	492	ACTGTAGTCTGGAAGACTCAC
NM_003365	UQCRC1	493	ACCTGCATGCCACAGCATTC
NM_003365	UQCRC1	494	ACGCTGTGCCCACTCTTACTC
NM_003366	UQCRC2	495	ACCTCAGGACCTTGAGTTTAC
NM_003366	UQCRC2	496	ACCAGAATGCCTTGGCTAATC
NM_003366	UQCRC2	497	ACAGCTGCTGGAGATGTTATC
NM_005143	HP	498	ACATGGCTATGTGGAGCACTC
NM_005143	HP	499	ACTCCCAAGTAGATATTGGGC
NM_005143	HP	500	ACCATAGCTGAGAATAATGC
NM_004413	DPEP1	501	ACCTTCCTGTATGTCACCAGC
NM_004413	DPEP1	502	ACGTCCTGAGGCTGGTGAAAC
NM_004413	DPEP1	503	ACGTCTCCAAGTATCCAGACC
NM_004476	FOLH1	504	ACCACCTTTTCAGTGCTTTCTC
NM_004476	FOLH1	505	ACCCTGCTGACTACTTTGCTC
NM_004476	FOLH1	506	ACAAATTCAGCGGCTATCCAC
NM_004613	TGM2	507	ACTTTGAGGGCCGCAACTACC
NM_004613	TGM2	508	ACCCAGCAGGGCTTTATCTAC
NM_004613	TGM2	509	ACCTTCTCATCGAGTACTTCC
NM_004651	USP11	510	ACAACAACCTCTACTACGGCC
NM_004651	USP11	511	ACATTGCTATCGACTGGGAGC
NM_004651	USP11	512	ACCCTCGTGGAGTTTCCTATC
NM_004279	PMPCB	513	ACAATGGAACAGCACACTTTC
NM_004279	PMPCB	514	ACAAGATGCCTTTGGCGCACC
NM_004279	PMPCB	515	ACTTGTCATGGCAATCTTTGC
NM_004390	CTSH	516	ACCTACAGTACGGAGGAGTAC
NM_004390	CTSH	517	ACTTCAATAATTACGGCTGCC
NM_004390	CTSH	518	ACGGGTACTTCCTCATCGAGC
NM_005110	GFPT2	519	ACACTTCGGCATTGCCACAC
NM_005110	GFPT2	520	ACACCTGTGTTTCAGGGATGAC
NM_005110	GFPT2	521	ACTGTGCTCCAAGGACGATAC
NM_005040	PRCP	522	ACATCGATACTATGGAGAGTC
NM_005040	PRCP	523	ACTCATTCAAGGATTCCAGAC
NM_005040	PRCP	524	ACTCTGGTTGCAGTCACCATC
NM_005468	NAALADASEL	525	ACAACCCTATGCTGCCTATGC
NM_005468	NAALADASEL	526	ACCCTCTGACTCCCTACCTTC
NM_005468	NAALADASEL	527	ACGGGCTCCGTAGTCACATTC
NM_005577	LPA	528	ACCACTGTCACAGGAAGGACC

NM_005577	LPA	529	ACTGTCACAGGAAGAACCTGC
NM_024492	APOARGC	529	ACTGTCACAGGAAGAACCTGC
NM_145727	APOARGC	529	ACTGTCACAGGAAGAACCTGC
NM_005577	LPA	530	ACCACACTCGCATAGTCGGAC
NM_005588	MEP1A	531	ACAGTTTGATGGGTGCTGGTC
NM_005588	MEP1A	532	ACATCACTCTGACAGAAACCC
NM_005588	MEP1A	533	ACTTCAGAGACCCATGTGACC
NM_003399	XPNPEP2	534	ACTCCTATTGTACCTGGCTC
NM_003399	XPNPEP2	535	ACTCGTGACAGACACCTACTC
NM_003399	XPNPEP2	536	ACCTCATCGATGTCAGCCTGC
NM_004055	CAPN5	537	ACTCTACTATAAGGGCACGCC
NM_004055	CAPN5	538	ACGATGAGACTAAGAGGAACC
NM_004055	CAPN5	539	ACACCTTCTTCCAGAACCCAC
NM_004121	GGTLA1	540	ACAGGGAAGGTGGAGGTCATC
NM_004121	GGTLA1	541	ACCACCACCTTGTAGAGACGC
NM_004121	GGTLA1	542	ACCAGCACCATCAACACACCC
NM_004131	GZMB	543	ACAAGACGACTTCGTGCTGAC
NM_004131	GZMB	544	ACGCCATTATTACGACAGTAC
NM_004131	GZMB	545	ACGAAACAATGGCATGCCTCC
NM_004969	IDE	546	ACCCTTTCCAAGAAGAACATC
NM_004969	IDE	547	ACACCCCTCATTTGAACATGCTC
NM_004969	IDE	548	ACATGACAGAAGAGGCCTTCC
NM_005317	GZMM	549	ACCTTCCACATCAAGGCAGCC
NM_005317	GZMM	550	ACATCAAGGCAGCCATCCAGC
NM_005317	GZMM	551	ACCCGCATGTGTAACAACAGC
NM_003793	CTSF	552	ACTTTCAGCTCAGTCATTTCC
NM_003793	CTSF	553	ACAGCTCAGTATGGAGTCACC
NM_003793	CTSF	554	ACAGCTACCAGGGTCACATGC
NM_005800	D13S106E	555	ACTGTGCTCGAAGGAGGAATC
NM_005800	D13S106E	556	ACTAATGACCAACACGCTCTC
NM_005800	D13S106E	557	ACTTGGTGGAAGGTCAGATTC
NM_005630	SLC21A2	558	ACAGCTGCAGTTAACTTGGTC
NM_005630	SLC21A2	559	ACCACCATCATCACCATCTCC
NM_005630	SLC21A2	560	ACTATGACAACGATGCTCTCC
NM_005925	MEP1B	561	ACATCAGACTTGATAGGGCAC
NM_005925	MEP1B	562	ACTTTGAGGATGTGATCGGCC
NM_005925	MEP1B	563	ACAGACCCATTTATGACCACC
NM_006191	PA2G4	564	ACATCGCCAACAGGGTACTTC
NM_006191	PA2G4	565	ACTTCGGTCCCTTGGTGGAAGC
NM_006191	PA2G4	566	ACTGTGTATGTCACTTCTCCC
XM_167030	LOC222530	566	ACTGTGTATGTCACTTCTCCC
NM_006290	TNFAIP3	567	ACGAACGGTGACGGCAATTGC
NM_006290	TNFAIP3	568	ACCAGCGTTCCAAGTCAGATC
NM_006290	TNFAIP3	569	ACAGCGTCCAGGTTCCAGAAC
NM_006447	USP16	570	ACGCCAAGATCTGAACCTCAC
NM_006447	USP16	571	ACGGAGACAGTGTAATGGACC

NM_006447	USP16	572	ACACACATGTGCAAGCTGTGC
NM_006528	TFPI2	573	ACAGGAAATAACGCGGAGATC
NM_006528	TFPI2	574	ACTACTACGACAGGTACACGC
NM_006528	TFPI2	575	ACTGGCTGTGGAGGGAATGAC
AF073344	AF073344	576	ACTGCCATTTGTGCCACAGGC
NM_006537	USP3	576	ACTGCCATTTGTGCCACAGGC
AF073344	AF073344	577	ACAGCAGGAAGGCGGACATAC
NM_006537	USP3	577	ACAGCAGGAAGGCGGACATAC
AF073344	AF073344	578	ACACCAGGCCAAAGCTGGATC
NM_006537	USP3	578	ACACCAGGCCAAAGCTGGATC
NM_006785	MALT1	579	ACTGAAGTTCTTCAGCTTCTC
NM_006785	MALT1	580	ACCAAGGAACCTACTGGTGTC
NM_006785	MALT1	581	ACCCATTCCATGGTGTTTACC
NM_007215	POLG2	582	ACAAAGAGCTGAGTAAGGAAC
NM_007215	POLG2	583	ACTTCAGCAGCAGTGAAGTGC
NM_007215	POLG2	584	ACATCTGAGAAGCAGAGACAC
NM_013270	TSP50	585	ACCACCATGGAGACCCCAATTC
NM_013270	TSP50	586	ACGGACTATGTGTTGAAGGAC
NM_013270	TSP50	587	ACCCATCTACCTACAGGTCTC
NM_013272	SLC21A11	588	ACCTGGAGCAGCAGTTTAACC
NM_013272	SLC21A11	589	ACTGTTCCCTATGGAAACAGC
NM_013272	SLC21A11	590	ACAATGTGGTCTACCGATACC
NM_016006	LOC51099	591	ACCCAGGTTTGACAGTGATGC
NM_016006	LOC51099	592	ACCCATCAAGGGTTAATCATC
NM_016006	LOC51099	593	ACCACTGTAATGTGCAGACTC
NM_001700	AZU1	594	ACGACCTGATGCTGCTTCAGC
NM_005099	ADAMTS4	595	ACTAGAGCTGGAGCAGGACTC
NM_005099	ADAMTS4	596	ACTGACTTCCTGGACAATGGC
NM_005099	ADAMTS4	597	ACACGCCTCCGATACAGCTTC
NM_022098	LOC63929	598	ACCTATGTGGATTCCAAGAGC
NM_022098	LOC63929	599	ACAAGCTTGGAGAACATCTAC
NM_022098	LOC63929	600	ACTCAGGACTCACCTCTCATC
NM_004555	NFATC3	601	ACAGTATGGACTTGGACACTC
NM_004555	NFATC3	602	ACATCTCTTAGCCCATACACC
NM_004555	NFATC3	603	ACTCAAGCACAAAGTACGGGC
NM_000027	AGA	604	ACCACACTAGATGCCATGATC
NM_000027	AGA	605	ACTTATCTACCAGTGCTTCTC
NM_000027	AGA	606	ACATGGCCGTGTAGGAGACTC
NM_004505	USP6	607	ACTCTCCGGAACCATGTCTTC
X63546	HSTRE210	607	ACTCTCCGGAACCATGTCTTC
X63547	HSTRE213	607	ACTCTCCGGAACCATGTCTTC
XM_165948	USP6	607	ACTCTCCGGAACCATGTCTTC
NM_004505	USP6	608	ACGATGACACCGTGCTCAAGC
X63546	HSTRE210	608	ACGATGACACCGTGCTCAAGC
X63547	HSTRE213	608	ACGATGACACCGTGCTCAAGC
XM_165948	USP6	608	ACGATGACACCGTGCTCAAGC

NM_000447	PSEN2	609	ACCCTCATCATGATCAGCGTC
NM_012486	PSEN2	609	ACCCTCATCATGATCAGCGTC
NM_000447	PSEN2	610	ACCTACAATGTGGCCATGGAC
NM_012486	PSEN2	610	ACCTACAATGTGGCCATGGAC
NM_000447	PSEN2	611	ACTTCATCTTCTACAGTGTGC
NM_012486	PSEN2	611	ACTTCATCTTCTACAGTGTGC
NM_000665	ACHE	612	ACTGTGCTGGTGTCCATGAAC
NM_015831	ACHE	612	ACTGTGCTGGTGTCCATGAAC
NM_001199	BMP1	613	ACAGCTCGTAAGTCCTCCATC
NM_006128	BMP1	613	ACAGCTCGTAAGTCCTCCATC
NM_006129	BMP1	613	ACAGCTCGTAAGTCCTCCATC
NM_006130	BMP1	613	ACAGCTCGTAAGTCCTCCATC
NM_006131	BMP1	613	ACAGCTCGTAAGTCCTCCATC
NM_006132	BMP1	613	ACAGCTCGTAAGTCCTCCATC
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NM_006131	BMP1	615	ACAAGAAGTGCATCTGGCAGC
NM_006132	BMP1	615	ACAAGAAGTGCATCTGGCAGC
NM_002390	ADAM11	616	ACTCAAACCTTCACCCTGGACC
NM_002390	ADAM11	617	ACCAGCAACTTTGCCAAGTCC
NM_021612	ADAM11	617	ACCAGCAACTTTGCCAAGTCC
NM_002390	ADAM11	618	ACGAGTACAACCAAGTTCTGC
NM_021612	ADAM11	618	ACGAGTACAACCAAGTTCTGC
NM_002390	ADAM11	619	ACCAACATCATCATTGGCTCC
NM_021612	ADAM11	619	ACCAACATCATCATTGGCTCC
NM_006350	FST	620	ACCGAGGAGGACGTGAATGAC
NM_013409	FST	620	ACCGAGGAGGACGTGAATGAC
NM_006350	FST	621	ACCGCAATGAATGTGCACTCC
NM_013409	FST	621	ACCGCAATGAATGTGCACTCC
NM_006350	FST	622	ACCTGAGAAAGGCTACCTGCC
NM_013409	FST	622	ACCTGAGAAAGGCTACCTGCC
NM_014244	ADAMTS2	623	ACAATGTACGGTCTTTGGCC
NM_021599	ADAMTS2	623	ACAATGTACGGTCTTTGGCC
NM_014244	ADAMTS2	624	ACCTGCACTCCTATGACTGCC
NM_021599	ADAMTS2	624	ACCTGCACTCCTATGACTGCC
NM_003183	ADAM17	625	ACCAGAGAATGGACACCATCC
NM_021832	ADAM17	625	ACCAGAGAATGGACACCATCC
NM_022790	MMP19	626	ACATGGGACTTCAGCATGAGC

NM_022791	MMP19	626	ACATGGGACTTCAGCATGAGC
NM_022792	MMP19	626	ACATGGGACTTCAGCATGAGC
NM_002426	MMP12	627	ACTGCTGTTCACGAGATTGGC
NM_005940	MMP11	628	ACCTCACCTACAGGATCCTTC
NM_005940	MMP11	629	ACCCTGTGAAGGTGAAGGCTC
NM_004142	MMPL1	630	ACATCCTCATCGACTTTGCCC
NM_022468	MMP25	630	ACATCCTCATCGACTTTGCCC
NM_022718	MMP25	630	ACATCCTCATCGACTTTGCCC
NM_004142	MMPL1	631	ACCCTAGCCCATGCCTTCTTC
NM_022468	MMP25	631	ACCCTAGCCCATGCCTTCTTC
NM_022718	MMP25	631	ACCCTAGCCCATGCCTTCTTC
NM_005941	MMP16	632	ACAGCCAGCACTGTGAAAGCC
NM_004530	MMP2	633	ACAACCTTCTTCCCTCGCAAGC
NM_004530	MMP2	634	ACCAAGGGTACAGCCTGTTC
NM_004530	MMP2	635	ACACCTACACCAAGAACTCC
NM_002423	MMP7	636	ACTGGAATGTTAAACTCCCGC
NM_002423	MMP7	637	ACTGCTGACATCATGATTGGC
NM_002423	MMP7	638	ACTCCTACCCATTGTGATGGGC
NM_004994	MMP9	639	ACAACATCACCTATTGGATCC
NM_004994	MMP9	640	ACGGCAATGCTGATGGGAAAC
NM_004994	MMP9	641	ACTTTCCTGGGTAAAGGAGTAC
NM_006690	MMP24	642	ACTGACCTTTGAAGAGGTGCC
NM_006690	MMP24	643	ACGCACAACCTCAAGCTGCCC
NM_006690	MMP24	644	ACCTACTATAAGCGGCCAGTC
NM_021801	MMP26	645	ACACAGCTCCTGCAACAATTC
NM_021801	MMP26	646	ACATGATATGAAGCCATCCGC
NM_021801	MMP26	647	ACACTGGTCAGCTTCAGACAC
NM_021251	CAPN10	648	ACCTACAAGGTTGTGCCCTCC
NM_023083	CAPN10	648	ACCTACAAGGTTGTGCCCTCC
NM_023084	CAPN10	648	ACCTACAAGGTTGTGCCCTCC
NM_023085	CAPN10	648	ACCTACAAGGTTGTGCCCTCC
NM_023086	CAPN10	648	ACCTACAAGGTTGTGCCCTCC
NM_023087	CAPN10	648	ACCTACAAGGTTGTGCCCTCC
NM_023088	CAPN10	648	ACCTACAAGGTTGTGCCCTCC
NM_021251	CAPN10	649	ACCATCGCAACCAGGATTGAC
NM_023083	CAPN10	649	ACCATCGCAACCAGGATTGAC
NM_023084	CAPN10	649	ACCATCGCAACCAGGATTGAC
NM_023085	CAPN10	649	ACCATCGCAACCAGGATTGAC
NM_023086	CAPN10	649	ACCATCGCAACCAGGATTGAC
NM_023087	CAPN10	649	ACCATCGCAACCAGGATTGAC
NM_023088	CAPN10	649	ACCATCGCAACCAGGATTGAC
NM_023089	CAPN10	650	ACTTCACCAGATTTCAGCCACC
NM_023089	CAPN10	651	ACCTGAACTCTACCAACAGC
NM_003474	ADAM12	652	ACAATCCCAGGAGATTGCTGC
NM_021102	SPINT2	653	ACTTCATCTATGGAGGCTGCC
NM_017493	HSHIN1	654	ACAGCAGTCTGCTGAAGTTTC

NM_000091	COL4A3	655	ACCAGGTACTCCAGGTCTTCC
NM_031362	COL4A3	655	ACCAGGTACTCCAGGTCTTCC
NM_031363	COL4A3	655	ACCAGGTACTCCAGGTCTTCC
NM_031364	COL4A3	655	ACCAGGTACTCCAGGTCTTCC
NM_031365	COL4A3	655	ACCAGGTACTCCAGGTCTTCC
NM_031366	COL4A3	655	ACCAGGTACTCCAGGTCTTCC
NM_032549	IMMP2L	656	ACACCGTGGTGACATTGTATC
NM_032549	IMMP2L	657	ACTTCTGCATGCCCATGCCAC
NG_000013	NG_000013	658	ACTGGAGTACGTGTGTCTTC
NM_001710	BF	658	ACTGGAGTACGTGTGTCTTC
NM_001710	BF	659	ACTTGACAGAGGTGATTCTGGC
NM_020249	ADAMTS9	660	ACTCAACAGATCGCATTGAGC
NM_015571	SUSP1	661	ACTGCAGTTCAGAAATAGGAC
AJ312398	HSA312398	662	ACACGCTCAGAAGTAACCCAC
AJ312399	HSA312399	662	ACACGCTCAGAAGTAACCCAC
NM_033029	LMLN	662	ACACGCTCAGAAGTAACCCAC
AJ312398	HSA312398	663	ACTTCTGTGAGCTCTGTCTTC
AJ312399	HSA312399	663	ACTTCTGTGAGCTCTGTCTTC
NM_033029	LMLN	663	ACTTCTGTGAGCTCTGTCTTC
NM_004346	CASP3	664	ACAGATGTGATGCAGCAAAC
NM_032991	CASP3	664	ACAGATGTGATGCAGCAAAC
NM_004346	CASP3	665	ACTGGACTGTGGCATTGAGAC
NM_032991	CASP3	665	ACTGGACTGTGGCATTGAGAC
NM_001229	CASP9	666	ACATCGACTGTGAGAAGTTGC
NM_001229	CASP9	667	ACTGCTGCGTGGTGGTCATTC
NM_001229	CASP9	668	ACTCTGAAGACCTGCAGTCCC
NM_032996	CASP9	668	ACTCTGAAGACCTGCAGTCCC
NM_001224	CASP2	669	ACCAGACTGCACAGGAAATGC
NM_032982	CASP2	669	ACCAGACTGCACAGGAAATGC
NM_032983	CASP2	669	ACCAGACTGCACAGGAAATGC
NM_032984	CASP2	669	ACCAGACTGCACAGGAAATGC
NM_001224	CASP2	670	ACCAAACGAGGTTCTTGGTAC
NM_032982	CASP2	670	ACCAAACGAGGTTCTTGGTAC
NM_032983	CASP2	670	ACCAAACGAGGTTCTTGGTAC
NM_032984	CASP2	670	ACCAAACGAGGTTCTTGGTAC
NM_001226	CASP6	671	ACTGGCTTGTTCAAAGGAGAC
NM_032992	CASP6	671	ACTGGCTTGTTCAAAGGAGAC
NM_001226	CASP6	672	ACTGTGAACGGCTCATGGTAC
NM_032992	CASP6	672	ACTGTGAACGGCTCATGGTAC
NM_001230	CASP10	673	ACAACCACAGCTTTACCTCCC
NM_032974	CASP10	673	ACAACCACAGCTTTACCTCCC
NM_032976	CASP10	673	ACAACCACAGCTTTACCTCCC
NM_032977	CASP10	673	ACAACCACAGCTTTACCTCCC
NM_032974	CASP10	674	ACTCTAAACTCTGAAACCAGC
NM_015984	UCH37	675	ACAACCTGCAGAGGAGGAACC
J04605	HUMPEPD	676	ACGTCACAGAAGCCCTCTGTC

NM_000285	PEPD	676	ACGTACACAGAAGCCCTCTGTC
J04605	HUMPEPD	677	ACGGCAAGTTCACTGCAGACC
NM_000285	PEPD	677	ACGGCAAGTTCACTGCAGACC
J04605	HUMPEPD	678	ACTTCCTGGGCATTGACGTGC
NM_000285	PEPD	678	ACTTCCTGGGCATTGACGTGC
NM_006102	PGCP	679	ACAGTCCTCACACAGGTATTC
NM_016134	PGCP	679	ACAGTCCTCACACAGGTATTC
NM_033292	CASP1	680	ACTGTATGAATGTCTGTGGGC
NM_033293	CASP1	680	ACTGTATGAATGTCTGTGGGC
NM_033294	CASP1	680	ACTGTATGAATGTCTGTGGGC
NM_033295	CASP1	680	ACTGTATGAATGTCTGTGGGC
NM_013379	DPP7	681	ACCTTCTTCTACACTGGGAAC
NM_023038	ADAM19	682	ACCTGGAGAAGAATGAGCAAC
NM_033274	ADAM19	682	ACCTGGAGAAGAATGAGCAAC
NM_023038	ADAM19	683	ACTGCCCTACCAACTTCTACC
NM_033274	ADAM19	683	ACTGCCCTACCAACTTCTACC
NM_023038	ADAM19	684	ACTGGAACCAAGTGTGGCTAC
NM_033274	ADAM19	684	ACTGGAACCAAGTGTGGCTAC
NM_030955	ADAMTS12	685	ACCTTTCAGGAATGTGTGACG
NM_005467	NAALAD2	686	ACTTGGGAGGAATTGCTCCAC
NM_005467	NAALAD2	687	ACTGATGCTCCTGGAAAGAGC
NM_004598	SPOCK	688	ACATGAACATGACCTCCTGC
NM_001971	ELA1	689	ACAGAACTGGGTGATGACAGC
NM_001227	CASP7	690	ACTGCTCTTGTGCCAAGATGC
NM_033338	CASP7	690	ACTGCTCTTGTGCCAAGATGC
NM_033339	CASP7	690	ACTGCTCTTGTGCCAAGATGC
NM_033340	CASP7	690	ACTGCTCTTGTGCCAAGATGC
NM_001227	CASP7	691	ACCGAGCTTGATGATGGCATC
NM_033338	CASP7	691	ACCGAGCTTGATGATGGCATC
NM_033339	CASP7	691	ACCGAGCTTGATGATGGCATC
NM_033340	CASP7	691	ACCGAGCTTGATGATGGCATC
NM_001227	CASP7	692	ACCTGGAAATCATGCAGATCC
NM_033338	CASP7	692	ACCTGGAAATCATGCAGATCC
NM_033339	CASP7	692	ACCTGGAAATCATGCAGATCC
NM_033340	CASP7	692	ACCTGGAAATCATGCAGATCC
NM_001228	CASP8	693	ACTACATTCCGCAAAGGAAGC
NM_033355	CASP8	693	ACTACATTCCGCAAAGGAAGC
NM_033356	CASP8	693	ACTACATTCCGCAAAGGAAGC
NM_033357	CASP8	693	ACTACATTCCGCAAAGGAAGC
NM_033358	CASP8	693	ACTACATTCCGCAAAGGAAGC
NM_001228	CASP8	694	ACTGCTTCATCTGCTGTATCC
NM_033355	CASP8	694	ACTGCTTCATCTGCTGTATCC
NM_033356	CASP8	694	ACTGCTTCATCTGCTGTATCC
NM_033357	CASP8	694	ACTGCTTCATCTGCTGTATCC
NM_003814	ADAM20	695	ACTTCTCCAGAAGTGGTGATC
NM_032857	MRPL56	696	ACAGTTATGCGAATTGCTAGC

NM_032857	MRPL56	697	ACATTATGTTCCCGAATTCCC
NM_004347	CASP5	698	ACTCTGGGTGAGAGACTCTCC
NM_020886	USP28	699	ACTATTCGACCCAATTCTCCC
NM_014296	CAPN7	700	ACAATAGTATCGGATTGCTCC
NM_006615	CAPN9	701	ACCCTGTTTGAGGATGCAGAC
NM_006615	CAPN9	702	ACCTGAGAGAAGTCTCCGACC
NM_053284	WFIKKN	703	ACGGCCTCACCTACTACAACC
NM_053284	WFIKKN	704	ACCTGATCATGCGCCCTGATC
NM_001266	CES1	705	ACGTGGTGGTGGTGACCATTC
NM_012122	CES3	705	ACGTGGTGGTGGTGACCATTC
NM_016280	LOC51716	705	ACGTGGTGGTGGTGACCATTC
NM_001266	CES1	706	ACCAGAAGGAAGGGTATCTGC
NM_000420	KEL	707	ACAACCTCCAGAAGTGTGGCC
NM_000420	KEL	708	ACCTGACTTACCTGAATCAGC
NM_000420	KEL	709	ACTCTCACGACACTCACAGCC
NM_004369	COL6A3	710	ACCAGAGTAAGCCTGAGATCC
NM_057164	COL6A3	710	ACCAGAGTAAGCCTGAGATCC
NM_057165	COL6A3	710	ACCAGAGTAAGCCTGAGATCC
NM_057166	COL6A3	710	ACCAGAGTAAGCCTGAGATCC
NM_057167	COL6A3	710	ACCAGAGTAAGCCTGAGATCC
NM_004369	COL6A3	711	ACTTCAGGAGGGACAGTTTCC
NM_057164	COL6A3	711	ACTTCAGGAGGGACAGTTTCC
NM_057165	COL6A3	711	ACTTCAGGAGGGACAGTTTCC
NM_057166	COL6A3	711	ACTTCAGGAGGGACAGTTTCC
NM_057167	COL6A3	711	ACTTCAGGAGGGACAGTTTCC
NM_004369	COL6A3	712	ACATCGACAGAACAGAGCTGC
NM_057165	COL6A3	712	ACATCGACAGAACAGAGCTGC
NM_057166	COL6A3	712	ACATCGACAGAACAGAGCTGC
NM_057167	COL6A3	712	ACATCGACAGAACAGAGCTGC
NM_052936	AUTL2	713	ACAGATGATGCTGGCTCAAGC
NM_052936	AUTL2	714	ACTCTATCCATCAAATGGCAC
NM_052936	AUTL2	715	ACTGGCCTCCCTTTGTACCTC
NM_005807	PRG4	716	ACACTACATGGAGTGCTGCCC
NM_005807	PRG4	717	ACCACCAGTTGTAGATGAAGC
NM_005807	PRG4	718	ACCCACTACTCCCAAGAAGCC
NM_014693	ECE2	719	ACCAGGCCATACTGAAGCACC
NM_014693	ECE2	720	ACCATTGGAGTTGAGTGACTC
NM_014693	ECE2	721	ACAATGCTTACAAAGCATGGC
NM_033423	CTLA1	722	ACTTTGTGCTGACAGCTGCTC
NM_033423	CTLA1	723	ACTGCAGGAAGTGTGCTGAC
NM_015528	DKFZP566H073	724	ACTTTGCAGACCTTCCAGCTC
NM_015528	DKFZP566H073	725	ACCTCAAGGTCTCTAAATGCCC
NM_015528	DKFZP566H073	726	ACACATACACCTCTGGTGACC
NM_006590	SAD1	727	ACAAGCAAGCCAAATTGTCCC
NM_021627	SEN2	728	ACAGAAGAACGGACGATCTCC
NM_021626	RISC	729	ACCAACTCCTGCAAGAACTTC

NM_030958	OATPRP4	730	ACCACCATTGAAAGGCGCTAC
NM_030958	OATPRP4	731	ACCTATTTATACCCTGGGACC
NM_030958	OATPRP4	732	ACCTTGACCAGAATGACCCTC
NM_033280	LOC90701	733	ACAAGCGCCAGCTCTATTACC
NM_033280	LOC90701	734	ACAGAGGAGACCTCCTGTTCC
NM_033280	LOC90701	735	ACCATATGTTGGTATGGTCAC
NM_032859	FLJ14906	736	ACGTGATGACTAGACCTGACC
NM_032859	FLJ14906	737	ACAATGACACATGGCAGTGCC
NM_018235	FLJ10830	738	ACCGTGTGCATTTACGGGCAC
NM_018235	FLJ10830	739	ACTTCAGTCACCCTCATTACC
NM_023112	FLJ21916	740	ACGTCGGCCTTCATCAGGAAC
NM_023112	FLJ21916	741	ACATCAAAGACTTCTGCACTC
NM_000094	COL7A1	742	ACAGTGCAGTACAGCGATGAC
NM_000094	COL7A1	743	ACCAAGTGACTGTGATTGCCC
NM_006660	CLPX	744	ACTCAGGCTGGATATGTAGGC
NM_006660	CLPX	745	ACTGAATGTTACTGAGGATGC
NM_002402	MEST	746	ACCGAGACCACATCACTATTC
NM_005632	SOLH	747	ACCTGGTCATGTGCCAAGTGC
NM_003652	CPZ	748	ACCTGACGTCCGAGTACTACC
NM_003652	CPZ	749	ACTTCACATCGCTGAGCACCC
NM_006732	FOSB	750	ACACCAGGCATGAGTGGCTAC
NM_006732	FOSB	751	ACGGCTTCTCTCTTTACACAC
NM_006732	FOSB	752	ACTTCTTCGTTTGTCTCACC
NM_003878	GGH	753	ACCGCCAAGAAGCCCATCATC
NM_004851	NAP1	754	ACAAGCCCATCTTCGTACCTC
NM_004851	NAP1	755	ACTGGGCGGGTAGATGGAATC
NM_004851	NAP1	756	ACGGCCCATGATTACGTCATC
NM_003710	SPINT1	757	ACTTCGTGTGCAAGTTTCGCGC
NM_003710	SPINT1	758	ACAGGACTCTGCAAGGAGAGC
NM_003710	SPINT1	759	ACGGAGCACCTGGTCTATAAC
NM_006012	CLPP	760	ACGACACGATGCAGTACATCC
NM_006012	CLPP	761	ACTCCCGTATCATGATCCACC
NM_002900	RBP3	762	ACATCATCTCCTACCTGCACC
NM_002900	RBP3	763	ACCTATGATCGCCGCACCAAC
NM_002900	RBP3	764	ACCTACCACGTGGATGACACC
NM_005133	RCE1	765	ACGTCTGGAAGAGCGAACTGC
NM_005133	RCE1	766	ACTGCTTTCCTCTTCATCCGC
NM_005133	RCE1	767	ACGCTATGAACTCTCACCGGC
NM_000537	REN	768	ACCAGCTCCATAGAGAAGCTC
NM_000537	REN	769	ACAGAGTTTGATCGGCGTAAC
NM_002792	PSMA7	770	ACTCCTGGAAGTGGTTTCAGTC
NM_000638	VTN	771	ACCGAGTCAATCTTCGCACAC
NM_025220	ADAM33	772	ACGAGATCTTTCGGATGGAGC
NM_025220	ADAM33	773	ACCATAACTGCCACTGTGCTC
NM_004654	USP9Y	774	ACATGAACTCTGTGATCCAGC
NM_004654	USP9Y	775	ACAGCCATATACAGGACCAGC

NM_001641	APEX	776	ACTCTCTCATCAATACTGGTC
NM_080648	APEX	776	ACTCTCTCATCAATACTGGTC
NM_080649	APEX	776	ACTCTCTCATCAATACTGGTC
NM_001641	APEX	777	ACCTAGCACTGTGACACCACC
NM_080648	APEX	777	ACCTAGCACTGTGACACCACC
NM_080649	APEX	777	ACCTAGCACTGTGACACCACC
NM_004652	USP9X	778	ACAGAATCAGACTTCATCGCC
NM_021906	USP9X	778	ACAGAATCAGACTTCATCGCC
NM_004652	USP9X	779	ACAGGCAGGGAAACATGAAGC
NM_021906	USP9X	779	ACAGGCAGGGAAACATGAAGC
NM_004652	USP9X	780	ACTCAGGCGACTACTTTACTC
NM_021906	USP9X	780	ACTCAGGCGACTACTTTACTC
NM_005857	ZMPSTE24	781	ACATGGCTTCAATCAACAGAC
NM_005857	ZMPSTE24	782	ACTGGTTGTTCTCAATGTGGC
NM_016155	MMP17	783	ACCTGTTTGCAGTGGCTGTCC
NM_016155	MMP17	784	ACAACATGACCAGAGCCGCTC
NM_004659	MMP23A	785	ACCTACAGGATCCTCTCCTTC
NM_006983	MMP23B	785	ACCTACAGGATCCTCTCCTTC
NM_032557	HP43.8KD	786	ACGAGCAGGTTTCCAAAGGAC
NM_032557	HP43.8KD	787	ACCCACCTCTACAGAAAGAAC
NM_007352	ELA3B	788	ACATCCTTCCCAACGAGACAC
NM_016280	LOC51716	789	ACCTTGTAACCTCCTATGTTT
NM_052830	GGTL3	790	ACTCCTTCCTGAAGTCTGCAC
NM_052830	GGTL3	791	ACGTGACTCATGATCTAGCCC
NM_052830	GGTL3	792	ACCCTGAAGATTGCATTAGCC
NM_130901	LOC161725	793	ACACACTTCAGCAAGAATGGC
NM_130901	LOC161725	794	ACGGATGTGAAGCTGAGCCTC
NM_001225	CASP4	795	ACTGAAGACAAAAGTTCGGGTC
NM_033306	CASP4	795	ACTGAAGACAAAAGTTCGGGTC
NM_033307	CASP4	795	ACTGAAGACAAAAGTTCGGGTC
NM_032236	FLJ23277	796	ACTCTACTTATGTCCAAGCAC
NM_032236	FLJ23277	797	ACTGTTTGCAACCAAGTGTGGC
NM_020398	SPINLW1	798	ACAAGATGTATGCGAAATGCC
NM_004656	BAP1	799	ACATGTTCTTTGCCACCAGC
NM_004656	BAP1	800	ACAAGTCTCAAGAGTCACAGC
NM_004656	BAP1	801	ACCCACAACACTACGATGAGTTC
NM_014375	FETUB	802	ACCCTGGATATTTCCCTTCCTC
NM_020241	SEMA6B	803	ACTCCAAGTGGTTCAAAGAGC
NM_032108	SEMA6B	803	ACTCCAAGTGGTTCAAAGAGC
NM_133327	SEMA6B	803	ACTCCAAGTGGTTCAAAGAGC
NM_032108	SEMA6B	804	ACGTCTGGGCTCAGTGTCTTC
NM_133327	SEMA6B	804	ACGTCTGGGCTCAGTGTCTTC
NM_052955	TGM7	805	ACGTACTATGACCGAAATGCC
NM_052955	TGM7	806	ACCTTAATGGTGGCTCTGAGC
NM_080830	CST11	807	ACTAGGTGTCCTGGAGTGTAC
NM_130794	CST11	807	ACTAGGTGTCCTGGAGTGTAC

NM_130794	CST11	808	ACTGACCACCTGGAGTATCAC
NG_000839	NG_000839	809	ACCTCAATGATGAGCGGGTAC
NM_001322	CST2	809	ACCTCAATGATGAGCGGGTAC
NM_000099	CST3	810	ACTACTTCTTGGACGTGGAGC
NG_000839	NG_000839	811	ACCTCAATGACAAGAGTGTGC
NM_001900	CST5	811	ACCTCAATGACAAGAGTGTGC
NG_000839	NG_000839	812	ACTGTCCCTTCAATGACCAGC
NM_001900	CST5	812	ACTGTCCCTTCAATGACCAGC
NM_005492	CST8	813	ACCTCTGTGACTACTTTATCC
NM_080610	CST9L	814	ACAGAGCAAGGACTACTATGC
NM_080610	CST9L	815	ACTCAGTTCAGCCTCCTGAAC
NM_006310	NPEPPS	816	ACAGTTTGAGGCTACTGATGC
NM_006310	NPEPPS	817	ACAGATTATTGAGGTTGTCCC
NM_005075	SLC21A3	818	ACGTGGAATGGGTGAAACTCC
NM_021094	SLC21A3	818	ACGTGGAATGGGTGAAACTCC
NM_134431	SLC21A3	818	ACGTGGAATGGGTGAAACTCC
NM_005075	SLC21A3	819	ACGGGAATAAACATGGTGTTC
NM_021094	SLC21A3	819	ACGGGAATAAACATGGTGTTC
NM_134431	SLC21A3	819	ACGGGAATAAACATGGTGTTC
NM_000628	IL10RB	820	ACATTCTACAGTGGGAGTCAC
NM_000628	IL10RB	821	ACCTTCTGTCTGTGGATGAC
NM_002794	PSMB2	822	ACTACACACCGACTATCTCAC
NM_002800	PSMB9	823	ACGAGCGCATCTACTGTGCAC
NM_002800	PSMB9	824	ACATGACAGGTGATCACGTAC
NM_006446	SLC21A6	825	ACTGCTTTGCCACATTTCTTC
NM_006446	SLC21A6	826	ACGTAGAGCAACAGTATGGTC
NM_006446	SLC21A6	827	ACTCAATGGTTATACGAGCAC
NM_018226	RNPEPL1	828	ACCTTCATCATCTCCTCCATC
NM_018226	RNPEPL1	829	ACGTCAATGTGTCTGCCTAGC
NM_024663	NPEPL1	830	ACACCCTGCAATGAGATGAAC
NM_024663	NPEPL1	831	ACCTTCCTCGAGGAGATTAAC
NM_001909	CTSD	832	ACCTACGTGAAGAATGGTACC
NM_001909	CTSD	833	ACAACCTGATGCAGCAGAAGC
NM_001909	CTSD	834	ACTGTGTTTGACCGTGACAAC
NM_005551	KLK2	835	ACAATATGAGCCTTCTGAAGC
NM_007282	RNF13	836	ACCAGAGAATGCCTGTGAACC
NM_007282	RNF13	837	ACTCTGACACAGACAGTAGTC
NM_003650	CST7	838	ACTTGTTCCCAGGACCTTAAC
NM_003650	CST7	839	ACGAACGACATGTTCTTGTTT
NM_003650	CST7	840	ACTGTGACTTCCAAACCAACC
NM_017509	KLK15	841	ACGCTTTAACTGTGGCGCTTC
NM_023006	KLK15	841	ACGCTTTAACTGTGGCGCTTC
NM_138563	KLK15	841	ACGCTTTAACTGTGGCGCTTC
NM_138564	KLK15	841	ACGCTTTAACTGTGGCGCTTC
NM_017509	KLK15	842	ACCGCAACGACATCATGTTGC
NM_023006	KLK15	842	ACCGCAACGACATCATGTTGC

NM_138563	KLK15	842	ACCGCAACGACATCATGTTGC
NM_138564	KLK15	842	ACCGCAACGACATCATGTTGC
NM_006200	PCSK5	843	ACGGATTTCATCAACATAGGAC
NM_006200	PCSK5	844	ACTCCCTCTCAGCTAAGGAAC
NM_006200	PCSK5	845	ACTGCCCTGATGGGTCATATC
NM_005213	CSTA	846	ACTTGGTACTTACTGGATACC
NM_020172	SPPL2B	847	ACCTCAGCAAGGCATCTTTCC
NM_020172	SPPL2B	848	ACGCAGTATGATGAGATTGGC
NM_020172	SPPL2B	849	ACATGCTGAAGACCATCCGTC
NM_139015	SPPL3	850	ACCAATAATTGGCTTCCAACC
NM_139015	SPPL3	851	ACGTTCTATCCCGGAAGCTCC
NM_139015	SPPL3	852	ACTGTGGCGTCTCGCATTAC
NM_022355	LOC64174	853	ACCACACTCAGTAGTCCCAGC
NM_022355	LOC64174	854	ACACTCAGAAATTGGCCTGCC
NM_022355	LOC64174	855	ACTGTGGCAGATCACTTCGAC
NM_031948	MPN	856	ACCTCTGAGACGTCCCTGTAC
NM_031948	MPN	857	ACACCGAGTTTGGCTACCAAC
NM_031948	MPN	858	ACTGGATCCATCGGATCATCC
NM_024922	FLJ21736	859	ACCTTCGAGATTCTGGAAGCC
NM_032324	MGC13186	860	ACTACCCGTCTTGAGGAATGC
NM_032929	MGC14793	861	ACTTGGCACAGACTTATACTC
NM_080920	GGTLA4	862	ACTGCTCACCTGTCTGTGGTC
NM_013325	Apg4B	863	ACGGACATCAACGAGGCCTAC
NM_030929	FKSG28	864	ACCTCTGTGTGCCTGTCTGTTT
NM_030929	FKSG28	865	ACCTCCAACAGGTTGTTTCCC
NM_030929	FKSG28	866	ACCAGGATTCTCCACTTCTTC
NM_002789	PSMA4	867	ACAGTATCAGGAGCCAATACC
NM_002789	PSMA4	868	ACTATGGCTTTTCAGCTCTATC
NM_002787	PSMA2	869	ACTTGGCTGCCATAGCATAAC
NM_006838	METAP2	870	ACATGTGCCAATAAGGCTTCC
NM_014300	SPC18	871	ACAAATCGAGTTGAAGATCCC
NM_014471	SPINK4	872	ACGAATGAATGCCAGCTCTGC
NM_014889	MP1	873	ACATCTGTTCCCGAGCTGTTC
NM_014889	MP1	874	ACATTGAGACCGTCAGAAGCC
NM_014889	MP1	875	ACTCACTTCCTGATGCCCTTC
NM_014968	MP1	875	ACTCACTTCCTGATGCCCTTC
NM_016014	LOC51104	876	ACGAGCAGACTGGCAGTATTC
NM_016014	LOC51104	877	ACTCTTCTCACATGGAAATGC
NM_016014	LOC51104	878	ACCGTCTGTGGATCTTGCTGC
NM_017659	FLJ20084	879	ACCCTTGCCCTGCCATTATGAC
NM_017659	FLJ20084	880	ACCCGTGCTCCATCTCATCTC
NM_017712	FLJ20208	881	ACCTGCATGTGTACGAGATTTC
NM_017712	FLJ20208	882	ACACTGGAGAAATGTGGACAC
NM_017712	FLJ20208	883	ACACCTCTTTGTACCAGAGTC
NM_001129	AEBP1	884	ACGACGAGATCGAGGAGTTCC
NM_001129	AEBP1	885	ACCACAGCTACAAGGACATGC

NM_001129	AEBP1	886	ACTGAGGAGGGCTTTGACATC
NM_001873	CPE	887	ACGGCATCTCCTTCGAGTACC
NM_001873	CPE	888	ACCAACGGTGGTGCTTGGTAC
NM_012100	DNPEP	889	ACCAGGAACTCCTCCACCATC
NM_012100	DNPEP	890	ACACAGAGATGCATCTAGTCC
NM_012100	DNPEP	891	ACAAGCATGAGGAGAACCACC
NM_139175	LOC168433	892	ACTGGAGTCTTTGGAAGAAGC
NM_139175	LOC168433	893	ACACATTGGACAACCTCCAAC
NM_139175	LOC168433	894	ACTGCCTGAAACCTTATCACC
NM_012105	BACE2	895	ACTTGGCCTAGCTTATGCCAC
NM_138991	BACE2	895	ACTTGGCCTAGCTTATGCCAC
NM_138992	BACE2	895	ACTTGGCCTAGCTTATGCCAC
NM_012105	BACE2	896	ACCAACGGAGGTAGTCTTGTC
NM_138991	BACE2	896	ACCAACGGAGGTAGTCTTGTC
NM_138992	BACE2	896	ACCAACGGAGGTAGTCTTGTC
NM_012105	BACE2	897	ACAATCCTGCCTCAGCTTTAC
NM_002769	PRSS1	898	ACTGGCACGAAGTGCCTCATC
NG_001337	NG_001337	899	ACATGTTCTGTGTGGGCTTCC
NM_002769	PRSS1	899	ACATGTTCTGTGTGGGCTTCC
NM_002770	PRSS2	899	ACATGTTCTGTGTGGGCTTCC
NM_002771	PRSS3	899	ACATGTTCTGTGTGGGCTTCC
NM_139000	TRY6	899	ACATGTTCTGTGTGGGCTTCC
NM_000193	SHH	900	ACTCCGAGCGATTTAAGGAAC
NM_000193	SHH	901	ACGAGTCCAAGGCACATATCC
NM_000193	SHH	902	ACTTCCTCACTTTCTCCTGGACC
NM_139025	ADAMTS13	903	ACCTGGTGAAGATGGTCATTC
NM_139026	ADAMTS13	903	ACCTGGTGAAGATGGTCATTC
NM_139027	ADAMTS13	903	ACCTGGTGAAGATGGTCATTC
NM_139028	ADAMTS13	903	ACCTGGTGAAGATGGTCATTC
NM_139025	ADAMTS13	904	ACCAGTGTCTACATTGCCAAC
NM_139026	ADAMTS13	904	ACCAGTGTCTACATTGCCAAC
NM_139027	ADAMTS13	904	ACCAGTGTCTACATTGCCAAC
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NM_139027	ADAMTS13	905	ACTTTCAGCTCCAAGACCAAC
NM_080722	ADAMTS14	906	ACCATGACCACGTTGTGTTCC
NM_139155	ADAMTS14	906	ACCATGACCACGTTGTGTTCC
NM_080722	ADAMTS14	907	ACCGCATTGTGGTGAAGAACC
NM_139155	ADAMTS14	907	ACCGCATTGTGGTGAAGAACC
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NM_139155	ADAMTS14	908	ACAAGATATCATCAACGGAGC
NM_005860	FSTL3	909	ACTGAGCGCCTGATTTAGGGC
NM_014263	YME1L1	910	ACCAGCATCGAGATGTAGTTC
NM_139312	YME1L1	910	ACCAGCATCGAGATGTAGTTC
NM_139313	YME1L1	910	ACCAGCATCGAGATGTAGTTC

NM_014263	YME1L1	911	ACCTGAAGCTCACCAAGATGC
NM_139312	YME1L1	911	ACCTGAAGCTCACCAAGATGC
NM_139313	YME1L1	911	ACCTGAAGCTCACCAAGATGC
NM_014263	YME1L1	912	ACCTATGAGACTTTGGATGCC
NM_139312	YME1L1	912	ACCTATGAGACTTTGGATGCC
NM_002774	KLK6	913	ACCATCCAGTGTGCATACATC
NM_005747	ELA3A	914	ACTCTGAGGAGCTGTTTGTGC
NM_005747	ELA3A	915	ACATCCTTCCCAACAAGACAC
NM_001948	DUT	916	ACGGACATTGAGATAGCGCTC
NM_001948	DUT	917	ACTATCAGCCCACTTGACCAC
NM_004205	USP2	918	ACCAACAACCTGCCTCAGCTAC
NM_004205	USP2	919	ACACTGAGACCTAAGTCCAAC
NM_004205	USP2	920	ACCAACCATGCTGTTTACAAC
NM_018561	DKFZP586D2223	921	ACTCAGTGTGGAGCCTGATCC
NM_024539	FLJ23516	922	ACAGCTGGTAAACCATGAAGC
NM_144691	MGC20576	923	ACCTCTGGAACCATGAACCTC
NM_144981	FLJ25059	924	ACCACTAGTCCATCAGATTTT
NM_015017	VDU1	925	ACTTAGGGCCAGAGGTCTTAC
NM_015017	VDU1	926	ACAATGGAAGAAGACAAGAGC
NM_015017	VDU1	927	ACGTTTATCGGCAAGCCCTCC
NM_000573	CR1	928	ACTCATTGGTTTCTCGTCTGC
NM_000651	CR1	928	ACTCATTGGTTTCTCGTCTGC
NM_000573	CR1	929	ACCCAAAGGGACAAGGACAAC
NM_000651	CR1	929	ACCCAAAGGGACAAGGACAAC
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NM_000651	CR1	930	ACCCAAACCAATGCATCTGAC
NM_004194	ADAM22	931	ACTCATGTTGACCAAGCAAGC
NM_016351	ADAM22	931	ACTCATGTTGACCAAGCAAGC
NM_021721	ADAM22	931	ACTCATGTTGACCAAGCAAGC
NM_021722	ADAM22	931	ACTCATGTTGACCAAGCAAGC
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NM_016351	ADAM22	932	ACGTGCTCAGGAAATTCAGC
NM_021721	ADAM22	932	ACGTGCTCAGGAAATTCAGC
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NM_021723	ADAM22	932	ACGTGCTCAGGAAATTCAGC
NM_016351	ADAM22	933	ACTGAGACTTTATCTCCTGCC
NM_021723	ADAM22	933	ACTGAGACTTTATCTCCTGCC
NM_007037	ADAMTS8	934	ACATCGGGACCATTGTGTGACC
NM_007037	ADAMTS8	935	ACACGAAGAATGGCAGCCTGC
NM_007037	ADAMTS8	936	ACAATGACATTGTCAACCATCC
NM_003816	ADAM9	937	ACAGTGTGTTCAAGGAGCCAC
NM_006799	PRSS21	938	ACATCAAAGAGGATGAGGCAC
NM_144956	PRSS21	938	ACATCAAAGAGGATGAGGCAC
NM_144957	PRSS21	938	ACATCAAAGAGGATGAGGCAC
NM_006799	PRSS21	939	ACTTTGAGTGGATCCAGAAGC

NM_144956	PRSS21	939	ACTTTGAGTGGATCCAGAAGC
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NM_013247	PRSS25	940	ACTGCAGAACACGATCACATC
NM_007173	SPUVE	941	ACGAAGAGGCCAAGCAATATC
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NM_144947	KLK11	942	ACCACCGCAATGACATCATGC
NM_145204	SENP8	943	ACTTTGCCAACAGTCAGTTTC
NM_145204	SENP8	944	ACCCACTGGAGTTTATTGGTC
NM_145204	SENP8	945	ACTGAGGCCTTGTGTGAGAAC
NM_032319	C2orf7	946	ACACAAGGTATGAGCAGATTTC
NM_032319	C2orf7	947	ACGGTTTCTTCATCCAGGACC
NM_032852	AUTL1	948	ACCTGCAGAGTCGGGATGTAC
NM_032852	AUTL1	949	ACTCTGAATCATGGACTTCCC
NM_032852	AUTL1	950	ACAGAGTGCTTCCATGACTTC
NM_017807	OSGEP	951	ACAGATGAAGTAGAGGTGACC
NM_022137	SMOC1	952	ACGAGTCCATGTGTGAGTACC
NM_021044	DHH	953	ACTCTACAAGCAATTTGTGCC
NM_021044	DHH	954	ACTGGGTCTACTACGAGTCCC
NM_021044	DHH	955	ACGCTGCTGGTGAACGATGTC
NM_005606	LGMN	956	ACTCTGAAGACAATCCCACTC
NM_005606	LGMN	957	ACACTGGAGAGGATGTTACCC
NM_005606	LGMN	958	ACCCACTGCTTCAACTGGCAC
NM_000484	APP	959	ACCAACTTGCATGACTACGGC
NM_000484	APP	960	ACGTCAAGCAAAGAACTTGCC
NM_000484	APP	961	ACACATGGCCAGAGTGGAAGC
NM_000484	APP	962	ACTGACCACTCGACCAGGTTC
NM_000484	APP	963	ACCATTGCTTCACTACCCATC
NM_001734	C1S	964	ACCTGTGGACTGTGGCATTCC
NM_001734	C1S	965	ACCAAATTCTACGCAGCTGGC
NM_025191	C1orf22	966	ACCCTGCTGATGAACATCATGC
NM_005700	DPP3	967	ACTCTGAGGTGACTTCCAAGC
NM_005700	DPP3	968	ACGTGATCTACGTGAACCTGGC
NM_017743	DPP8	969	ACATGATGGCTAAGGCACCAC
NM_130434	DPP8	969	ACATGATGGCTAAGGCACCAC
NM_130434	DPP8	970	ACTTAGATCGTGTGGGCATCC
NM_000131	F7	971	ACGGAGTACATGTTCTGTGCC
NM_019616	F7	971	ACGGAGTACATGTTCTGTGCC
NM_004341	CAD	972	ACACCAGCTATTGGCCTTAGC
NM_004341	CAD	973	ACACCATTGGTATCAGCCAGC
NM_014265	ADAM28	974	ACAGACTTCAGTTCCTGCAGC
NM_021777	ADAM28	974	ACAGACTTCAGTTCCTGCAGC
NM_021778	ADAM28	974	ACAGACTTCAGTTCCTGCAGC
NM_021778	ADAM28	975	ACCAATTGCTCATCCAAGTGC
NM_014265	ADAM28	976	ACCAATTGCTCATCTAAGTGC
NM_021777	ADAM28	977	ACCAGGTAGGAGGACAAATCC
NM_019029	CPVL	978	ACAGAAGTGTTTCCATGCCAC

NM_031311	CPVL	978	ACAGAAAGTGTTCATGCCAC
NM_019029	CPVL	979	ACTCTTTGTGGAACATGGGCC
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NM_019029	CPVL	980	ACTCCCAGAGGTGAGACAAGC
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NM_002257	KLK1	982	ACAGAGCCTGCTGATACCATC
NM_002257	KLK1	983	ACTTCATGCTGTGTGTCGGAC
NM_014893	KIAA0951	984	ACTACTCAGAAGGTCTCTTCC
NM_002776	KLK10	985	ACTCGCTCTGTTGTCCATCCC
NM_145888	KLK10	985	ACTCGCTCTGTTGTCCATCCC
NM_002776	KLK10	986	ACCTGCTCCAGCATCACTATC
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NM_002776	KLK10	987	ACAACATGATATGTGCTGGAC
NM_145888	KLK10	987	ACAACATGATATGTGCTGGAC
NM_015596	KLK13	988	ACCACGACCATGACATCATGC
NM_015596	KLK13	989	ACCCGTGTCTCAAGATACGTC
NM_001648	KLK3	990	ACTCAATTTCTCTGAGGACAC
NM_012427	KLK5	991	ACAAAGTGCTTGGTGTCTGGC
NM_147191	MMP21	992	ACGACGACGAGCACTTCACAC
NM_147191	MMP21	993	ACAGTGACAAGGATCAGGCCC
NM_147191	MMP21	994	ACAGAATTCCTGGCTTCCTGC
NM_006523	XPNPEP1	995	ACTTTGTGGACCTGAGCTTCC
NM_020383	XPNPEP1	995	ACTTTGTGGACCTGAGCTTCC
AF311940	AF311940	996	ACCAGACACTGAAGGAAATGC
AJ278348	HSA278348	996	ACCAGACACTGAAGGAAATGC
AF311940	AF311940	997	ACGTGGAGTGTAACAACATGC
AJ278348	HSA278348	997	ACGTGGAGTGTAACAACATGC
AF483215	AF483215	998	ACAGTACCAGCTGCTCTTCAC
AJ420895	HSA420895	998	ACAGTACCAGCTGCTCTTCAC
X59417	HSPROS27	999	ACAGAATGCTGAAATGAGGCC
X59417	HSPROS27	1000	ACCTGTGTGTTTGGTAACAAC
XM_043669	TRABID	1001	ACGCTTGCTGAATCGTCCCTC
XM_043669	TRABID	1002	ACAGCCTGCATGACTGTTAC
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XM_067027	LOC140038	1004	ACAATGGACTGAGCCTGAATC
XM_067027	LOC140038	1005	ACCTGCAGCAAGTCCATTGAC
XM_067027	LOC140038	1006	ACAGACACCACAACAGGAGAC
XM_065537	LOC130028	1007	ACTCTTATAGAGATGTGACGC
XM_068321	LOC133384	1008	ACCTGCCTTATGTCCAGAAAC
XM_068321	LOC133384	1009	ACGAACACAAGATGAGTGTGC
XM_065874	CPO	1010	ACAAGGAAGTGGTGACACAGC
XM_065874	CPO	1011	ACACTTGGACAACATGATCGTC
XM_065874	CPO	1012	ACCTTAGATATGGCCGTTGGC
XM_062003	LOC120332	1013	ACATCATAGGCATGACGATGC
XM_066484	LOC139116	1014	ACGAGGTAGAGGACAGCCTTC

XM_070928	LOC138482	1015	ACCATGTACCGAGAAGTGCGC
XM_061692	LOC119795	1016	ACAATATCTGTCAACCATCCC
XM_061692	LOC119795	1017	ACCTGAGAAGGCTTCCACTGC
XM_062575	LOC121302	1018	ACCACCTGGAGTTGGTTACAC
XM_062575	LOC121302	1019	ACCATCTCTAAAGGAACCTCGC
XM_062575	LOC121302	1020	ACGCCCCGAGTCTTACACAAC
XM_062734	LOC121656	1021	ACTTTGCAGCTCTCATAGCTC
XM_062734	LOC121656	1022	ACTATAGATATGGGCTTCAGC
XM_063398	LOC122985	1023	ACGGTTACTCGTGGATTATTC
XM_065124	LOC126502	1024	ACATAAGTCCTCACACCTTAC
XM_065124	LOC126502	1025	ACCAGTCCTCACACCTTACTC
XM_066005	C20orf137	1026	ACGTGAAGTAGCCTGTGTTGC
XM_066031	LOC128559	1027	ACAAACGGCATCCTTCCCTGC
XM_066924	LOC139853	1028	ACACCCACCAAGAACCTCTGC
XM_058785	LOC124221	1029	ACAGACTGGATTTCAGAGAACC
XM_060237	LOC126906	1030	ACTAGTGTGTACTATGTCGTC
XM_060237	LOC126906	1031	ACTGGAATTAGCAGATGAAGC
XM_060237	LOC126906	1032	ACTGATGTCAACCGCTTCACC
XM_087628	LOC153218	1033	ACTGGACCCTGATTACAATGC
XM_058378	LOC119180	1034	ACAGATGCGATTATCTGTGCC
XM_086031	LOC148066	1035	ACCTAGCAGCACACAGACAGC
XM_086031	LOC148066	1036	ACCACTGCAAATGCATTGACC
XM_086868	LOC257456	1037	ACGCTGATCACACTCCCATGC
XM_086868	LOC257456	1038	ACCCAGATCGCATCCACTTTC
XM_086138	LOC148293	1039	ACTTCTGTGATGTCTACTAC
XM_086138	LOC148293	1040	ACATTGTATTTGTGGGCCATC
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XM_061638	LOC119714	1042	ACTACTGGCTTCGCTTTTCATC
XM_061638	LOC119714	1043	ACTAGAGCAGCCATGTGTAGC
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XM_059364	LOC129526	1045	ACCCGGCATGTACAGGAGTTC
XM_059364	LOC129526	1046	ACATTTGTTTCCTGCAGGAAC
XM_055924	ADAM7	1047	ACGAGTTCCCATGCACCTGTC
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XM_070231	LOC137098	1049	ACTGAAACCCACACCAAGTGAC
XM_068418	LOC133590	1050	ACCTATGCCCCAACACTCTGTC
XM_064073	LOC124294	1051	ACTCAAAGAACACGCTCTACC
XM_060074	KIAA0951	1052	ACAGTATCCAGTTGTCAACAC
XM_060074	KIAA0951	1053	ACACCATTACCCAGTGAGATC
XM_068225	LOC133177	1054	ACGCTGTGGAATAAGGATGAC
XM_068000	LOC132722	1055	ACAGGATAGAGTGCTATGTGC
XM_068000	LOC132722	1056	ACTCTGGAGGACCACTAGTTC
XM_068002	LOC132724	1057	ACCACTAGCTTACCCTGATTC
XM_068002	LOC132724	1058	ACTCGAGTGACTTCTTATCGC
XM_087521	LOC152779	1059	ACTTCGGTTGTGTTTGTCTCC
XM_087521	LOC152779	1060	ACAAGCCCAATGACGTTGTCC

XM_087521	LOC152779	1061	ACCAACCAGATCACAGGTGCC
XM_087526	LOC152805	1062	ACCTCCAAGGCCAAAGAACTC
XM_086178	AGRN	1063	ACACACCAGATCAGCCTGCAC
XM_086178	AGRN	1064	ACAGCCAGGAGCATTGAGAGC
XM_086178	AGRN	1065	ACCACTTTGAACTGAGCCTGC
XM_086914	LOC150426	1066	ACAATGGCTCTTACGTGATTC
XM_070195	LOC137042	1067	ACCTCTGTGATGATTTGGCTC
XM_093962	LOC152697	1067	ACCTCTGTGATGATTTGGCTC
XM_172434	LOC253804	1067	ACCTCTGTGATGATTTGGCTC
XM_172437	LOC255606	1067	ACCTCTGTGATGATTTGGCTC
XM_172440	LOC255609	1067	ACCTCTGTGATGATTTGGCTC
XM_070195	LOC137042	1068	ACATCAACTGTTTCCACTGCC
XM_070195	LOC137042	1069	ACCTTTGACCCTTACCTGGAC
XM_059830	LOC136242	1070	ACCTCAAGTCTCACTTCAACC
XM_063287	LOC122706	1071	ACCTTCCTGCAGATCCATGGC
XM_063287	LOC122706	1072	ACTGGATCTCTGTGTGGCCAC
XM_063287	LOC122706	1073	ACGTGGAGTTACAGAAGCTCC
XM_027341	LOC89932	1074	ACCCACCCAGTGTTTAGCCTC
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XM_066522	LOC139171	1076	ACATCAATCACCAGTGTGTAC
XM_066522	LOC139171	1077	ACCGGCATTGTACTAGCAAAC
XM_066860	LOC139736	1078	ACTGCAAGGAACATGAGTTCC
XM_042698	USP22	1079	ACGGACAGTCTCAACAATGAC
XM_064383	LOC124975	1080	ACTTTGCCATGCTGATGGGAC
XM_064383	LOC124975	1081	ACTGCTCCTTTGGCTCTGCAC
XM_063846	LOC123788	1082	ACCAGGGATGTGTATCTGTAC
XM_063846	LOC123788	1083	ACCTGCTACCTGATGGCTGTC
XM_063846	LOC123788	1084	ACCTGCTACACGATGGCCATC
XM_092572	LOC165417	1085	ACAGTCAGACAATCATGGAGC
XM_108675	LOC157788	1086	ACAACGTGTGCTTTGGGAACCC
XM_108675	LOC157788	1087	ACCTGTGGAGGGTGTCTCTGC
XM_090337	LOC160507	1088	ACCCATCCTGAATACAACAGC
XM_090337	LOC160507	1089	ACAACCATGTGAAGGCATCAC
XM_090337	LOC160507	1090	ACCTGAAGGAATCAACAGAGC
XM_091358	LOC162106	1091	ACACCTCTGCCACCTCCTTAC
XM_092901	LOC164646	1092	ACTCGGGTCTTGGAACCATC
XM_092901	LOC164646	1093	ACCCATGAATTCCTACATGGC
XM_092483	LOC165262	1094	ACCGTTCATGTGTAAACGCAC
XM_092483	LOC165262	1095	ACACTGCACCAAGCAAGATGC
XM_092483	LOC165262	1096	ACCAGGGAGCAAATGTCAGTC
XM_166526	FLJ12697	1097	ACACCACCTCTTGCCAATTAC
XM_166526	FLJ12697	1098	ACAACAAGTTGCCTGTTCGCC
XM_166526	FLJ12697	1099	ACCCATGACCCTAAACGGTGC
XM_114325	USP19	1100	ACACCCATGGAGCATGTAACC
XM_114325	USP19	1101	ACCTGAGAACATTGGCTACCC
XM_114325	USP19	1102	ACTGCCCACAGTGCAAACAGC

XM_093373	LOC165693	1103	ACAGGCTGTCAGATCCCACAC
XM_092016	LOC163126	1104	ACTGCCTCTGAAGTTATCAAC
XM_092016	LOC163126	1105	ACACTACTTCAAGAGAACCTC
XM_091055	LOC145914	1106	ACGGCAAAGGCCTTCAGTTTC
XM_091055	LOC145914	1107	ACCTGTCATATAGGAGAGTGC
XM_091055	LOC145914	1108	ACCCGGTGCAATGCAACTATC
XM_096824	LOC145624	1109	ACACTTCCATAGACTTAGGCC
XM_090422	LOC160662	1110	ACAGTATGGTTGGTCTGCATC
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XM_090078	LOC160131	1112	ACAGAACATCTTTGTGGGTTC
XM_168015	LOC221191	1113	ACCATCATCATCCATGAGGAC
XM_168015	LOC221191	1114	ACACCACCAGTCTTGCAAGAC
NM_014157	HSPC065	1115	ACCAAGGTGGAAGACTACAGC
XM_168015	LOC221191	1115	ACCAAGGTGGAAGACTACAGC
XM_053531	FIBL-6	1116	ACAAGTTCTGGTCAAGTGTTT
XM_053531	FIBL-6	1117	ACACAGGTATAGGATGACCTC
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XM_061219	LOC118945	1119	ACTTCATGGATAATCCCTTCC
XM_166631	LOC219343	1119	ACTTCATGGATAATCCCTTCC
XM_066765	LOC139562	1120	ACTACAACCTCCGTGACACCGC
XM_067587	LOC131875	1121	ACCTGGTAATGCTGGCTTTCC
XM_067587	LOC131875	1122	ACTACCTATGGTCCTTGTTCC
XM_067587	LOC131875	1123	ACGCTGAAGTCCTATGCAGAC
XM_088514	LOC158219	1124	ACTTCAGAATTCAGGCAGCTC
XM_091623	LOC162540	1125	ACATGCTGGTCATCTTCATCC
XM_091623	LOC162540	1126	ACACTGGGCATTTCTACTGC
XM_091623	LOC162540	1127	ACTTGGATCCTAATGAGCTGC
XM_092184	LOC164832	1128	ACACAGCGGACATTGAATATC
XM_113763	DKFZP434I1735	1129	ACACAATCTTGGCACCACAGC
XM_113763	DKFZP434I1735	1130	ACAGCACTTCTCCTGATGTGC
XM_113763	DKFZP434I1735	1131	ACCAGCCTTCACTTCAGAGAC
XM_114040	LOC199858	1132	ACAGGCTAAGAAAGGAGTTGC
XM_114823	LOC205016	1133	ACCCTGAGTTCCCAGCATGTC
XM_115647	LOC199783	1134	ACACTTACCATGCTCTGCACC
XM_116753	LOC206841	1135	ACTGGCCTTGAATCTCTTCC
XM_116753	LOC206841	1136	ACATTGGTGGTGGGTTCTGAC
XM_116753	LOC206841	1137	ACCGTTGATAAACCTAACTGC
XM_116823	LOC206969	1138	ACTCTGATGTCTTCATGGGCC
XM_116823	LOC206969	1139	ACAGAATGGCGTCTTGTCGAC
XM_172791	LOC254584	1139	ACAGAATGGCGTCTTGTCGAC
XM_116823	LOC206969	1140	ACGAAGTAGCAACTCGAGCTC
XM_172791	LOC254584	1140	ACGAAGTAGCAACTCGAGCTC
XM_119439	LOC205174	1141	ACTGACACACTTGCTGGCCAC
XM_119439	LOC205174	1142	ACTGCAGCTTTGACAACAGCC
XM_119439	LOC205174	1143	ACATCCTCCATCCTTGGTTCC
XM_119808	LOC205081	1144	ACCACCAGTCGGTCTAGAGAC

XM_120869	LOC206100	1145	ACCATTCTGGTTCTCTTGGAC
XM_120869	LOC206100	1146	ACTTCCTGATTCCCACCTATC
XM_166942	LOC220369	1147	ACGCTGACGCTCGTCTACTTC
XM_167306	LOC222978	1148	ACACTGCTGTTACTGGCCAAC
XM_167306	LOC222978	1149	ACTGACCCAGAGCATGTTTAC
XM_167306	LOC222978	1150	ACTACCTCATCTGAGGCCACC
XM_167616	LOC219743	1151	ACCTTTGGAAAGAAGAGTGAC
XM_171147	LOC255779	1152	ACTCAAAGAACAGTGCAGGGC
XM_171147	LOC255779	1153	ACAATGATGAAGGCAGACCAC
XM_171300	LOC254639	1154	ACCCAGTGGTATGAGGTGAAC
XM_171300	LOC254639	1155	ACTCCAGAAGTGAACCTTACC
XM_171586	LOC256652	1156	ACATGGTGAGGATTGGAGAAC
XM_171629	LOC257238	1157	ACGTGGCCAGATCCTCATAGC
XM_171739	LOC253335	1158	ACAAGAGGGTGGTATGGATGC
XM_171739	LOC253335	1159	ACTTTGTCTGGGCTACATGCC
XM_171739	LOC253335	1160	ACTTGGAGGGTCTGTGATTTT
XM_171781	LOC257157	1161	ACGAAGGTGGTTGAGATCGTC
XM_171781	LOC257157	1162	ACCACACTGAGCGGTTTGAGC
XM_171781	LOC257157	1163	ACCTATTTCATCTGGGTCGGC
XM_171997	LOC253005	1164	ACTCTAACAGGACAACCTCGC
XM_171997	LOC253005	1165	ACATGCCACTCCACCTGAAAC
XM_171997	LOC253005	1166	ACAGGATCTAATAACCCTTCC
XM_172410	LOC255555	1167	ACTGGAGAGATGATGGAGGCC
XM_172437	LOC255606	1168	ACAAGTGTGGGATGAAGAACC
XM_172440	LOC255609	1168	ACAAGTGTGGGATGAAGAACC
XM_172524	LOC256138	1169	ACTGTGGTGAGTTCCAGGACC
NG_001333	NG_001333	1170	ACCACGAAGACCTTCATCTTC
XM_172637	LOC254737	1170	ACCACGAAGACCTTCATCTTC
NG_001333	NG_001333	1171	ACCTGTCAGACGAATGCTGTC
XM_172637	LOC254737	1171	ACCTGTCAGACGAATGCTGTC
XM_172713	LOC254580	1172	ACTTCTGCGATGATTTGGCGC
XM_172713	LOC254580	1173	ACAAACACTGCAAGAGGGCTC
XM_172789	LOC254989	1174	ACCAGGGTCACCTACTTCATC
XM_173817	LOC254333	1175	ACCGACTCCCTTTATGGAGGC
XM_173817	LOC254333	1176	ACGCAGATGAACACGCGGTTT
XM_174302	LOC254190	1177	ACCTGGTTCTTTCAGGCTCTCC
XM_174302	LOC254190	1178	ACAAGGGTCAATCTCTTTGCC
XM_174302	LOC254190	1179	ACATTCTCTACGCTGTCTTTC
ENSG00000117094	ENSG00000117094	1180	ACAAGTTCCCGAACGATCACC
ENSG00000117094	ENSG00000117094	1181	ACAAGTGTGAGCTGCTTCCGC
ENSG00000117094	ENSG00000117094	1182	ACCTAGCAGAGCTTCTCTCCC
ENSG00000115257	ENSG00000115257	1183	ACCAGCCATCTTCTGTGGTTC
ENSG00000115257	ENSG00000115257	1184	ACACCAACAGCATCCACACGC
ENSG00000115257	ENSG00000115257	1185	ACTCCTGACCTCAGACAACAC
ENSG00000170967	ENSG00000170967	1186	ACGATGCTCTACATTAAGTGC
ENSG00000145784	ENSG00000145784	1187	ACGTGTGCCATATTGGTGTGC

ENSG00000145784	ENSG00000145784	1188	ACTCCTAATCATCTCTAACCC
ENSG00000145784	ENSG00000145784	1189	ACTGGCCATTCAAGCAATAGC
ENSG00000175194	ENSG00000175194	1190	ACATTTGTTTCGGCATAGCTGC
NM_000041	APOE	1191	ACCATGAAGGAGTTGAAGGCC
NM_000041	APOE	1192	ACAAATCGGAACTGGAGGAAC
NM_000247	MICA	1193	ACCAGAGACTTGACAGGGAAC
NM_000247	MICA	1194	ACCCTGGCTCATATCAAGGAC
NM_000247	MICA	1195	ACACTATCACGCTATGCATGC
NM_000247	MICA	1196	ACAGCGGGAATCACAGCACTC
NM_000270	NP	1197	ACTTTCCTCGAAGTACAGTGC
NM_000270	NP	1198	ACCTTTCCTCACTTTCTTCTAC
NM_000305	PON2	1199	ACCGGCACATTTCTATGCCAC
NM_000305	PON2	1200	ACAGAGCCTTGTATTGTGAAC
NM_000362	TIMP3	1201	ACCGAGGCTTCACCAAGATGC
NM_000362	TIMP3	1202	ACCGACATGCTCTCCAATTTC
NM_000382	ALDH3A2	1203	ACTGATAGGAGCCATCGCTGC
NM_000382	ALDH3A2	1204	ACCTGGACATTGTTTGCAGAC
NM_000382	ALDH3A2	1205	ACCAATTCTTCCAATAGTGCC
NM_000382	ALDH3A2	1206	ACGGATGATTGATGAGACATC
NM_000418	IL4R	1207	ACGTGTATCCCTGAGAACAAC
NM_000418	IL4R	1208	ACCAAGTGGCACAACCTCTAC
NM_000418	IL4R	1209	ACACCTGGAGGAAGTAGAACC
NM_000418	IL4R	1210	ACCTGAAACAGTGTCTATGGCC
NM_000852	GSTP1	1211	ACCTGTACCAGTCCAATACC
M24902	HUMPAPA	1212	ACAAGGATTTGGCCAACTCAC
NM_001099	ACPP	1212	ACAAGGATTTGGCCAACTCAC
NM_001099	ACPP	1213	ACACTACTGTGAGTGGCCTAC
M24902	HUMPAPA	1214	ACTCCTTCCTCCCTATGCTTC
NM_001099	ACPP	1214	ACTCCTTCCTCCCTATGCTTC
NM_001099	ACPP	1215	ACGGAGTGTATGACCACAAAC
NM_001152	SLC25A5	1216	ACACTGCAAAGGGAATGCTTC
NM_001152	SLC25A5	1217	ACATCATGTACACAGGCACGC
NM_001634	AMD1	1218	ACAAGCAGGAAGCTTATGTAC
NM_001634	AMD1	1219	ACAGTGGGTTTGACTCAATTC
NM_001634	AMD1	1220	ACCAGGTTCTGTCTATTGATGC
NM_001634	AMD1	1221	ACCTCCTATGATGACCTGATC
NM_001676	ATP12A	1222	ACGCCTGAGATCGTCAAGTTC
NM_001676	ATP12A	1223	ACTGACCCAGAACAGGATGAC
NM_001676	ATP12A	1224	ACTGGCATGGAGCTGAAGGAC
NM_001677	ATP1B1	1225	ACATATCAGGACCGAGTGGCC
NM_001677	ATP1B1	1226	ACTTATGGCTACAAAGAGGGC
NM_001677	ATP1B1	1227	ACCATGGACACTGAAATTCGC
NM_002068	GNA15	1228	ACCACGTTTGAGAAGCGCTAC
NM_002068	GNA15	1229	ACCACTGGCATCAACGAGTAC
NM_002068	GNA15	1230	ACGAGATCAACCTGCTGTGAC
NM_002079	GOT1	1231	ACCTGGGAGTGGGAGCATATC

NM_002080	GOT2	1232	ACCGGGATGATAATGGAAAGC
NM_002080	GOT2	1233	ACCATTCTCTGGAACTGGAGCC
NM_002080	GOT2	1234	ACCTTGCCCATGCCATTCCACC
NM_002455	MTX1	1235	ACCAGTCATGGAGAGGTCATC
NM_002455	MTX1	1236	ACATGGAACGGCTACAGCTGC
NM_002455	MTX1	1237	ACCCACATTCTCAGTCTCTAC
NM_002462	MX1	1238	ACAATCAGCCTGGTGGTGGTC
NM_002629	PGAM1	1239	ACATCTGCTTCACCTCAGTGC
NM_002629	PGAM1	1240	ACAGCAACATCAGTAAGGATC
NM_002629	PGAM1	1241	ACCTCACAGAAGATCAGCTAC
NM_002715	PPP2CA	1242	ACCAAGCTGCAATCATGGAAC
NM_002962	S100A5	1243	ACTATGGTGACCACGTTTCAC
NM_003129	SQLE	1244	ACAGTGGAAAGGTCTTGATGCC
NM_003129	SQLE	1245	ACTGGAGATATCAAGGAAGTC
NM_003129	SQLE	1246	ACTTACTGGTGGAGGAATGAC
NM_003132	SRM	1247	ACCAGGAGATGATCGCCAACC
NM_003132	SRM	1248	ACTCTAGCTCGAAGGTGACCC
NM_003132	SRM	1249	ACCAGCTCATGAAGACAGCCC
NM_003246	THBS1	1250	ACGGCCAACAACAGGTGTGC
NM_003345	UBE2I	1251	ACCAAATATCCAAGACCCAGC
NM_003345	UBE2I	1252	ACAAGCCAAGAAGTTTGCGCC
NM_003364	UP	1253	ACCTTAACAAGAAGCTGGTGC
NM_004000	CHI3L2	1254	ACCTCCTGTCTTTGACTTCC
NM_004000	CHI3L2	1255	ACTGGATACATAAGGGAATGC
NM_004358	CDC25B	1256	ACGAGCAGTTTGCCATCAGAC
NM_021872	CDC25B	1256	ACGAGCAGTTTGCCATCAGAC
NM_021873	CDC25B	1256	ACGAGCAGTTTGCCATCAGAC
NM_021874	CDC25B	1256	ACGAGCAGTTTGCCATCAGAC
NM_004358	CDC25B	1257	ACTGTGAATTCTCATCTGAGC
NM_021872	CDC25B	1257	ACTGTGAATTCTCATCTGAGC
NM_021873	CDC25B	1257	ACTGTGAATTCTCATCTGAGC
NM_021874	CDC25B	1257	ACTGTGAATTCTCATCTGAGC
NM_004358	CDC25B	1258	ACAAGGAGTTCTTCCCTCAGC
NM_021872	CDC25B	1258	ACAAGGAGTTCTTCCCTCAGC
NM_021873	CDC25B	1258	ACAAGGAGTTCTTCCCTCAGC
NM_021874	CDC25B	1258	ACAAGGAGTTCTTCCCTCAGC
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NM_004730	ETF1	1260	ACAAATTCACTGTGGATCTCC
NM_004730	ETF1	1261	ACAAAGAGACCGGACAGGAAC
NM_005116	SLC23A1	1262	ACAGAACACATCTGGTATCCC
NM_005116	SLC23A1	1263	ACAGCTGTTGGCCTCTCTAAC
NM_005729	PPIF	1264	ACGAGAACTTTTACACTGAAGC
NM_005729	PPIF	1265	ACAGACTGTGGCCAGTTGAGC
NM_005729	PPIF	1266	ACTCCACTGTCACAGTGTGCC
NM_006198	PCP4	1267	ACCAGAGACAGAACGTGCAGC
NM_006198	PCP4	1268	ACACCCTAGAGAGAAGTCATC

NM_006198	PCP4	1269	ACACACGCATAGCAAACCTCC
NM_012319	LIV-1	1270	ACCATGAGCATCACTCAGACC
NM_012319	LIV-1	1271	ACACTGTCTCTGAAGGAATC
NM_014226	RAGE	1272	ACCTACGAGAGATCCAAGCAC
NM_014226	RAGE	1273	ACACGGAATACATCTCCACCC
NM_014226	RAGE	1274	ACTGATGGGTTCTACACGTAC
NM_014226	RAGE	1275	ACCCCTGAAGTGCATCCCTGC
NM_000021	PSEN1	1276	ACAGCCAGTGGAGACTGGAAC
NM_007318	PSEN1	1276	ACAGCCAGTGGAGACTGGAAC
NM_007319	PSEN1	1276	ACAGCCAGTGGAGACTGGAAC
NM_000021	PSEN1	1277	ACGACAGACGGAGCCTTG GCC
NM_007318	PSEN1	1277	ACGACAGACGGAGCCTTG GCC
NM_007319	PSEN1	1277	ACGACAGACGGAGCCTTG GCC
NM_000021	PSEN1	1278	ACAGGTGCTATAAGGTCATCC
NM_007318	PSEN1	1278	ACAGGTGCTATAAGGTCATCC
NM_007319	PSEN1	1278	ACAGGTGCTATAAGGTCATCC
NM_000021	PSEN1	1279	ACCTATAACGTTGCTGTGGAC
NM_007318	PSEN1	1279	ACCTATAACGTTGCTGTGGAC
NM_007319	PSEN1	1279	ACCTATAACGTTGCTGTGGAC
NM_000021	PSEN1	1280	ACTTCGTATGCTGGTTGAAAC
NM_007318	PSEN1	1280	ACTTCGTATGCTGGTTGAAAC
NM_007319	PSEN1	1280	ACTTCGTATGCTGGTTGAAAC
NM_000396	CTSK	1281	ACCCACAGGAAGCAATATAAC
NM_000396	CTSK	1282	ACCTGAAGTATATTTCCATCC
NM_000396	CTSK	1283	ACATATGAACTGGCTATGAAC
NM_000396	CTSK	1285	ACGCCTGTGGCATTGCCAACC
NM_001065	TNFRSF1A	1286	ACCTTCACCTCCAGCTCCACC
NM_001065	TNFRSF1A	1287	ACTGTCCCAACTTTGCGGCTC
NM_001065	TNFRSF1A	1288	ACCAAGTGCCACAAAGGAACC
NM_001065	TNFRSF1A	1289	ACCTCTCCTGCCAGGAGAAAC
NM_001065	TNFRSF1A	1290	ACCAACGGTGGAAGTCCAAGC
NM_001110	ADAM10	1291	ACCACAGACTTCTCCGGAATC
NM_001110	ADAM10	1292	ACACTGGAATTATTACTGTTC
NM_001110	ADAM10	1293	ACAATGTGGATTCAATTACACC
NM_001110	ADAM10	1294	ACTCTGCCATTTCACTCTGTC
NM_001110	ADAM10	1295	ACCTCAAGAAGAACATGCTGC
NM_001278	CHUK	1296	ACAGCTGCGTAAAGTGTGGGC
NM_001278	CHUK	1297	ACGTCTGTCTGTACCAGCATC
NM_001278	CHUK	1298	ACTGTTCTGGAGGAGATCTCC
NM_001278	CHUK	1299	ACTTGATGGAATCTCTGGAAC
NM_001278	CHUK	1300	ACTCCCTAAGGTGGAAGTGGC
NM_002355	M6PR	1301	ACAGTGGTAGGGAGACTCAAC
NM_002355	M6PR	1302	ACAACCACTGTGGCAAGGAGC
NM_002355	M6PR	1303	ACTGTGGCAAGGAGCAGCGTC
NM_002355	M6PR	1304	ACTTAGCCTTCTGGCAGGATC
NM_002355	M6PR	1305	ACCTCGAAATGTGCCTGCAGC

NM_004348	RUNX2	1306	ACTTCCTGTGCTCGGTGCTGC
NM_004348	RUNX2	1307	ACCAGATGGGACTGTGGTTAC
NM_004348	RUNX2	1308	ACCTTGACCATAACCGTCTTC
NM_004348	RUNX2	1309	ACCATGGTGGAGATCATCGCC
NM_004348	RUNX2	1310	ACAAGGACAGAGTCAGATTAC
NM_005037	PPARG	1311	ACTACTGTTGACTTCTCCAGC
NM_015869	PPARG	1311	ACTACTGTTGACTTCTCCAGC
NM_138711	PPARG	1311	ACTACTGTTGACTTCTCCAGC
NM_138712	PPARG	1311	ACTACTGTTGACTTCTCCAGC
NM_005037	PPARG	1312	ACCTGAAACTTCAAGAGTACC
NM_015869	PPARG	1312	ACCTGAAACTTCAAGAGTACC
NM_138711	PPARG	1312	ACCTGAAACTTCAAGAGTACC
NM_138712	PPARG	1312	ACCTGAAACTTCAAGAGTACC
NM_005037	PPARG	1313	ACAATAAGCCTCATGAAGAGC
NM_015869	PPARG	1313	ACAATAAGCCTCATGAAGAGC
NM_138711	PPARG	1313	ACAATAAGCCTCATGAAGAGC
NM_138712	PPARG	1313	ACAATAAGCCTCATGAAGAGC
NM_005037	PPARG	1314	ACAGATGTGATCTTAAGTGTC
NM_015869	PPARG	1314	ACAGATGTGATCTTAAGTGTC
NM_138711	PPARG	1314	ACAGATGTGATCTTAAGTGTC
NM_138712	PPARG	1314	ACAGATGTGATCTTAAGTGTC
NM_005037	PPARG	1315	ACAACAGACAAATCACCATT
NM_015869	PPARG	1315	ACAACAGACAAATCACCATT
NM_138711	PPARG	1315	ACAACAGACAAATCACCATT
NM_138712	PPARG	1315	ACAACAGACAAATCACCATT
NM_012104	BACE	1316	ACTCGCTGTACACAGGCAGTC
NM_138971	BACE	1316	ACTCGCTGTACACAGGCAGTC
NM_138972	BACE	1316	ACTCGCTGTACACAGGCAGTC
NM_138973	BACE	1316	ACTCGCTGTACACAGGCAGTC
NM_012104	BACE	1317	ACCACCAACCTTCGTTTGCCC
NM_138971	BACE	1317	ACCACCAACCTTCGTTTGCCC
NM_138972	BACE	1317	ACCACCAACCTTCGTTTGCCC
NM_138973	BACE	1317	ACCACCAACCTTCGTTTGCCC
NM_012104	BACE	1318	ACCATCCTTCCGCAGCAATAC
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NM_138973	BACE	1318	ACCATCCTTCCGCAGCAATAC
NM_012104	BACE	1319	ACTTTGCAGTGGGTGCTGCCC
NM_138971	BACE	1319	ACTTTGCAGTGGGTGCTGCCC
NM_138972	BACE	1319	ACTTTGCAGTGGGTGCTGCCC
NM_138973	BACE	1319	ACTTTGCAGTGGGTGCTGCCC
NM_012104	BACE	1320	ACTGAATCAGACAAGTTCTTC
NM_138972	BACE	1320	ACTGAATCAGACAAGTTCTTC
NM_000346	SOX9	1321	ACGGCTCCAGCAAGAACAAGC
NM_000346	SOX9	1322	ACGGAGCAGACGCACATCTCC
NM_000346	SOX9	1323	ACGCCATCTTCAAGGCGCTGC

NM_000346	SOX9	1324	ACGAGTTTGACCAGTACCTGC
NM_000346	SOX9	1325	ACGTGTGGATGTCCAAGCAGC
AF031416	AF031416	1326	ACAATCAGGAAACAGGTGAGC
BC006231	BC006231	1326	ACAATCAGGAAACAGGTGAGC
SK176	IKKb	1326	ACAATCAGGAAACAGGTGAGC
XM_032491	IKBKB	1326	ACAATCAGGAAACAGGTGAGC
AF031416	AF031416	1327	ACCTTGCTGAGTGACATTGCC
BC006231	BC006231	1327	ACCTTGCTGAGTGACATTGCC
SK176	IKKb	1327	ACCTTGCTGAGTGACATTGCC
XM_032491	IKBKB	1327	ACCTTGCTGAGTGACATTGCC
AF031416	AF031416	1328	ACTGGAGCAGCAGAAGTACAC
BC006231	BC006231	1328	ACTGGAGCAGCAGAAGTACAC
SK176	IKKb	1328	ACTGGAGCAGCAGAAGTACAC
XM_032491	IKBKB	1328	ACTGGAGCAGCAGAAGTACAC
AF031416	AF031416	1329	ACTACTGGAGCTTCGGCACCC
BC006231	BC006231	1329	ACTACTGGAGCTTCGGCACCC
SK176	IKKb	1329	ACTACTGGAGCTTCGGCACCC
XM_032491	IKBKB	1329	ACTACTGGAGCTTCGGCACCC
AF031416	AF031416	1330	ACAGTGTCTTGCTGAGCGAC
SK176	IKKb	1330	ACAGTGTCTTGCTGAGCGAC
XM_032491	IKBKB	1330	ACAGTGTCTTGCTGAGCGAC
NM_000516	GNAS	1332	ACAGATCGACGTGATCAAGC
NM_016592	GNAS	1332	ACAGATCGACGTGATCAAGC
NM_080425	GNAS	1332	ACAGATCGACGTGATCAAGC
NM_080426	GNAS	1332	ACAGATCGACGTGATCAAGC
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BC011399	BC011399	1336	ACGTCTGCCTCCTCAAGAAGC
NM_003177	SYK	1336	ACGTCTGCCTCCTCAAGAAGC
SK363	SYK	1336	ACGTCTGCCTCCTCAAGAAGC
Z29630	HSSYKPTK	1336	ACGTCTGCCTCCTCAAGAAGC
BC011399	BC011399	1337	ACCATGCAGCAGCTGGACAAC
NM_003177	SYK	1337	ACCATGCAGCAGCTGGACAAC
SK363	SYK	1337	ACCATGCAGCAGCTGGACAAC
Z29630	HSSYKPTK	1337	ACCATGCAGCAGCTGGACAAC
BC011399	BC011399	1338	ACTTGTGCACAGAGATCTGGC

NM_003177	SYK	1338	ACTTGTGCACAGAGATCTGGC
SK363	SYK	1338	ACTTGTGCACAGAGATCTGGC
Z29630	HSSYKPTK	1338	ACTTGTGCACAGAGATCTGGC
BC011399	BC011399	1339	ACACTACTACAAGGCCAGAC
NM_003177	SYK	1339	ACACTACTACAAGGCCAGAC
SK363	SYK	1339	ACACTACTACAAGGCCAGAC
Z29630	HSSYKPTK	1339	ACACTACTACAAGGCCAGAC
BC011399	BC011399	1340	ACAGGAGAGCGGATGGGGTGC
NM_003177	SYK	1340	ACAGGAGAGCGGATGGGGTGC
SK363	SYK	1340	ACAGGAGAGCGGATGGGGTGC
Z29630	HSSYKPTK	1340	ACAGGAGAGCGGATGGGGTGC
NM_001401	EDG2	1341	ACTCGGAGACTGACTGTTAGC
NM_000516	GNAS	1342	ACCGATGTGACTGCCATCATC
NM_016592	GNAS	1342	ACCGATGTGACTGCCATCATC
NM_080425	GNAS	1342	ACCGATGTGACTGCCATCATC
NM_080426	GNAS	1342	ACCGATGTGACTGCCATCATC
AF031416	AF031416	1343	ACCTTAAAGCTGGTTCATATC
SK176	IKKb	1343	ACCTTAAAGCTGGTTCATATC
XM_032491	IKBKB	1343	ACCTTAAAGCTGGTTCATATC
AF031416	AF031416	1344	ACAGAATCATCCATCGGGATC
BC006231	BC006231	1344	ACAGAATCATCCATCGGGATC
SK176	IKKb	1344	ACAGAATCATCCATCGGGATC
XM_032491	IKBKB	1344	ACAGAATCATCCATCGGGATC
AF031416	AF031416	1345	ACCGTCGACTACTGGAGCTTC
BC006231	BC006231	1345	ACCGTCGACTACTGGAGCTTC
SK176	IKKb	1345	ACCGTCGACTACTGGAGCTTC
XM_032491	IKBKB	1345	ACCGTCGACTACTGGAGCTTC
NM_005037	PPARG	1346	ACTACTGTTGACTTCTCCAGC
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NM_138711	PPARG	1346	ACTACTGTTGACTTCTCCAGC
NM_138712	PPARG	1346	ACTACTGTTGACTTCTCCAGC
NM_005037	PPARG	1347	ACTTGAACGACCAAGTAACTC
NM_015869	PPARG	1347	ACTTGAACGACCAAGTAACTC
NM_138711	PPARG	1347	ACTTGAACGACCAAGTAACTC
NM_138712	PPARG	1347	ACTTGAACGACCAAGTAACTC
NM_005037	PPARG	1348	ACATTCAAGACAACCTGCTAC
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NM_138711	PPARG	1348	ACATTCAAGACAACCTGCTAC
NM_138712	PPARG	1348	ACATTCAAGACAACCTGCTAC
NM_002355	M6PR	1349	ACGGAAGTAATTGGATCATGC
NM_004348	RUNX2	1350	ACCCGCACCATGGTGGAGATC
NM_000478	ALPL	1351	ACCGAGATGCCCCCTGAGGCC
NM_004573	PLCB2	1352	ACTCGCTTTGGGAAGTTTGCC
NM_004573	PLCB2	1353	ACTTCTTACCATGCTAAGGCC
NM_004573	PLCB2	1354	ACATGACGCAGCCACTCAATC
NM_004573	PLCB2	1355	ACTTCCAGACGATGGACTTGC

NM_004573	PLCB2	1356	ACTAACTCCATCAATCCTGTC
AF258451	AF258451	1357	ACCTTCTAGAATGTGCCTGGC
NM_000125	ESR1	1357	ACCTTCTAGAATGTGCCTGGC
NM_001437	ESR2	1358	ACAAGGGCATGGAACATCTGC
NM_018417	SAC	1359	ACTGCAATGACTGAGAAGTTC
NM_018417	SAC	1360	ACCTCACAAGTGGTGTGACAG
NM_018417	SAC	1361	ACAAGCTCATAATGGGACACC
NM_001438	ESRRG	1362	ACAGTTCAACCATGAATGGCC
NM_001438	ESRRG	1363	ACAGCCCATACCTGAACCCCTC
NM_001438	ESRRG	1364	ACCAGTCCAAATTAGCAGGCC
NM_000720	CACNA1D	1365	ACATCTTCACCAACCTCATCC
NM_000720	CACNA1D	1366	ACGGCTCTTAAGATCAAGACC
NM_000719	CACNA1C	1367	ACATACCCAATGCTCTCCCTC
NM_000582	SPP1	1368	ACAGTAGACACATATGATGGC
NM_017442	TLR9	1369	ACCAGCCTTTTCCTTGTCCTCC
NM_138688	TLR9	1369	ACCAGCCTTTTCCTTGTCCTCC
NM_017442	TLR9	1370	ACCCACCTGTCACTCAAGTAC
NM_138688	TLR9	1370	ACCCACCTGTCACTCAAGTAC
NM_002210	ITGAV	1371	ACGCAGTCCCATCTCAAATCC
NM_002210	ITGAV	1372	ACCAACTCCACATTGGTTACC
NM_016584	IL23A	1373	ACAGAAGCTCTGCACACTGGC
NM_016584	IL23A	1374	ACAACAGTCAGTTCTGCTTGC
NM_016584	IL23A	1375	ACTGGGAGACTCAGCAGATTC
NM_016584	IL23A	1376	ACTCAGCAGATTCCAAGCCCTC
NM_000965	RARB	1377	ACAGGCCTTCTCAGTGCCATC
NM_016152	RARB	1377	ACAGGCCTTCTCAGTGCCATC
NM_021005	NR2F2	1378	ACATACGGATCTTCCAAGAGC
NM_021005	NR2F2	1379	ACTGGCCGTATATGGCAATTC
NM_000475	NR0B1	1380	ACTAGCTCAAAGCAAACGCAC
NM_000475	NR0B1	1381	ACGCTGCGCTTCGTCAAGTAC
NM_016346	NR2E3	1382	ACCCACTCATCTGTCCCTGAC
NM_021969	NR0B2	1383	ACAGTGGCCCTTCCTCAGGAAC
NM_021724	NR1D1	1384	ACAACCTCCAATGGCAGCTTCC
XM_051522	RDC1	1385	ACCTACTACCTGAAGACCGTC
XM_051522	RDC1	1386	ACTACATCCCTTTTCACCTGCC
NM_002831	PTPN6	1397	ACTACCAGTACCTGAGCTGGC
NM_080548	PTPN6	1397	ACTACCAGTACCTGAGCTGGC
NM_080549	PTPN6	1397	ACTACCAGTACCTGAGCTGGC
NM_000176	NR3C1	1399	ACAGACCAAAGCACCTTTGAC
XM_051522	RDC1	1400	ACGTGCAAAGTCACACACCTC
NM_000176	NR3C1	1401	ACCTGGATGACCAAATGACCC
NM_000901	NR3C2	1402	ACATGCTAGCAATGTGGGCTC
NM_000901	NR3C2	1403	ACTGTGGGATCTATCTGTAGC
NM_000926	PGR	1404	ACGGTGATGGATTTTCATCCAC
NM_000926	PGR	1405	ACAGCTTCGAGTCATTACCTC
NM_000964	RARA	1406	ACGTGTCAACCGGGACAAGAAC

NM_000964	RARA	1407	ACCGACCTGGTCTTTGCCTTC
L27586	HUMTR4OR	1408	ACACTGGCAAATGTAGTGACC
NM_003298	NR2C2	1408	ACACTGGCAAATGTAGTGACC
U10990	HSU10990	1408	ACACTGGCAAATGTAGTGACC
L27586	HUMTR4OR	1409	ACTGGCAAATGTAGTGACCTC
NM_003298	NR2C2	1409	ACTGGCAAATGTAGTGACCTC
U10990	HSU10990	1409	ACTGGCAAATGTAGTGACCTC
NM_005036	PPARA	1410	ACCAGTATTTAGGAAGCTGTC
NM_006186	NR4A2	1411	ACAGCTCCGATTTCTTAACCTC
NM_017532	HSAJ2425	1412	ACAGGAGGAAAGATGGCGTAC
NM_006981	NR4A3	1413	ACACCAAGCTGACCATGGACC
NM_006981	NR4A3	1414	ACTGCCCAGTAGACAAGAGAC
NM_006981	NR4A3	1415	ACTTTCCATCAGGTCAAACAC
NM_000461	THRB	1416	ACACTGAAGTAGCCCTCCTTC
NM_005123	NR1H4	1417	ACAGAACCTGGAAGTGGAACC
NM_005123	NR1H4	1418	ACAGTGAAGGTCGTGACTTGC
NM_004451	ESRRA	1419	ACTAAAGGCCTTGGCCCTTGC
NM_134260	RORA	1420	ACTCCATCAGTGTATCCTGTC
NM_002943	RORA	1421	ACCCAGACATTGTGCGACTTC
NM_134260	RORA	1421	ACCCAGACATTGTGCGACTTC
NM_134261	RORA	1421	ACCCAGACATTGTGCGACTTC
NM_134262	RORA	1421	ACCCAGACATTGTGCGACTTC
NM_006914	RORB	1422	ACCTATCTATGACCTCACATC
NM_006914	RORB	1423	ACCATCACGGCAGTTTGCAAC
NM_005060	RORC	1424	ACAGGAACCAGTGGTCAAGAC
NM_005060	RORC	1425	ACTGGCTACCAGAGGAAGTCC
AF124247	AF124247	1426	ACAACCTCATGAGTCATGCAC
AF146343	AF146343	1426	ACAACCTCATGAGTCATGCAC
NM_003822	NR5A2	1426	ACAACCTCATGAGTCATGCAC
U80251	HSU80251	1426	ACAACCTCATGAGTCATGCAC
U93553	HSU93553	1426	ACAACCTCATGAGTCATGCAC
NM_004959	NR5A1	1427	ACGGTGCAGAACAAAGCAC
NM_004959	NR5A1	1428	ACCTTCATCTCCATCGTGGAC
NM_005234	NR2F6	1429	ACGCCCATTGAGACACTGATC
NM_003250	THRA	1430	ACCAGCATGTGAGGGTATATC
NM_003250	THRA	1431	ACTGGGCAAGTCACTCTCTGC
NM_003297	NR2C1	1432	ACAACACCTGCAGCTCCTAAC
NM_003297	NR2C1	1433	ACATGTAGCTTTCAGGCTCAC
NM_003297	NR2C1	1434	ACTCTTCAGTCCAGATCATCC
NM_005122	NR1I3	1435	ACATGGGCACCATGTTTGAAC
NM_005693	NR1H3	1436	ACACATATGTGGAAGCCCTGC
U22662	HSU22662	1436	ACACATATGTGGAAGCCCTGC
NM_000044	AR	1437	ACACTTGAAGTCCCGTCTACC
M73069	HUMANRE	1438	ACGACCAGATGGCTGTCTATTC
NM_000044	AR	1438	ACGACCAGATGGCTGTCTATTC
NM_003269	NR2E1	1439	ACGTTCTATTAGCCCATCAAC

NM_000457	HNF4A	1440	ACCAAGAGATCCATGGTGTTC
X76930	HSHNF4	1440	ACCAAGAGATCCATGGTGTTC
X87870	HSHNF4AGN	1440	ACCAAGAGATCCATGGTGTTC
X87871	HSHNP4BGN	1440	ACCAAGAGATCCATGGTGTTC
X87872	HSHNF4CGN	1440	ACCAAGAGATCCATGGTGTTC
Z49825	HSHNF4A	1440	ACCAAGAGATCCATGGTGTTC
NM_000457	HNF4A	1441	ACGGACAGATGTGTGAGTGGC
X76930	HSHNF4	1441	ACGGACAGATGTGTGAGTGGC
X87871	HSHNP4BGN	1441	ACGGACAGATGTGTGAGTGGC
Z49825	HSHNF4A	1441	ACGGACAGATGTGTGAGTGGC
NM_002135	NR4A1	1442	ACTTCTCCACACCTTGAGGGC
NM_002135	NR4A1	1443	ACAAGATCTTCATGGACACGC
NM_006917	RXRG	1444	ACAGGGAAGCCAATGGACAGC
NM_002957	RXRA	1445	ACACCTTCCTTATGGAGATGC
NM_004452	ESRRB	1446	ACTACATCATGGATGAGGAGC
NM_004452	ESRRB	1447	ACAAACTCTTCCTGGAGATGC
D16815	D16815	1448	ACACTGGAGGAAGAATGCATC
M73069	HUMANRE	1449	ACATCCTGCTCAAGACGCTTC
NM_000044	AR	1449	ACATCCTGCTCAAGACGCTTC
AF258451	AF258451	1450	ACAGGCTTTGTGGATTTGACC
NM_000125	ESR1	1450	ACAGGCTTTGTGGATTTGACC
NM_003150	STAT3	1451	ACCCTCAAGAGTCAAGGAGAC
NM_139276	STAT3	1451	ACCCTCAAGAGTCAAGGAGAC
NM_003150	STAT3	1452	ACCTAGAGACCCACTCCTTGC
NM_139276	STAT3	1452	ACCTAGAGACCCACTCCTTGC
NM_003150	STAT3	1453	ACCTTTGACATGGAGTTGACC
NM_139276	STAT3	1453	ACCTTTGACATGGAGTTGACC
AF014402	AF014402	1454	ACCCTGTCTGTTTACTGTAAC
AF014403	AF014403	1454	ACCCTGTCTGTTTACTGTAAC
NM_003711	PPAP2A	1454	ACCCTGTCTGTTTACTGTAAC
AF014402	AF014402	1455	ACTGCAATTTGGTCTTGTTGC
AF014403	AF014403	1455	ACTGCAATTTGGTCTTGTTGC
NM_003711	PPAP2A	1455	ACTGCAATTTGGTCTTGTTGC
AF017999	AF017999	1456	ACTGTAAAGCTGGAAAGGGAC
BC038293	BC038293	1456	ACTGTAAAGCTGGAAAGGGAC
NG_001337	NG_001337	1456	ACTGTAAAGCTGGAAAGGGAC
NM_000314	PTEN	1456	ACTGTAAAGCTGGAAAGGGAC
AF017999	AF017999	1457	ACTATTCCAATGTTTCAGTGGC
BC038293	BC038293	1457	ACTATTCCAATGTTTCAGTGGC
NG_001337	NG_001337	1457	ACTATTCCAATGTTTCAGTGGC
NM_000314	PTEN	1457	ACTATTCCAATGTTTCAGTGGC
AF024579	AF024579	1458	ACTTTCCAACCTGGTTTCTCC
NM_002711	PPP1R3A	1458	ACTTTCCAACCTGGTTTCTCC
AF086924	AF086924	1459	ACCTACCAGGTCCATGACTAC
BC032954	BC032954	1459	ACCTACCAGGTCCATGACTAC
AF086924	AF086924	1460	ACCAACAACCTGTACATCTTC

BC032954	BC032954	1460	ACCAACAACCTGTACATCTTC
AF213044	AF213044	1461	ACCTTCTGGATCTCTACCAGC
AF213045	AF213045	1461	ACCTTCTGGATCTCTACCAGC
AF213048	AF213048	1461	ACCTTCTGGATCTCTACCAGC
AF213050	AF213050	1461	ACCTTCTGGATCTCTACCAGC
NM_005192	CDKN3	1461	ACCTTCTGGATCTCTACCAGC
AF213044	AF213044	1462	ACAATATCACCAGAGCAAGCC
AF213045	AF213045	1462	ACAATATCACCAGAGCAAGCC
AF213048	AF213048	1462	ACAATATCACCAGAGCAAGCC
AF213050	AF213050	1462	ACAATATCACCAGAGCAAGCC
NM_005192	CDKN3	1462	ACAATATCACCAGAGCAAGCC
AF233436	AF233436	1463	ACAGGGCAGGCATTGAGATAC
AF233437	AF233437	1463	ACAGGGCAGGCATTGAGATAC
NM_021090	MTMR3	1463	ACAGGGCAGGCATTGAGATAC
AF233436	AF233436	1464	ACACAGACACGATCCAACAGC
AF233437	AF233437	1464	ACACAGACACGATCCAACAGC
NM_021090	MTMR3	1464	ACACAGACACGATCCAACAGC
AF290614	AF290614	1465	ACGCACATTACCTGCATCAGC
BC004881	BC004881	1465	ACGCACATTACCTGCATCAGC
AF318616	AF318616	1466	ACCATCCAGTCCAACCTCTTC
AF331843	AF331843	1467	ACATTCCGTCTGACACCACTC
AF331843	AF331843	1468	ACCATCTGTCTGGCATACTTC
NM_004418	DUSP2	1468	ACCATCTGTCTGGCATACTTC
AF368319	AF368319	1469	ACCCAGTACCAGACCATCATC
NM_001566	INPP4A	1469	ACCCAGTACCAGACCATCATC
NM_004027	INPP4A	1469	ACCCAGTACCAGACCATCATC
AF368319	AF368319	1470	ACTGGATCAGACCAGAAGACC
AF368319	AF368319	1471	ACACTGGAGCAGTGCCTGATC
NM_001566	INPP4A	1471	ACACTGGAGCAGTGCCTGATC
NM_004027	INPP4A	1471	ACACTGGAGCAGTGCCTGATC
AF458589	AF458589	1472	ACACGTTCAAGTCCC
NM_002480	PPP1R12A	1472	ACACGTTCAAGTCCC
AF458589	AF458589	1473	ACGCAGATCATACCTCACTCC
NM_002480	PPP1R12A	1473	ACGCAGATCATACCTCACTCC
AF508727	AF508727	1474	ACATCGAGACGGCCATCAACC
AF508727	AF508727	1475	ACAGAGTACTCTGAGCACTGC
AF518728	AF518728	1476	ACATGTTATCACAAGGGTGGC
AF518729	AF518729	1476	ACATGTTATCACAAGGGTGGC
AF518728	AF518728	1477	ACAGCTATGGAGGAGCAGTTC
AF518729	AF518729	1477	ACAGCTATGGAGGAGCAGTTC
AF518728	AF518728	1478	ACCTCCAAGATCTTTGGTTTC
AF518729	AF518729	1478	ACCTCCAAGATCTTTGGTTTC
AY040091	AY040091	1479	ACCGCTTTGAGCTGTGGAAGC
AY040091	AY040091	1480	ACACAGAAGATGGTGGGAAGCC
AY040091	AY040091	1481	ACCATATCGATGAGGTCTGGC
NM_016364	LOC51207	1481	ACCATATCGATGAGGTCTGGC

BC001175	BC001175	1482	ACCCATAGCCGTGATGTTGTC
NM_006245	PPP2R5D	1482	ACCCATAGCCGTGATGTTGTC
BC001175	BC001175	1483	ACGTGTACACCATCAAGGCAC
NM_006245	PPP2R5D	1483	ACGTGTACACCATCAAGGCAC
BC008216	BC008216	1484	ACAATGTACACATTGAGCTTGC
BC017943	BC017943	1485	ACTGGTCTGCAGCAAGAAGGC
BC021714	BC021714	1486	ACACCTTATTGACAGCCACCC
BC031614	BC031614	1487	ACCAGGGCAACATGTACTGAC
BC033103	BC033103	1488	ACATTGGATAATGGGCTTCGC
BC033103	BC033103	1489	ACAGTTGGCCTCCACCGTTTC
BC036539	BC036539	1490	ACTTCTCTTCGGAATTTCCC
XM_045128	DKFZP566K0524	1490	ACTTCTCTTCGGAATTTCCC
ENSG00000139304	ENSG00000139304	1491	ACTCCTCACTGTACTCTCACC
NM_000151	G6PC	1492	ACGTGATGGTCACATCTACTC
NM_000252	MTM1	1493	ACATATGTCCTTTCAATGGCC
NM_000252	MTM1	1494	ACATGGAGCTCTTAGCCTTAC
NM_000276	OCRL	1495	ACCTTATGGCAAGACAGACTC
NM_001587	OCRL	1495	ACCTTATGGCAAGACAGACTC
NM_000296	PKD1	1496	ACAGCGGATGTAACTACATC
NM_000478	ALPL	1497	ACTATGCTCACAACAACCTACC
NM_000507	FBP1	1498	ACGGAGGGATATTTCTGTACC
NM_000507	FBP1	1499	ACGTCATTCCCACAGACATTC
NM_001107	ACYP1	1500	ACAATTGCAAGGTCCCATCTC
NM_001246	ENTPD2	1501	ACAGCTTCCTCTGCTATGGCC
NM_001246	ENTPD2	1502	ACATGCTGAACCTGACCAACC
NM_001247	ENTPD6	1503	ACTGCGGATGTTTAAACAGGAC
NM_001248	ENTPD3	1504	ACCGGAGTGGTCAGTCAAACC
NM_001249	ENTPD5	1505	ACTTGGTTTGAGGGTATCTTC
NM_001567	INPPL1	1506	ACAGGACATGAGCTCCACAGC
NM_001567	INPPL1	1507	ACATGGATATCCAGGAGATCC
NM_001610	ACP2	1508	ACAATTTCTGGACATGGTGGC
NM_001611	ACP5	1509	ACATCAATGACAAGAGGTTCC
NM_001611	ACP5	1510	ACTATGGGACTGAAGACTCAC
NM_001631	ALPI	1511	ACATGGACATTGACGTGATCC
NM_001632	ALPP	1511	ACATGGACATTGACGTGATCC
NM_001631	ALPI	1512	ACGTGTTCAACTCAGGCGTGC
NM_001632	ALPP	1513	ACGGTCCTCCTATACGGAAAC
NM_031313	ALPPL2	1513	ACGGTCCTCCTATACGGAAAC
NM_001776	ENTPD1	1514	ACGTTAAGTATGGGATTGTGC
NM_001776	ENTPD1	1515	ACTTTGGGCTACATGCTGAAC
NM_001946	DUSP6	1516	ACCGACACAGTGGTGCTCTAC
NM_022652	DUSP6	1516	ACCGACACAGTGGTGCTCTAC
NM_001946	DUSP6	1517	ACCTTATGCAGAAGCTCAATC
NM_022652	DUSP6	1517	ACCTTATGCAGAAGCTCAATC
NM_001946	DUSP6	1518	ACAACAGGGTTCCAGCACAGC
NM_022652	DUSP6	1518	ACAACAGGGTTCCAGCACAGC

NM_002194	INPP1	1519	ACCATCTCTAGAAGAAACGGC
NM_002706	PPM1B	1520	ACCCAGGATCACAAACCTTGC
NM_002706	PPM1B	1521	ACCAGCTGCCACAGCTACTTC
NM_002708	PPP1CA	1522	ACGAGTGTGCCAGCATCAACC
S57501	S57501	1522	ACGAGTGTGCCAGCATCAACC
NM_002709	PPP1CB	1523	ACCTACTGATGTCCCTGATAC
NM_002709	PPP1CB	1524	ACCTCGAACAGCTAATCCGCC
NM_002712	PPP1R7	1525	ACAGTGATCCTGGAGCGGAAC
NM_002716	PPP2R1B	1526	ACTTTGCCCCACTGTCTGCTGC
NM_002717	PPP2R2A	1527	ACTACACTACGAGTGCCAGTC
NM_002718	PPP2R3A	1528	ACAGCACAGTCATTTCATTGCC
NM_002719	PPP2R5C	1529	ACCCATAATCGGAATGTGATC
NM_002720	PPP4C	1530	ACGCAGGTCTATGGCTTCTAC
NM_002720	PPP4C	1531	ACTGAGATCTTTGACTACCTC
NM_002828	PTPN2	1532	ACAGATACAGAGATGTAAGCC
NM_080422	PTPN2	1532	ACAGATACAGAGATGTAAGCC
NM_080423	PTPN2	1532	ACAGATACAGAGATGTAAGCC
XM_171634	LOC255048	1532	ACAGATACAGAGATGTAAGCC
NM_002828	PTPN2	1533	ACTGTAGTGCAGGCATTGGGC
NM_080422	PTPN2	1533	ACTGTAGTGCAGGCATTGGGC
NM_080423	PTPN2	1533	ACTGTAGTGCAGGCATTGGGC
NM_002829	PTPN3	1534	ACATCAGCGACAGAAACAGGC
NM_002829	PTPN3	1535	ACCTGCATTCCCTAAGCTGAAC
NM_002829	PTPN3	1536	ACAGTGACACATCTCCAGTAC
NM_002830	PTPN4	1537	ACTGTGGGAGAACTGAAGTCC
NM_002830	PTPN4	1538	ACACCTGCTGACCTCTGTGTC
NM_002830	PTPN4	1539	ACAATGAGAGATCAGCGAGCC
NM_002831	PTPN6	1540	ACCATCATCCACCTCAAGTAC
NM_080548	PTPN6	1540	ACCATCATCCACCTCAAGTAC
NM_080549	PTPN6	1540	ACCATCATCCACCTCAAGTAC
NM_002831	PTPN6	1541	ACCCACATCAAGGTCATGTGC
NM_080548	PTPN6	1541	ACCCACATCAAGGTCATGTGC
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NM_002832	PTPN7	1542	ACCCATCTGCTCTGTGAACAC
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NM_080589	PTPN7	1542	ACCCATCTGCTCTGTGAACAC
NM_002832	PTPN7	1543	ACCTATGGACCCCTTCCAGATC
NM_080588	PTPN7	1543	ACCTATGGACCCCTTCCAGATC
NM_080589	PTPN7	1543	ACCTATGGACCCCTTCCAGATC
NM_002833	PTPN9	1544	ACCTGCTGAAGGGAGCATTTTC
NM_002834	PTPN11	1545	ACCCACATCAAGATTCAGAAC
NM_080601	PTPN11	1545	ACCCACATCAAGATTCAGAAC
NM_002834	PTPN11	1546	ACACTACAACAACAGGAGTGC
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NM_002837	PTPRB	1547	ACAGATAGCCTGACGGTGAAC
NM_002838	PTPRC	1548	ACATTCTGTCAATGGTCTGTC

NM_080921	PTPRC	1548	ACATTCTGTCAATGGTCCTGC
NM_080922	PTPRC	1548	ACATTCTGTCAATGGTCCTGC
NM_002839	PTPRD	1549	ACGAACACCCGTTGATCAGAC
NM_130391	PTPRD	1549	ACGAACACCCGTTGATCAGAC
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NM_002839	PTPRD	1550	ACCTCAATTGGAGATGGTCCC
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NM_130392	PTPRD	1550	ACCTCAATTGGAGATGGTCCC
NM_130393	PTPRD	1550	ACCTCAATTGGAGATGGTCCC
NM_002841	PTPRG	1551	ACGGAGCAGCAAGACCATGTC
NM_002841	PTPRG	1552	ACCAGGAGTAGGAGGAAAGAC
NM_002842	PTPRH	1553	ACTGAGGCTCAGTACGTATTC
NM_002843	PTPRJ	1554	ACCTCGTACAACATCAGCATC
NM_002845	PTPRM	1555	ACTTCTGGAGGATGGTGTGGC
NM_002846	PTPRN	1556	ACATGGACATCTCCACGGGAC
NM_002847	PTPRN2	1557	ACAGTACCTTCTGCGTGCACC
NM_130842	PTPRN2	1557	ACAGTACCTTCTGCGTGCACC
NM_130843	PTPRN2	1557	ACAGTACCTTCTGCGTGCACC
NM_002847	PTPRN2	1558	ACGAAGGAGCAGTTTGAGTTC
NM_130842	PTPRN2	1558	ACGAAGGAGCAGTTTGAGTTC
NM_130843	PTPRN2	1558	ACGAAGGAGCAGTTTGAGTTC
NM_002848	PTPRO	1559	ACAGAGAAGTCAACATCAGGC
NM_030667	PTPRO	1559	ACAGAGAAGTCAACATCAGGC
NM_002848	PTPRO	1560	ACTGGCCATTACGGAAGAAC
NM_030667	PTPRO	1560	ACTGGCCATTACGGAAGAAC
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NM_002848	PTPRO	1561	ACACTTCCGGATCAACTATGC
NM_030667	PTPRO	1561	ACACTTCCGGATCAACTATGC
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NM_030670	PTPRO	1561	ACACTTCCGGATCAACTATGC
NM_030671	PTPRO	1561	ACACTTCCGGATCAACTATGC
NM_002849	PTPRR	1562	ACAAGCTGAACATAACCTTGC
NM_002851	PTPRZ1	1563	ACAGTTAGCATCTCTGAAAGC
NM_002851	PTPRZ1	1564	ACAATGAAGCCAAGACTAACC
NM_002851	PTPRZ1	1565	ACACCTCTTCAACCTTCCTAC
NM_003584	DUSP11	1566	ACCAGAGGATTTGCCAGAAAC
NM_003584	DUSP11	1567	ACCAGAGACACCATCTCCCTC
NM_003620	PPM1D	1568	ACTATGACGGGTCTTCCTAGC
NM_003626	PPFIA1	1569	ACAGGAGCGCTTGGAATTGGC
NM_003626	PPFIA1	1570	ACAAGCTGGTGTTCGAGAC
NM_003671	CDC14B	1571	ACAAGGTGATAGACTTCGGGC

NM_033331	CDC14B	1571	ACAAGGTGATAGACTTCGGGC
NM_033332	CDC14B	1571	ACAAGGTGATAGACTTCGGGC
NM_003672	CDC14A	1572	ACAACATCGTGCGAAGGTTCC
NM_033312	CDC14A	1572	ACAACATCGTGCGAAGGTTCC
NM_033313	CDC14A	1572	ACAACATCGTGCGAAGGTTCC
NM_003672	CDC14A	1573	ACCAACCTCTTGAATGGCAGC
NM_033312	CDC14A	1573	ACCAACCTCTTGAATGGCAGC
NM_003712	PPAP2C	1574	ACACAGACCGGCTCTATTCTC
NM_003712	PPAP2C	1575	ACCGAGGCCAGGTTGTCTTTC
NM_003713	PPAP2B	1576	ACTGCTCTGAAGGCTACATTC
NM_003713	PPAP2B	1577	ACCTTGATCATGATGGCCTTC
NM_003800	RNGTT	1578	ACCACTGAGAATACTGAGACC
NM_003800	RNGTT	1579	ACCCTGTCACCAAGGAGATGC
NM_003832	PSPHL	1580	ACATCCATTGTCATACAGCTC
NM_003866	INPP4B	1581	ACGCTAAGAAGAGACATCGTC
NM_003912	MTMR2	1582	ACTTTGTGATACATACCCTGC
NM_016156	MTMR2	1582	ACTTTGTGATACATACCCTGC
NM_003912	MTMR2	1583	ACGTCTGTGGTAGTGCAATTGC
NM_016156	MTMR2	1583	ACGTCTGTGGTAGTGCAATTGC
NM_003978	PSTPIP1	1584	ACAGCAACCAGCTCTCCATGC
NM_003978	PSTPIP1	1585	ACGATTATACAGCGCAGAACC
NM_004090	DUSP3	1586	ACGACACACAGGAGTTCAACC
NM_004090	DUSP3	1587	ACGCTAGTTATCGCCTACCTC
NM_004156	PPP2CB	1588	ACACTGGATCATATAAGAGCC
NM_004300	ACP1	1589	ACTACTTGGGAGCTATGATCC
NM_007099	ACP1	1589	ACTACTTGGGAGCTATGATCC
NM_004300	ACP1	1590	ACTTTGAGACGGTGTACCAGC
NM_007099	ACP1	1590	ACTTTGAGACGGTGTACCAGC
NM_004419	DUSP5	1591	ACGGCTGACATTAGCTCCAC
NM_004419	DUSP5	1592	ACTGATAGGCCATTTGCAGAC
NM_004420	DUSP8	1593	ACAGGTTCTGTAAGGACAGGC
M64930	HUMPROP2AB	1594	ACGAAGAGTATTTGCCAACGC
NM_004576	PPP2R2B	1594	ACGAAGAGTATTTGCCAACGC
M64930	HUMPROP2AB	1595	ACCTTCGTGTACAGCAGCAGC
NM_004576	PPP2R2B	1595	ACCTTCGTGTACAGCAGCAGC
NM_004577	PSPH	1596	ACGCGGTGTCAGAAATGACAC
NM_004577	PSPH	1597	ACAGAGCGCTTAGCCCTCATC
NM_004687	MTMR4	1598	ACCTCTGGACAGCTGTTTATC
NM_004715	CTDP1	1599	ACTTCCCGATAGAGAAGACGC
NM_048368	CTDP1	1599	ACTTCCCGATAGAGAAGACGC
NM_004715	CTDP1	1600	ACAAAGAGGTGGACGACATCC
NM_004901	LYSAL1	1601	ACACCTCTCTACATTCTCTGC
NM_005134	PPP4R1	1602	ACAAGTCAGGCCAGAGGATAC
NM_005134	PPP4R1	1603	ACAAGATGTTGTACCTCAGGC
NM_005398	PPP1R3C	1604	ACTGCGATCCATGTCTTCTCC
NM_005401	PTPN14	1605	ACCTGACTAGTGTGAAGGAGC

NM_005536	IMPA1	1606	ACAGCAGCTGTTAATATGTGC
NM_005670	EPM2A	1607	ACACGTTCTGGTACAAGTTCC
NM_005704	PTPRU	1608	ACTTCATAGCCACTCAAGGGC
NM_133177	PTPRU	1608	ACTTCATAGCCACTCAAGGGC
NM_133178	PTPRU	1608	ACTTCATAGCCACTCAAGGGC
NM_005704	PTPRU	1609	ACATGGTGGAGACCATGGATC
NM_133177	PTPRU	1609	ACATGGTGGAGACCATGGATC
NM_133178	PTPRU	1609	ACATGGTGGAGACCATGGATC
NM_005765	ATP6M8-9	1610	ACCCTTTGGAGAATGCAGTTC
NM_005765	ATP6M8-9	1611	ACTCTGTTCTCAGTTCCTCC
NM_006085	BPNT1	1612	ACTGAAGCAACCATGCCCATC
NM_006085	BPNT1	1613	ACTGTGTTGCTGCTATGAACC
NM_006239	PPEF2	1614	ACAGAGGAAACCATGAGGACC
NM_006239	PPEF2	1615	ACAACCTGCAATTCTTGATCC
NM_006240	PPEF1	1616	ACCGAGGTTACAAAGCTCGAC
NM_006240	PPEF1	1617	ACTCACATACAACTTCTCCC
NM_006243	PPP2R5A	1618	ACATCTTCCGTACACTTCCTC
NM_006243	PPP2R5A	1619	ACACTAACAGAGCCAGTGATC
NM_006243	PPP2R5A	1620	ACCCTAATGGAAATGAATGGC
NM_006244	PPP2R5B	1621	ACCTCAAGACCATCCTGCACC
NM_006244	PPP2R5B	1622	ACTCTGACAGAGCACGTGATC
NM_006244	PPP2R5B	1623	ACCATCGTATCACTGATCTAC
NM_006246	PPP2R5E	1624	ACAGAAGAGGTGCGAAAGTTC
NM_006246	PPP2R5E	1625	ACTTCAATGGTGTAGCTGAAC
NM_006246	PPP2R5E	1626	ACAGCACCATGTTTGACGAGC
NM_006305	ANP32A	1627	ACAATCAACGTAGGCCTCACC
NM_006305	ANP32A	1628	ACCTCAGCACAATAGAGCCAC
NM_012403	ANP32C	1628	ACCTCAGCACAATAGAGCCAC
NM_006741	PPP1R1A	1629	ACATCTCAAGTCCACTTTGGC
NM_006741	PPP1R1A	1630	ACGAAAGAGGCAGTAAGGAAC
NM_006903	SID6-306	1631	ACGTGCAGATATCTGATAGCC
NM_007039	PTPN21	1632	ACTTACTTCAGCCTCTGGTAC
NM_007039	PTPN21	1633	ACAATGAGGTGCTGGACATCC
NM_007050	PTPRT	1634	ACCTCTTTGTGGGTCTGTACC
NM_133170	PTPRT	1634	ACCTCTTTGTGGGTCTGTACC
NM_007050	PTPRT	1635	ACGGAGACATTAAAGTCACCC
NM_133170	PTPRT	1635	ACGGAGACATTAAAGTCACCC
NM_007099	ACP1	1636	ACACAGCCCATAAAGCAAGAC
NM_007207	DUSP10	1637	ACTTCACATAGTCCTCGAGTC
NM_007240	DUSP12	1638	ACTGTCAATGCAGGAGTCAGTC
NM_007240	DUSP12	1639	ACACCATCTTCCATGCTTACC
NM_012404	ANP32D	1640	ACAATCAACATAGGCCTCACC
NM_012404	ANP32D	1641	ACTAAGCAGTAACAGAGCCTC
NM_012411	PTPN22	1642	ACTATTGAACCAGGAGTCAGC
NM_015967	PTPN22	1642	ACTATTGAACCAGGAGTCAGC
NM_013239	PR48	1643	ACTTCTACGAGGAGCAGTGCC

NM_013315	TPTE	1644	ACCACTATCGAGTCTACAATC
NM_130785	TPIP	1644	ACCACTATCGAGTCTACAATC
XM_166267	LOC220115	1644	ACCACTATCGAGTCTACAATC
NM_013315	TPTE	1645	ACAGGAAGTATGGTTTGTGCC
NM_002713	PPP1R8	1646	ACCATTGACCACCAGTCTTGC
NM_014110	PPP1R8	1646	ACCATTGACCACCAGTCTTGC
NM_138558	PPP1R8	1646	ACCATTGACCACCAGTCTTGC
NM_002713	PPP1R8	1647	ACAGAGTTCAACACTGCCCAC
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NM_138558	PPP1R8	1647	ACAGAGTTCAACACTGCCCAC
NM_014225	PPP2R1A	1648	ACGTCAAGAGTGAGATCATCC
NM_014225	PPP2R1A	1649	ACCAACATGTCAAGTCTGCCC
NM_014225	PPP2R1A	1650	ACATCACCACCAAGCACATGC
NM_014241	PTPLA	1651	ACAGAGATCACTCGCTATTCC
NM_014369	PTPN18	1652	ACAGAGGAGCAGTACAGGTTT
NM_014395	DAPP1	1653	ACAGAAGATGACCTTGTGCCC
NM_014395	DAPP1	1654	ACTTCAAAGACCAGATGTCAC
NM_014634	FEM-2	1655	ACCTTGCTGGATGCCCCAAGC
NM_014634	FEM-2	1656	ACTTTGCTGTGTTTGATGGTC
NM_014787	DNAJC6	1657	ACAGGCTAAGGTGACCAACAC
NM_014906	POPX1	1658	ACAAATTAGTGGCATCAGCTC
NM_015216	KIAA0433	1659	ACATCTAGTGAAGAGGAGGAC
NM_016086	LOC51657	1660	ACCTCATGCATAGTAACGAGC
NM_016147	PME-1	1661	ACAAGAGTGGTTCAGAGGGTC
NM_016361	LOC51205	1662	ACCCACAGGAGGTCTTTATTC
NM_016361	LOC51205	1663	ACGGATGATCGAACAGAGAGC
NM_016532	SKIP	1664	ACATCGACATCAGCAATATCC
NM_130766	SKIP	1664	ACATCGACATCAGCAATATCC
NM_017607	PPP1R12C	1665	ACTGTGAACCAGGCAGACAAC
NM_017607	PPP1R12C	1666	ACCTCAACCCAGAACCTGAGC
NM_017677	FLJ20126	1667	ACATGGATTGCACTCCATCAC
NM_017813	FLJ20421	1668	ACCCTGAGTGGTGAAGAAATC
NM_003120	SPI1	1669	ACTACCAGTTCCTGTTGGACC
NM_017823	FLJ20442	1669	ACTACCAGTTCCTGTTGGACC
NM_018159	NUDT11	1670	ACAGAACGTACGTGTATGTAC
NM_018159	NUDT11	1671	ACGCCGAATATCTGGAGAAAC
NM_018276	SSH-3	1672	ACCTACCACAATGTGCGCCTC
NM_017857	SSH-3	1673	ACCAGTGACATGCCAGAGGTC
NM_018276	SSH-3	1673	ACCAGTGACATGCCAGAGGTC
NM_018444	PDP	1674	ACTGTTCTCTGATGCCATGCC
NM_018444	PDP	1675	ACTGGCAAGAGCTTATAGACC
NM_018444	PDP	1676	ACCTAACTGGCATGCATCACC
NM_018461	MDS026	1677	ACATGATGACCAGAGACTTAC
NM_019061	3-PAP	1678	ACCATGGTTTGTGTTACCGC
NM_019892	PPI5PIV	1679	ACACGCATCGTGTCTCAGATC
NM_020185	MKPX	1680	ACACTGGTGATCGCATACATC

NM_020354	LALP1	1681	ACATTGGAGTGCTTCATTACC
NM_021003	PPM1A	1682	ACATTAGCGAGTGAGAACATC
NM_021129	PP	1683	ACATGGTAGTTGAAGTACCAC
NM_021129	PP	1684	ACCGACTGGAAAGTCATTGCC
NM_021176	IGRP	1685	ACAGACTGACCTGGTCATTTC
NM_002287	LAIR1	1686	ACAAGGCCACAGTCAATGGAC
NM_021706	LAIR1	1686	ACAAGGCCACAGTCAATGGAC
NM_021708	LAIR1	1686	ACAAGGCCACAGTCAATGGAC
NM_022076	LOC63904	1687	ACCATCGATATGAGGCAGGGC
NM_022126	LHPP	1688	ACTACAAGGAGACCTCTGGCC
NM_022648	TNS	1689	ACAGCCAATGAGGAGAACTTC
NM_022648	TNS	1690	ACAGTATGAGAACCAGTCTCC
NM_024025	MGC1136	1691	ACCGTTCAACATCCTTTTCCTC
NM_024025	MGC1136	1692	ACCAGGACATGGCTAACAACC
NM_030768	ILKAP	1693	ACATGGAGGAATTCGAGCCTC
NM_030791	LOC81537	1694	ACCTGATTGACAACTTCAACC
NM_030949	PPP1R14C	1695	ACAGCCTAACCAAGGATTATC
NM_031313	ALPPL2	1696	ACAGTGTAGACAAGCATGTGC
NM_032781	FLJ14427	1697	ACCAACATCGAGGAGATGAAC
NM_032781	FLJ14427	1698	ACATCCTGAAGACCACGTGCC
NM_033068	ACPT	1699	ACTCAGCTCATGACAGCACCC
NM_080789	ACPT	1699	ACTCAGCTCATGACAGCACCC
NM_080790	ACPT	1699	ACTCAGCTCATGACAGCACCC
NM_080791	ACPT	1699	ACTCAGCTCATGACAGCACCC
NG_001182	NG_001182	1700	ACCTGTGCTGGTTGCACTTGC
NM_003479	PTP4A2	1700	ACCTGTGCTGGTTGCACTTGC
NM_080391	PTP4A2	1700	ACCTGTGCTGGTTGCACTTGC
NM_004648	PTPNS1	1701	ACCTACTACTGTGTGAAGTTC
NM_006065	SIRPB1	1701	ACCTACTACTGTGTGAAGTTC
NM_080792	PTPNS1	1701	ACCTACTACTGTGTGAAGTTC
NM_004648	PTPNS1	1702	ACACCCTCACCTATGCTGACC
NM_080792	PTPNS1	1702	ACACCCTCACCTATGCTGACC
NM_006750	SNTB2	1703	ACCAAGGACAGGAAGATCATC
NM_130845	SNTB2	1703	ACCAAGGACAGGAAGATCATC
NM_002850	PTPRS	1704	ACAGGCTGCTTTATCGTCATC
NM_130853	PTPRS	1704	ACAGGCTGCTTTATCGTCATC
NM_130854	PTPRS	1704	ACAGGCTGCTTTATCGTCATC
NM_130855	PTPRS	1704	ACAGGCTGCTTTATCGTCATC
NM_002850	PTPRS	1705	ACCGCCTGGTGAACATCATGC
NM_130853	PTPRS	1705	ACCGCCTGGTGAACATCATGC
NM_130854	PTPRS	1705	ACCGCCTGGTGAACATCATGC
NM_130855	PTPRS	1705	ACCGCCTGGTGAACATCATGC
NM_030764	SPAP1	1706	ACCTCTCTTTGACTGCAGAAC
NM_138738	SPAP1	1706	ACCTCTCTTTGACTGCAGAAC
NM_138739	SPAP1	1706	ACCTCTCTTTGACTGCAGAAC
NM_139283	TA-PP2C	1707	ACGGTTCGTACCTAGTAATCC

NM_139283	TA-PP2C	1708	ACTCCATTCCAGCTCTCAATC
NM_147180	PPP3R2	1709	ACTTGGACAAATCAGGGTCTC
NM_005605	PPP3CC	1710	ACCATTTGGTAAAGGAAGGAC
S46622	S46622	1710	ACCATTTGGTAAAGGAAGGAC
NM_005605	PPP3CC	1711	ACCAGCAGTTTCTCTGTGTAC
S46622	S46622	1711	ACCAGCAGTTTCTCTGTGTAC
XM_030846	SSH2	1712	ACATGAATGTCCACCTACTGC
XM_030846	SSH2	1713	ACTGCTTACCAGAGAGGGAGC
XM_038489	PIB5PA	1714	ACACAGTCAGCGACCACAAGC
XM_043826	KIAA1348	1715	ACAAGGATGTCACATCTGTGC
XM_043826	KIAA1348	1716	ACAATGGCATGTGGTCTGTGC
XM_043826	KIAA1348	1717	ACTACTACACTCCACCCTACC
XM_044665	LOC92370	1718	ACTCCTGCCCAATGATTGGTC
XM_046577	MTMR1	1719	ACGGACTTTAAGCTGTACTTC
XM_046577	MTMR1	1720	ACCCTGCCATCATTGTTGTGC
XM_054936	LOC114971	1721	ACGTGCATTGTAAGGCTGGGC
XM_054936	LOC114971	1722	ACGGGCAACAAAGGATGGGAC
XM_058886	LOC124997	1723	ACGTCTTGTTATGTTGGACCC
XM_059988	LOC138639	1724	ACTATTCTCTGCGTGTGCAC
XM_061101	LOC118707	1725	ACATCTGCTGCTCCAAGCTGC
XM_114902	LOC203688	1725	ACATCTGCTGCTCCAAGCTGC
XM_171375	LOC256242	1725	ACATCTGCTGCTCCAAGCTGC
XM_061191	LOC118879	1726	ACCTCAGTGTCTTCTTCTACC
XM_067153	LOC131015	1727	ACGATGTTGGTGGAGGAGAAC
XM_067153	LOC131015	1728	ACGTCAAAGAAAGCACCACCTC
XM_069073	LOC134897	1729	ACAGCAAGTGTAAGTGACCC
XM_069073	LOC134897	1730	ACTGGTCTGAAGAGGATGCTC
XM_086863	LOC150290	1731	ACACGTGGACCAAGTCATGCC
XM_086863	LOC150290	1732	ACTGTGCACATGGTCAGTTCC
XM_087562	LOC152926	1733	ACCCAGATGGTAGTGGGAGTC
XM_087562	LOC152926	1734	ACTTTGCAGTGTATGATGGAC
XM_089436	LOC159193	1735	ACATCAAATCAGCGAACACCC
XM_093300	LOC165582	1736	ACTTTCAAGACCCACCAACAC
XM_093300	LOC165582	1737	ACTTGCGAGCTTCCAAAGGAC
XM_095533	LOC169142	1738	ACACCCTGAAGATACAACAGC
XM_114343	LOC201562	1739	ACGGCGTACCTGGTCATCTAC
XM_114343	LOC201562	1740	ACAATATATGCAGCTCTGCCC
XM_115330	LOC197099	1741	ACCAGCTTCTGGCTGTGCTTC
XM_115330	LOC197099	1742	ACCCTGAAGATTTACATGGGC
XM_166125	KIAA1274	1743	ACGCCTTTGTCAGTGTTCTCC
XM_166125	KIAA1274	1744	ACTTGGAGCGCTATGTCTGCC
XM_166267	LOC220115	1745	ACTGCAGAGGAAAGATTGTAC
XM_167349	LOC223021	1746	ACCTCACTTACATCACGGAGC
XM_167349	LOC223021	1747	ACGCATAGGAGTGGTCATATC
XM_170949	INPP5B	1748	ACAATGTAAATGGGCAGTCCC
XM_170949	INPP5B	1749	ACCATGATGTGATCTTGTGGC

XM_170949	INPP5B	1750	ACGAGCTTTACCGGAAGACAC
XM_171208	LOC257019	1751	ACTAGTGTACAACCCAAGTGC
XM_171208	LOC257019	1752	ACTGGCCATATTTCGGGTGAAC
XM_171312	LOC256415	1753	ACGCACATCATGACTCACTCC
XM_171312	LOC256415	1754	ACAAGTGTTCCTGGGACTGGC
XM_171634	LOC255048	1755	ACAATGGGAACAGAATTGGTC
XM_174405	LOC253944	1756	ACCGACGAGGTGAAGACCATC
XM_174405	LOC253944	1757	ACCTGGGAGTTCAAGAACCAC
XM_174405	LOC253944	1758	ACTTTACAAGTGCAATCGGGC
NM_000283	PDE6B	1759	ACCTGTCTGCCATCACCAAGC
NM_000440	PDE6A	1760	ACTGCTGCTTTCTGCCATGAC
NM_000440	PDE6A	1761	ACGGAAGGAAATCGTTATGGC
NM_000921	PDE3A	1762	ACTGCCAAATAACTCAGCACC
NM_000923	PDE4C	1763	ACTGCGATATCTTCCAGAACC
NM_000924	PDE1B	1764	ACAGACATGTCCTGCCATTTT
NM_001083	PDE5A	1765	ACAAGAGAAATCAGGTGCTGC
NM_033430	PDE5A	1765	ACAAGAGAAATCAGGTGCTGC
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NM_033437	PDE5A	1765	ACAAGAGAAATCAGGTGCTGC
NM_001083	PDE5A	1766	ACTGACTTTAGCTTCAGTGAC
NM_033430	PDE5A	1766	ACTGACTTTAGCTTCAGTGAC
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NM_033437	PDE5A	1766	ACTGACTTTAGCTTCAGTGAC
NM_002599	PDE2A	1767	ACCAACTACCTCGAGGACATC
NM_002599	PDE2A	1768	ACCGGGAGAAGGCCTATATCC
NM_002600	PDE4B	1769	ACGTGGCATATCACAACAGCC
NM_002606	PDE9A	1770	ACATCTCACCGCTGGAGAACC
NM_005019	PDE1A	1771	ACAGGTATCATGCACTGGCTC
NM_005019	PDE1A	1772	ACCTGGTGGACATCATTCAGC
NM_005020	PDE1C	1773	ACATTCAGTCAGATGCTGTGC
NM_005020	PDE1C	1774	ACTTGTCTCATTTGTGGAGGC
NM_005021	ENPP3	1775	ACACTACTTTGTGGTGCTGAC
NM_006202	PDE4A	1776	ACAGAATGAAGTGAGATCCC
NM_006202	PDE4A	1777	ACACGATGGTGACATACATGC
NM_006202	PDE4A	1778	ACTGCGACATCTTCCAGAACC
NM_006203	PDE4D	1779	ACAGCGATTATGACCTCTCTC
NM_006203	PDE4D	1780	ACCATGCTGATGTGGCCTATC
NM_006203	PDE4D	1781	ACTCCAAGACTCTTTGTACTC
NM_006204	PDE6C	1782	ACACTGTGAGGAAAGGGTACC
NM_006204	PDE6C	1783	ACTAGCTGATGAGTATGATGC
NM_006209	ENPP2	1784	ACCGCTATGGATTACAGCCAC
NM_006209	ENPP2	1785	ACCTGCAGTGCTTTATCGGAC
NM_006209	ENPP2	1786	ACTCATGAAGATGCACACAGC
NM_006661	PDE10A	1787	ACTGCAACCTGGATTTTCATCC
NM_014936	ENPP4	1788	ACAGGCTTGTATGAAGAAAGC
NM_014936	ENPP4	1789	ACCAGTGGTGCATTAATCTCC

NM_015474	SAMHD1	1790	ACATGGAAGCCTATACTAAGC
NM_015474	SAMHD1	1791	ACTCCCTCTCCTGCACAATTC
NM_016641	MIR16	1792	ACTTCTGACGGGATTCTGTGTC
NM_016953	PDE11A	1793	ACTCAAATGAGGTGCAGGTCC
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NM_017711	FLJ20207	1795	ACTGATGTGATGGTCAGCTCC
NM_017711	FLJ20207	1796	ACCTACCTAATCATATGGGTC
NM_018945	PDE7B	1797	ACTACCTTGGACAAGCAAGGC
NM_024307	MGC4171	1798	ACACCCATGAGCGTAGAGATC
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NM_030792	PP1665	1800	ACCAACGTGGAGGAGGAGTTC
NM_030792	PP1665	1801	ACATATGCCAACAGCACCGCC
XM_031443	PDE8A	1802	ACTGTGCAGGTCTATCAGATC
XM_037534	PDE7A	1803	ACAGTCGAGCAGTGAGGACAC
XM_041695	PDE8B	1804	ACCAAGTGATCTTGTGGAGGC
XM_041695	PDE8B	1805	ACTGCTGTTCTGGAGAGTCAC
XM_041695	PDE8B	1806	ACTGGAAGACACTAGATGACC
XM_045585	KIAA1434	1807	ACAGCTTGTCTCTTATCATCC
XM_059626	LOC133121	1808	ACTACATCAGTGATGAGGCGC
XM_059626	LOC133121	1809	ACTGTCCTGAAGTACATGACC
XM_059626	LOC133121	1810	ACTTTAGTGGCTGATGAAGGC
NM_000068	CACNA1A	1811	ACAACAACACCAACAAGAGCC
NM_023035	CACNA1A	1811	ACAACAACACCAACAAGAGCC
XM_059898	LOC137057	1812	ACACGGAGCCTTTGGATGAGC
XM_059898	LOC137057	1813	ACGTAGTGACGGTCCATCAGC
XM_093333	LOC165622	1814	ACATGCCAGCTGTTTACCACC
XM_115430	LOC204524	1815	ACCACCGAAGAAAGGATCCAC
XM_166251	LOC220032	1816	ACCTATCAAGAATGCTGTAC
NM_000069	CACNA1S	1817	ACTCCATCTTCAAGGCCATGC
NM_000084	CLCN5	1818	ACATTGCCTGGTGTGGGAAGC
NM_000084	CLCN5	1819	ACATCCGTCTCAATGGATACC
NM_000085	CLCNKB	1820	ACTGGTACTTCCTGATGACCC
NM_004070	CLCNKA	1820	ACTGGTACTTCCTGATGACCC
NM_000085	CLCNKB	1821	ACCATCTTTGGGACCCCTTGCC
NM_004070	CLCNKA	1821	ACCATCTTTGGGACCCCTTGCC
NM_000085	CLCNKB	1822	ACTTCCCTGCATGAGGCACAC
NM_000087	CNGA1	1823	ACTACCATTGGTGAAACACCC
NM_000217	KCNA1	1824	ACGCCATCCTCTACTACTACC
NM_002235	KCNA6	1824	ACGCCATCCTCTACTACTACC
NM_000217	KCNA1	1825	ACCACGGTCATCTACAATTCC
NM_000219	KCNE1	1826	ACCATCTGGCCATAGAACAAC
NM_000220	KCNJ1	1827	ACAGAACAGTGTGCCACTGCC
NM_000238	KCNH2	1828	ACCCTCAACTTTGTGGACCTC
NM_000238	KCNH2	1829	ACCAACTCAGAGAAGATCTTC
NM_000238	KCNH2	1830	ACTCGCTTTCTCAGGTTTCCC
NM_000297	PKD2	1831	ACCTACGGCATGATGAGCTCC

NM_000297	PKD2	1832	ACAACCATGTCTCGATGTGCC
NM_000334	SCN4A	1833	ACAGAGTTTGTGGACTTGGGC
NM_000334	SCN4A	1834	ACCATCTGCATCGTGCTCAAC
NM_000336	SCNN1B	1835	ACTTCACGTCCATCTTCTACC
NM_000338	SLC12A1	1836	ACTCAGAATCAGCTTTAGGCC
NM_000338	SLC12A1	1837	ACTGGGATTCTTGCTGGTGCC
NM_000342	SLC4A1	1838	ACTTCGAAGGCGCTATCAGTC
NM_000342	SLC4A1	1839	ACGGGCATCCAGATCATCTGC
NM_000492	CFTR	1840	ACTGAGTGGAGGTCAACGAGC
NM_000525	KCNJ11	1841	ACCATGTCCCTTCCGTGCAGC
NM_000540	RYR1	1842	ACTGTGTCCCTCATTGAGAGTC
NM_000544	TAP2	1843	ACAAAGTCTTGATGTGGAGGC
NM_018833	TAP2	1843	ACAAAGTCTTGATGTGGAGGC
NM_000544	TAP2	1844	ACCCTCCTTTCTCTGCTGCAC
NM_018833	TAP2	1844	ACCCTCCTTTCTCTGCTGCAC
NM_000544	TAP2	1845	ACAGCCAAATCTGCCTTCACC
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NM_000544	TAP2	1846	ACAGTGCTGGTGATTGCTCAC
NM_000617	SLC11A2	1847	ACAAATATGGCTTGCGGAAGC
NM_000617	SLC11A2	1848	ACCTATTCTGGCCAGTTTGTC
NM_000701	ATP1A1	1849	ACCGTGGAAGACATTGCTGCC
NM_000701	ATP1A1	1850	ACTTGGGCACTGACATGGTTC
NM_000702	ATP1A2	1851	ACGGATGAGCTGAACTTTCCC
NM_000702	ATP1A2	1852	ACAGATCGGGATGATCCAGGC
NM_000703	ATP1A3	1853	ACTGTGTGCAGGGTTTGACCC
NM_000703	ATP1A3	1854	ACAAGAAAGTGGCTGAGATTC
NM_000704	ATP4A	1855	ACCTGAATGAGAAGGACTACC
NM_000705	ATP4B	1856	ACACACCGGACTACCAAGACC
NM_000705	ATP4B	1857	ACCAAGTTCTCCTGCAAGTTC
NM_000705	ATP4B	1858	ACCTTCAGTCTGCACTACTTC
NM_000718	CACNA1B	1859	ACTCATCTTTGCAGCACCACC
NM_000721	CACNA1E	1860	ACCATCATTGCCAACTGCATC
NM_000725	CACNB3	1861	ACACCATCAACCACCCAGCAC
NM_000726	CACNB4	1862	ACAGACATGATGCAGAAAGCC
NM_000742	CHRNA2	1863	ACTGAGATCATCCCGTCCACC
NM_000744	CHRNA4	1864	ACCTCACTGGTCATCCCACCTC
NM_000745	CHRNA5	1865	ACGTGTTCCCTTCAGACTCTTC
NM_000747	CHRNA1	1866	ACTATGGTGTTTCAGCTCCTAC
NM_000747	CHRNA1	1867	ACCTCATGTTTACCATGGTCC
NM_000748	CHRNA2	1868	ACCTCATGTTTACCATGGTGC
NM_000750	CHRNA4	1868	ACCTCATGTTTACCATGGTGC
NM_000748	CHRNA2	1869	ACCATGGTGCTTGTCACCTTC
NM_000749	CHRNA3	1870	ACCCTGTCCATCATTGTTACC
NM_000750	CHRNA4	1871	ACCTATGAGGTGTCTGTCTAC
NM_000806	GABRA1	1872	ACCAGTATGACCTTCTTGAC
NM_000806	GABRA1	1873	ACTGTCAAGAATAGCCTTCCC

NM_000807	GABRA2	1874	ACCATCTCCAAGAGTGCAACC
NM_000808	GABRA3	1875	ACTGAAGTTTGGAAGCTATGC
NM_000808	GABRA3	1876	ACCAGCACTACCTTCAACATC
NM_000809	GABRA4	1877	ACATTCTTTGCCCAAAGTGTC
NM_000809	GABRA4	1878	ACTTCCATCTGCTTCTCCTAC
NM_000810	GABRA5	1879	ACCATGACGACCCTCAGCATC
NM_000810	GABRA5	1880	ACCCCTCTGAAGAGAAGACTTC
NM_000811	GABRA6	1881	ACTCAAGTTTGGGAGCTATGC
NM_000811	GABRA6	1882	ACCAC'TTTGAGCATCAGTGCC
NM_000811	GABRA6	1883	ACAATCAACACCTGTCAACACC
NM_000812	GABRB1	1884	ACTCCGAATCACAACCACAGC
NM_000813	GABRB2	1885	ACAGCTGCCTGCATGATGGAC
NM_021911	GABRB2	1885	ACAGCTGCCTGCATGATGGAC
NM_000813	GABRB2	1886	ACCACAATCAACACCCACCTC
NM_021911	GABRB2	1886	ACCACAATCAACACCCACCTC
NM_000814	GABRB3	1887	ACAATCGAGTGGCTGACCAGC
NM_021912	GABRB3	1887	ACAATCGAGTGGCTGACCAGC
NM_000815	GABRD	1888	ACCACGGAGCTGATGAACTTC
NM_000816	GABRG2	1889	ACTGTCTTGACAATGACCACC
NM_000824	GLRB	1890	ACCAAAC'TTCAAAGGCATTCC
NM_000824	GLRB	1891	ACTTTGCAGGTTGGTGAGACC
NM_000824	GLRB	1892	ACAACGGACTTGGGAAATCTC
NM_000826	GRIA2	1893	ACAGAGGCTTATCAACACTGC
NM_000826	GRIA2	1894	ACGGCTAACTTAGCTGCCTTC
NM_000827	GRIA1	1895	ACTGTCAACATGCTGACCTCC
NM_000827	GRIA1	1896	ACATTGGAGTGAGTGTGTCC
NM_000828	GRIA3	1897	ACACCATCAGCATAGGTGGAC
NM_007325	GRIA3	1897	ACACCATCAGCATAGGTGGAC
NM_000828	GRIA3	1898	ACAGGTTTCCAGATTGTCAAC
NM_007325	GRIA3	1898	ACAGGTTTCCAGATTGTCAAC
NM_000828	GRIA3	1899	ACATTGGTCCGTGAAGAAGTC
NM_007325	GRIA3	1899	ACATTGGTCCGTGAAGAAGTC
NM_000830	GRIK1	1900	ACACCCTACGAGTGGTATAAC
NM_000831	GRIK3	1901	ACCACAGATGACCGTGAATC
NM_000831	GRIK3	1902	ACACGCATCATTGGTGGCATC
NM_000831	GRIK3	1903	ACACATTCAATGACCGCCGGC
NM_000832	GRIN1	1904	ACCTGCTCATCAAGCTGGCAC
NM_007327	GRIN1	1904	ACCTGCTCATCAAGCTGGCAC
NM_021569	GRIN1	1904	ACCTGCTCATCAAGCTGGCAC
NM_000869	HTR3A	1905	ACAGGAGTGTCTTCATGAACC
NM_000869	HTR3A	1906	ACTTTGTGGTGTGCATGGCTC
NM_000890	KCNJ5	1907	ACAACCATTGGGTATGGCTTC
NM_000890	KCNJ5	1908	ACCTATGAGACCAACACACCC
NM_000891	KCNJ2	1909	ACGAGACTCTTGTCTTCAGTC
NM_001035	RYR2	1910	ACACATGGACGAGTGTCTCAC
NM_001035	RYR2	1911	ACTCATGGACAAAGAGAAAGC

NM_001035	RYR2	1912	ACCCAAGAATTACCAGCTGAC
NM_001036	RYR3	1913	ACATCAAGTCGATCATCTCCC
NM_001039	SCNN1G	1914	ACTGTGCTCAAATGACACCTC
NM_001039	SCNN1G	1915	ACATCATGGCACAGGTGCCTC
NM_001046	SLC12A2	1916	ACAAACTGTACTTCTGCAGCC
NM_001095	ACCN2	1917	ACTTCAAGGTGGTCTTCACAC
NM_020039	ACCN2	1917	ACTTCAAGGTGGTCTTCACAC
NM_001095	ACCN2	1918	ACGCCTACGAGGTCATTAAGC
NM_020039	ACCN2	1918	ACGCCTACGAGGTCATTAAGC
NM_001194	HCN2	1919	ACCATCGGGAAGAAGATGTAC
NM_001285	CLCA1	1920	ACAATGGAATCCACCAAGACC
NM_001285	CLCA1	1921	ACAGCACCATTCTTGGCATTTC
NM_001286	CLCN6	1922	ACCTTTGTCTTCTTGGCAAGC
NM_021735	CLCN6	1922	ACCTTTGTCTTCTTGGCAAGC
NM_021736	CLCN6	1922	ACCTTTGTCTTCTTGGCAAGC
NM_021737	CLCN6	1922	ACCTTTGTCTTCTTGGCAAGC
NM_001286	CLCN6	1923	ACCTTCACCCTCAACTTCTTC
NM_021735	CLCN6	1923	ACCTTCACCCTCAACTTCTTC
NM_021736	CLCN6	1923	ACCTTCACCCTCAACTTCTTC
NM_021737	CLCN6	1923	ACCTTCACCCTCAACTTCTTC
NM_001288	CLIC1	1924	ACTGTGGCTCAAGGGAGTCAC
NM_001288	CLIC1	1925	ACAATCTGGAGAAGGGACTCC
NM_001297	CNGB1	1926	ACTCATTGACCCTGACGTCAC
NM_001298	CNGA3	1927	ACAGAGACAAGGACCAACTAC
NM_001298	CNGA3	1928	ACGCTGAAGAAGGTTGCGATC
NM_001542	IGSF3	1929	ACTGTGAAACAGCCAGACAGC
NM_001542	IGSF3	1930	ACCATCCTTCTGGTGCCTTTC
NM_001678	ATP1B2	1931	ACCAGCTGGGCCTTTATCCTC
NM_001679	ATP1B3	1932	ACCGTGACCAGATTCTTAGCC
NM_001682	ATP2B1	1933	ACTCACCGCTTAAGGCTGTGC
NM_001683	ATP2B2	1934	ACGGTGATCATCTGGTGCTC
NM_001684	ATP2B4	1935	ACTCTCAGACTGGAATCATCC
NM_001829	CLCN3	1936	ACTGAGGCAGTGCCTTGTAAC
NM_002042	GABRR1	1937	ACCATGATTTTACGATGAGGC
NM_002042	GABRR1	1938	ACTACTGGAAGGACGAGAGGC
NM_002042	GABRR1	1939	ACTCCAAACGCTCCTTCATCC
NM_002043	GABRR2	1940	ACTGCCATGTGCAACATGGAC
NM_002043	GABRR2	1941	ACTCTGATGGTCATGCTGTCC
NM_002063	GLRA2	1942	ACAACCTTCACAGACCCTATC
NM_002088	GRIK5	1943	ACCTTGATCATCATCTCCTCC
NM_002222	ITPR1	1944	ACATGCATGTGGACCGAGATC
NM_002222	ITPR1	1945	ACCAGCAGAATCAAGCTTTGC
NM_002224	ITPR3	1946	ACATGATGTCCACCATGGTGC
NM_002232	KCNA3	1947	ACGCCATCCTCTACTACTATC
NM_002233	KCNA4	1948	ACGTGTGGTGATAAATGTGTC
NM_000217	KCNA1	1949	ACATCAACATCTCCGGGCTGC

NM_002234	KCNA5	1949	ACATCAACATCTCCGGGCTGC
NM_002234	KCNA5	1950	ACCACGTGCGTCATCTGGTTTC
NM_002236	KCNF1	1951	ACGAGCTGGAGCTGATGGAAC
NM_002237	KCNG1	1952	ACTATCCTGACCTTCCTGCGC
NM_002237	KCNG1	1953	ACCTGGAGCTCAAAACAGGAGC
NM_002238	KCNH1	1954	ACTGGCCATGGAGTTCCAGAC
NM_002239	KCNJ3	1955	ACCAAGATGTTATCTGATCCC
NM_002240	KCNJ6	1956	ACCAGCCAAAGTTGCCTAAGC
NM_002240	KCNJ6	1957	ACATGGACCACATAGAGGACC
NM_002240	KCNJ6	1958	ACCCAAGAAGAGGGCAGAGAC
NM_002241	KCNJ10	1959	ACCACCATTGGCTATGGCTTC
NM_002241	KCNJ10	1960	ACTTTCCAAGTAGACACAGCC
NM_002243	KCNJ15	1961	ACTGTCAAATTCCACGTGGAC
NM_002244	KCNJN1	1962	ACGAGAAGTCACAGCGCTACC
NM_021012	KCNJ12	1962	ACGAGAAGTCACAGCGCTACC
NM_002244	KCNJN1	1963	ACGCAGAACACCATCAGCTAC
NM_002244	KCNJN1	1964	ACCACAGCTTTCTGGTGTAC
NM_002245	KCNK1	1965	ACTGTGTCTGCTTCTTCTTC
NM_002245	KCNK1	1966	ACTGTCCTTCTCCTCGATCAC
NM_002246	KCNK3	1967	ACCTTCTTCCAGGCCTACTAC
NM_002249	KCNN3	1968	ACAAGATCAACTTCAACACCC
NM_002250	KCNN4	1969	ACCTTCTTACTCCTCTGCCTC
NM_002250	KCNN4	1970	ACCTTTCAGACACACTTTGGC
NM_002250	KCNN4	1971	ACATGATCCTGTATGACCTGC
NM_002420	TRPM1	1972	ACTTTGAGATGCAGCCCAAGC
NM_002420	TRPM1	1973	ACGTATCTGCTCCAGATCAGC
NM_002558	P2RX1	1974	ACCAACTACCGTCACCTCTTC
NM_002559	P2RX3	1975	ACCTCGGTCTTTGTATCATC
NM_002559	P2RX3	1976	ACTTTGAGAAGGGAAACCTCC
NM_002559	P2RX3	1977	ACTGTTCTCTGTGACATCATC
NM_002561	P2RX5	1978	ACCTGGTCGTATGGGTGTTCC
NM_002976	SCN7A	1979	ACAAAGACTGTCAACTCCCAC
NM_002976	SCN7A	1980	ACAAGAGGCAGTTTCAGCAAC
NM_002978	SCNN1D	1981	ACCTTCTTCTGCACCAATGCC
NM_002978	SCNN1D	1982	ACTATGTGGATATCCTGGCCC
NM_003040	SLC4A2	1983	ACGGGATCCAGTTCTATGAGC
NM_003048	SLC9A2	1984	ACATCACTTTGCTCCAGAACC
NM_003048	SLC9A2	1985	ACAGTTTGACTGAAGGCATCC
NM_003052	SLC34A1	1986	ACCTCTGTACCAACACCATC
NM_003304	TRPC1	1987	ACCATACGTCTAGTGACGAGC
NM_003307	TRPM2	1988	ACAAGCAGCTCAAGAACAAGC
NM_003740	KCNK5	1989	ACAGGGAACCAGACCTTCAAC
NM_003740	KCNK5	1990	ACTTTGTGGCCGGTGTGAACC
NM_003759	SLC4A4	1991	ACATGTATGGAGAAAGGATCC
NM_003759	SLC4A4	1992	ACTCACTATTCTGAGCAGCAC
NM_003759	SLC4A4	1993	ACGGTCATCTCCATTGCTCAC

NM_004137	KCNMB1	1994	ACCGGTGGCCTCCTCATTATC
NM_004174	SLC9A3	1995	ACCAAGCATGTGCGTATCATC
NM_004174	SLC9A3	1996	ACGCAGATTCCCTACTCTCCC
NM_004198	CHRNA6	1997	ACAATGCTGTTGGTGACTTCC
NM_004198	CHRNA6	1998	ACAGCCACTACTTGGGAACAC
NM_004366	CLCN2	1999	ACCTGAACCGGAAGATTGTCC
NM_004366	CLCN2	2000	ACAGCACAGGGTGTGAAAGTC
NM_004518	KCNQ2	2001	ACCGCAAGCTGCAGAATTTCC
NM_004518	KCNQ2	2002	ACGTCTTTGCCACATCTGCGC
NM_004518	KCNQ2	2003	ACTCAGAAGAAGCAAGCCTCC
NM_004519	KCNQ3	2004	ACTGAAGTTTGCCAGGAAGCC
NM_004519	KCNQ3	2005	ACAGTGACACACCTCTGTCCC
NM_004621	TRPC6	2006	ACGGTTCTCCCATGATGTGAC
NM_004700	KCNQ4	2007	ACTGGGCATCTCTTTCTTTGC
NM_004727	SLC24A1	2008	ACCATCCGCAGCACCATCTAC
NM_004769	ACCN3	2009	ACTCCCTGGATGACATGCTGC
NM_020321	ACCN3	2009	ACTCCCTGGATGACATGCTGC
NM_020322	ACCN3	2009	ACTCCCTGGATGACATGCTGC
NM_004769	ACCN3	2010	ACCAGACCTTTGTTTCTTGCC
NM_020321	ACCN3	2010	ACCAGACCTTTGTTTCTTGCC
NM_020322	ACCN3	2010	ACCAGACCTTTGTTTCTTGCC
NM_004769	ACCN3	2011	ACTACCTCTGTGAGGTGTTCC
NM_020321	ACCN3	2011	ACTACCTCTGTGAGGTGTTCC
NM_020322	ACCN3	2011	ACTACCTCTGTGAGGTGTTCC
NM_004769	ACCN3	2012	ACTCCAGCACCAATCTGCTTC
NM_020321	ACCN3	2012	ACTCCAGCACCAATCTGCTTC
NM_004770	KCNB2	2013	ACTGCAACACACACGAGAGCC
NM_004823	KCNK6	2014	ACAGTCTACCTCTTCCTGGGC
NM_004823	KCNK6	2015	ACACCGACTACGCTTCCATCC
NM_004858	SLC4A8	2016	ACAGCATGAGGGTTAAAGTGC
NM_004858	SLC4A8	2017	ACCGAGATGCACTCAGCTTAC
NM_004909	TRAG3	2018	ACCAGGTGGACTGGAGTATAC
NM_004909	TRAG3	2019	ACCAACACCAAAGAGGTTCCC
NM_004961	GABRE	2020	ACTGTTGAGATCGCCGTCAAC
NM_004974	KCNA2	2021	ACTCTGCATCATCTGGTTCTC
NM_004974	KCNA2	2022	ACAAGTGTAGGCTATGGAGAC
NM_004976	KCNC1	2023	ACAGCCACTTCGACTATGACC
NM_004976	KCNC1	2024	ACTCTCCACACCACAGTACTC
NM_004978	KCNC4	2025	ACCACTTCTGCCTGGAGACC
NM_004978	KCNC4	2026	ACACCGACTTCAAGAACATCC
NM_004979	KCND1	2027	ACTTGGAAGAATACGCTGGAC
NM_004979	KCND1	2028	ACTCACAGGGCTTGAGGATTC
NM_004980	KCND3	2029	ACCACGAGTTTATTGATGAGC
NM_004981	KCNJ4	2030	ACGTTGCTGTTTCAGCCACCAC
NM_004981	KCNJ4	2031	ACTTTGAGATCGTGGTCATCC
NM_021012	KCNJ12	2031	ACTTTGAGATCGTGGTCATCC

XM_171828	LOC254633	2031	ACTTTGAGATCGTGGTCATCC
NM_004982	KCNJ8	2032	ACCATGTCTCTCCTCTGCAGC
NM_004983	KCNJ9	2033	ACATACCGCTACCTGACGGAC
NM_004983	KCNJ9	2034	ACATAGTGAGGGCTCCATCC
NM_005070	SLC4A3	2035	ACTGCTCTGGGTGGTCAAGTC
NM_005072	SLC12A4	2036	ACAATGAGACAGTGGCCACCC
NM_005072	SLC12A4	2037	ACCATTGTTGGTTCTGTCTATC
NM_005072	SLC12A4	2038	ACGAGAACTACATGGAGTTCC
NM_005074	SLC17A1	2039	ACCTCCTATGGTGTCTCATCTC
NM_005074	SLC17A1	2040	ACAATCTCTGCCTATCAAGGC
NM_005135	SLC12A6	2041	ACATGGAGTTCCTAGAGGTGC
NM_005136	KCNE2	2042	ACAACAGCTGAGCAAGAGGCC
NM_005173	ATP2A3	2043	ACCACCAATCAGATGTCTGTCT
NM_005173	ATP2A3	2044	ACTTCCTCATCCTGCTCGTGC
NM_005199	CHRNA1	2045	ACCAGAAAGGTGGTGTCTTACC
NM_005199	CHRNA1	2046	ACTCATCAGCAAGTACCTGAC
NM_005446	P2RX1	2047	ACCCACAGGACCTGTGAGATC
NM_005446	P2RX1	2048	ACCTTCAGCAAGTTCAACTTC
NM_005472	KCNE3	2049	ACAGCAATTTGCTCTGCCGGC
NM_005472	KCNE3	2050	ACCTGGCCGTGATGACAACTC
NM_005477	HCN4	2051	ACACCGTCTTCATCCTCCTTC
NM_005549	KCNA10	2052	ACAGACTTCGACTCAACCAGC
NM_005549	KCNA10	2053	ACTCTCATCACAGAGCTAGTC
NM_005832	KCNMB2	2054	ACTGCTCCTTCAGCTGTGGTC
NM_005832	KCNMB2	2055	ACTTCTCCTGCTATTCTGACC
NM_006028	HTR3B	2056	ACCAAGGCCACCACAGTCTAC
NM_006071	PKDREJ	2057	ACAACCTCTCTACCGAGGTAGC
NM_006071	PKDREJ	2058	ACTGTGACTAAGCTGGAAGAC
NM_006359	SLC9A6	2059	ACCTGCTCATCTTCATCCTGC
NM_006424	SLC34A2	2060	ACTGTCCATGACTTCTTCAAC
NM_006424	SLC34A2	2061	ACCTACAAGGAGAACATCGCC
NM_006529	GLRA3	2062	ACTGGAAAGCTTTGGGTACAC
NM_006529	GLRA3	2063	ACAGAGTTCAGGATCACGAGC
NM_006922	SCN3A	2064	ACCACCACTGAAACGGAAGTC
NM_006922	SCN3A	2065	ACTGTGAGGCTCTTGGAAGC
NM_007332	ANKTM1	2066	ACATGTGACGATATGGACACC
NM_007332	ANKTM1	2067	ACCGCATAGAGCTTCTCAATC
NM_012128	CLCA4	2068	ACACACTCATGGCAGGATTAC
NM_012128	CLCA4	2069	ACATTGATCCTACTCCTACTC
NM_012226	P2RX2	2070	ACCATCCTCATCAAGAACAGC
NM_016318	P2RX2	2070	ACCATCCTCATCAAGAACAGC
NM_012281	KCND2	2071	ACCGTGACCCAGACATCTTCC
NM_012281	KCND2	2072	ACCATGGCTATCATCATCTTC
NM_012281	KCND2	2073	ACGAGCAGACAAACGAAGGGC
NM_012283	KCNG2	2074	ACATCATTTGACATCCTGGCGC
NM_012285	KCNH4	2075	ACGTGACAGCCATCATCCAGC

NM_012285	KCNH4	2076	ACTTGAGACCTTCCATATTGC
NM_012471	TRPC5	2077	ACCTCTCATCAGAACCATGCC
NM_013348	KCNJ14	2078	ACGCTGGTCTTCAGCGAGAAC
NM_013943	CLIC4	2079	ACACGTAAATTTCTGGATGGC
NM_013943	CLIC4	2080	ACGAGTTCACCAATACCTGTC
NM_014139	SCN12A	2081	ACAATCTACCGCTTCAGTGCC
NM_014139	SCN12A	2082	ACTGAGCTGGCCATCACCATC
NM_014211	GABRP	2083	ACTCTGTGCGTGGACTGGAAC
NM_014217	KCNK2	2084	ACCTCCAATCAAATCAGTCAC
NM_014217	KCNK2	2085	ACCACAATCAGGAGCTGACTC
NM_014274	ABP/ZF	2086	ACCTTTGCCTGCCAGATGTAC
NM_018646	TRPV6	2086	ACCTTTGCCTGCCAGATGTAC
NM_019841	TRPV5	2086	ACCTTTGCCTGCCAGATGTAC
NM_014274	ABP/ZF	2087	ACACTGCTCATGCTCAACCTC
NM_018646	TRPV6	2087	ACACTGCTCATGCTCAACCTC
NM_014382	ATP2C1	2088	ACTGAGGTTACTGGAGTTGGC
NM_014382	ATP2C1	2089	ACTCATTGCCTCAGGAGTATC
NM_014386	PKD2L2	2090	ACAAGTTCATTGACCTTCGAC
NM_014407	KCNMB3	2091	ACTGACTCTGCTAGGTGGTGC
NM_014505	KCNMB4	2092	ACATTTGTGGTGGGCGTTCTC
NM_014619	GRIK4	2093	ACCGGCCACATTGAATTCAAC
NM_016112	PKD2L1	2094	ACTCGAGTGGTGTTCATCGAC
NM_016112	PKD2L1	2095	ACCTATGTCTTCTTCGTCTTC
NM_016121	LOC51133	2096	ACGAGTGATTGTACAACACCC
NM_016179	TRPC4	2097	ACTGGAATCTCGAGGATTAGC
NM_016601	KCNK9	2098	ACAGCATGGTCATTACATCC
NM_016611	KCNK4	2099	ACCAACTCGACCAGCAACAGC
NM_033310	KCNK4	2099	ACCAACTCGACCAGCAACAGC
NM_033311	KCNK4	2099	ACCAACTCGACCAGCAACAGC
NM_016929	CLIC5	2100	ACCTCAAGAACGCCTATGCCC
NM_017662	TRPM6	2101	ACCTGGAGAAGTACCTCTCTC
NM_017662	TRPM6	2102	ACATGCAGGTCCATATGTGAC
NM_017915	FLJ20641	2103	ACACAGTATCTCCTAGTCAAC
NM_018298	MCOLN3	2104	ACAGTTCGTCATCAAGAACTC
NM_018298	MCOLN3	2105	ACAGATTAGAAGATGACCCCTC
NM_018558	GABRQ	2106	ACCACTACAGCAGCTTGTTCC
NM_018658	KCNJ16	2107	ACATCTCACCAATCTAGAAGC
NM_018658	KCNJ16	2108	ACACCTTATCAGAAAGCTCTC
NM_018674	ASIC4	2109	ACATCTTCCACCTGGCCAATC
NM_018674	ASIC4	2110	ACCATCTGCCCACCAATATC
NM_018674	ASIC4	2111	ACGTTGCTGGAGATCCTCGAC
NM_018896	CACNA1G	2112	ACCAGCAGCCCATCATGAACC
NM_018992	FLJ20040	2113	ACCCGAAATCCTTCCTGTACC
NM_019098	CNGB3	2114	ACAGCCAATCAGAACTACTTC
NM_019098	CNGB3	2115	ACTCATTATCAGCATGGCTCC
NM_019841	TRPV5	2116	ACCTGGACAAGCTTCATATGC

NM_019841	TRPV5	2117	ACTCAGACAAGGAGGATGACC
NM_020344	SLC24A2	2118	ACACCGTCATTCACAGATTCC
NM_020389	trp7	2119	ACAAGTGGTGGCCTTCAGACC
NM_020402	CHRNA10	2120	ACTCTATAACAAAGCCGACGC
NM_020402	CHRNA10	2121	ACTATGACCATGGTCACATTC
NM_020402	CHRNA10	2122	ACCATTGCCAATACCTTCCGC
NM_020533	MCOLN1	2123	ACATCCAGGAGTGTAAGCACC
NM_020689	NCKX3	2124	ACAGCAAGAACTGCACCGAAC
NM_020689	NCKX3	2125	ACCGTACACACCATTCGACAC
NM_021007	SCN2A2	2126	ACGCATTGCAGAAGAGAAAGC
NM_021096	CACNA1I	2127	ACATGGAACCGCCTGGATTTTC
NM_021096	CACNA1I	2128	ACCAACATCCTGGAGATCTGC
NM_021096	CACNA1I	2129	ACTCATCTCCTCCCTCAAGCC
NM_021097	SLC8A1	2130	ACTACCAAGTCCTAAGTCAGC
NM_021097	SLC8A1	2131	ACTTGTGGAGAGCTCGAATTC
NM_021097	SLC8A1	2132	ACGAATATGATGACAAGCAGC
NM_021098	CACNA1H	2133	ACCTGTGAGCTGAAGAGCTGC
NM_021137	TNFAIP1	2134	ACCATGCTCAAGGCCATGTTTC
NM_021137	TNFAIP1	2135	ACCAGCCTGTGTGCAACATCC
NM_021161	KCNK10	2136	ACAACCTCCAGCACAGCCATGC
NM_138317	KCNK10	2136	ACAACCTCCAGCACAGCCATGC
NM_138318	KCNK10	2136	ACAACCTCCAGCACAGCCATGC
NM_021196	SLC4A5	2137	ACCCTCATGGTAGATGATCTC
NM_033323	SLC4A5	2137	ACCCTCATGGTAGATGATCTC
NM_133478	SLC4A5	2137	ACCCTCATGGTAGATGATCTC
NM_133479	SLC4A5	2137	ACCCTCATGGTAGATGATCTC
NM_021196	SLC4A5	2138	ACTCCATTCTGGGAACGCTGC
NM_033323	SLC4A5	2138	ACTCCATTCTGGGAACGCTGC
NM_021614	KCNN2	2139	ACTTACAATGCTGAGCGGTCC
NM_021949	ATP2B3	2140	ACTACAAAGAGATTCCGGCCC
NM_022054	KCNK13	2141	ACCATCTTGTTCTTCAACCTC
NM_022055	KCNK12	2142	ACCATCCTGTTCTTCAACCTC
NM_022055	KCNK12	2143	ACCTTCAGCACCATCGGCTTC
NM_022058	SLC4A10	2144	ACTGTGTGGAACCGCATAATC
NM_022358	KCNK15	2145	ACGCTGGTCACTTTCCAGAGC
NM_024076	MGC2628	2146	ACCGGAGACGTCATGTGCAAC
NM_024080	TRPM8	2147	ACTGGAAGATTATCCTGTGTC
NM_024681	FLJ12242	2148	ACAGGAGAAAGGTTCCCGTCC
NM_031460	KCNK17	2149	ACCACCATTGGCTATGGCAAC
NM_031460	KCNK17	2150	ACAGAGGGGCTTCTACTTCGCC
NM_031886	KCNA7	2151	ACGCCGTGCTCTACTACTACC
NM_032115	KCNK16	2152	ACCAGTTTCAGTTGGAGAAGC
NM_032115	KCNK16	2153	ACTATGTTGTTGGCACAGACC
NM_032591	SLC9A7	2154	ACCATCTGGCTCTTCAAGCAC
NM_032591	SLC9A7	2155	ACTGTCCCTCGTCTATTGTTGC
NM_032591	SLC9A7	2156	ACCACCCTTCTCATTGTGTTTC

NM_033223	GABRG3	2157	ACCCTCAACTACTATTCCAGC
NM_033223	GABRG3	2158	ACTGGGTTGGATACCTGTATC
NM_033272	KCNH7	2159	ACCAAGAGGCATGATATTGCC
NM_033272	KCNH7	2160	ACGTTACAATGACAGTGACTC
NM_005714	KCNK7	2161	ACAGGTTATGGCCACATGGCC
NM_033347	KCNK7	2161	ACAGGTTATGGCCACATGGCC
NM_033348	KCNK7	2161	ACAGGTTATGGCCACATGGCC
NM_033455	KCNK7	2161	ACAGGTTATGGCCACATGGCC
NM_033456	KCNK7	2161	ACAGGTTATGGCCACATGGCC
NM_053054	CATSPER1	2162	ACCATTACGAGTTGCACCATC
NM_053054	CATSPER1	2163	ACCCACTCCTTCGCCATCTAC
NM_053054	CATSPER1	2164	ACCATGCTGAAGCGGCTCATC
NM_054020	CATSPER2	2165	ACCATGTTGTCCCTGCTTCCC
NM_018727	TRPV1	2166	ACGCTGAGGTCTTCAAGAGTC
NM_080704	TRPV1	2166	ACGCTGAGGTCTTCAAGAGTC
NM_080705	TRPV1	2166	ACGCTGAGGTCTTCAAGAGTC
NM_080706	TRPV1	2166	ACGCTGAGGTCTTCAAGAGTC
NM_130770	HTR3C	2167	ACCAACTACAGCATCCCTACC
NM_130770	HTR3C	2168	ACTGGACATCTTCTACTTCCC
NM_130770	HTR3C	2169	ACACTTCTGCTGGGCTACAAC
NM_133329	KCNG3	2170	ACGAGTACTTCTTCGACCGGC
NM_133329	KCNG3	2171	ACCTACACCTTCTACTCGGCC
NM_133329	KCNG3	2172	ACAGGCGAGAAGTCTCAACTC
NM_133497	Kv11.1	2173	ACTTCTCTGCGGCTGTCTAC
NM_138392	LOC92799	2174	ACCCAGTTTCTAGTCTGCTAC
NM_138392	LOC92799	2175	ACACCTCCCAAGATGAAGCTC
NM_138444	LOC115207	2176	ACAGCAAAGGCCGCTTCTTTC
NM_139075	TPC2	2177	ACCAGATGACTGTGGAGCTCC
XM_030524	KIAA0939	2178	ACACCGAAGATGATGTTTCATC
XM_030524	KIAA0939	2179	ACTCTCACCAACAAGTGGTAC
SK423	ChaK1	2180	ACAGAGCTAAGTATGTGAGGC
XM_030709	TRPM7	2180	ACAGAGCTAAGTATGTGAGGC
XM_036123	TRPM3	2181	ACTTCTCCAACCTTAATGCCC
XM_038736	SLC4A9	2182	ACTCTACATTTACCTGGCCAC
XM_038736	SLC4A9	2183	ACACCAAAGCTCATGGTACCC
XM_044785	KCNJ13	2184	ACCAGTTTCACAGCTGCATTC
XM_044785	KCNJ13	2185	ACAGGACTGACCTGGATATCC
XM_046881	SLC9A1	2186	ACCTCCCGATTTACCTCCCAC
XM_059638	LOC133308	2187	ACAAGAAACACCAACTGAAGC
XM_059638	LOC133308	2188	ACCTGCTGGGTTTACCATGGC
XM_062645	LOC121456	2189	ACCATATGGCTCTTCAAGTAC
XM_062645	LOC121456	2190	ACACAAGCTCATTACACCTTC
XM_062909	LOC122032	2191	ACAGAAAGCACAGGCTTTGCC
XM_063451	SLC24A4	2192	ACCTTCATGGCTGCAGGAAGC
XM_063451	SLC24A4	2193	ACGAGATTATGAGCTCCAGCC
XM_063919	LOC123948	2194	ACTCAGAATCTAAGCCAACCC

XM_063919	LOC123948	2195	ACCCGTTACAACAACCTGATC
XM_066258	LOC128944	2196	ACCACAGATTGGCCTCCAATC
XM_066258	LOC128944	2197	ACACTTAGCCAGAGGTTTGGC
XM_066360	LOC128997	2198	ACCAGCTCATTACTCTAGGTC
XM_066360	LOC128997	2199	ACAAGGTCACCAGCATAGTCC
XM_066668	LOC139390	2200	ACCCTGATGCCAAGAAAGTCC
XM_069849	LOC136363	2201	ACGTCACTTGGAGGAGCAGTC
XM_070698	LOC137979	2202	ACCATCTATAGACCACCAGCC
XM_072244	LOC130535	2203	ACAGATGAGCAAACCCGCATC
XM_084997	bA430M15.1	2204	ACAGTGGTCGTCAGCATGTAC
XM_085367	LOC146212	2205	ACAGCTGGGTGGAGCTTACAC
XM_085367	LOC146212	2206	ACTCCATCCTGGGAAAGTACC
XM_086379	MGC25056	2207	ACTCTTGGCTGCATTTCTGTC
XM_086565	KIAA1535	2208	ACATCTTCCTAGTGGTGGAGC
NM_005477	HCN4	2209	ACTCATCCAGTCCCTGGACTC
XM_086565	KIAA1535	2209	ACTCATCCAGTCCCTGGACTC
XM_091397	LOC162163	2210	ACTGCTGGTCAGCATCCATAC
XM_092804	CLIC6	2211	ACATCCCGAATCTAATTCCGC
XM_092804	CLIC6	2212	ACACGCATATTCTAGATGTTGC
XM_093929	LOC166538	2213	ACCAAGCAGAACTCTCTCAAC
XM_094080	LOC166765	2214	ACAGCATTGGACCAGTTGATC
XM_094080	LOC166765	2215	ACAACCCTGAGTACAATTGCC
XM_095739	LOC206980	2216	ACACCTAACGTACTAAGGCTC
XM_095780	LOC169572	2217	ACTTTGTGATGGTACAGAGCC
XM_095797	LOC169596	2217	ACTTTGTGATGGTACAGAGCC
XM_095780	LOC169572	2218	ACCTCAGAGAAAGGATCACGC
XM_095797	LOC169596	2218	ACCTCAGAGAAAGGATCACGC
NM_002295	LAMR1	2219	ACTCCAATTGCTGGCCGCTTC
XM_095780	LOC169572	2219	ACTCCAATTGCTGGCCGCTTC
XM_114305	LOC200845	2220	ACCAGATTGAGCCCTTGATTC
XM_166742	LOC219896	2221	ACTTTCACGGGACCATTTCATC
XM_166943	LOC220370	2222	ACTGAACCAGCGTGTGCAGAC
XM_166943	LOC220370	2223	ACAAGCAGATCAACAGCTTCC
XM_170731	LOC254387	2224	ACAAAGCCAGGGAATGTAACC
XM_170803	LOC253980	2225	ACCATGCTCAAAGCCATGTTC
XM_170803	LOC253980	2226	ACATCCTCATCTACGAGACTC
XM_170908	LOC255231	2227	ACATGTTTGCAACCTTTGCC
XM_170908	LOC255231	2228	ACAGAATGGGTTTCCTGAAAC
XM_171197	LOC253971	2229	ACCTTCTTCAGTGGACTCATC
XM_171318	LOC255695	2230	ACAACAGAATCCTCATAGTCC
XM_171318	LOC255695	2231	ACTCCTGAAACATGGTCCCTCC
XM_171318	LOC255695	2232	ACTGCAGATTCCAATGTGGTC
XM_171384	LOC256342	2233	ACGTGGAACATGGCCTTCATC
XM_171720	LOC253188	2234	ACCTCATGCAAACCTTCACGTC
XM_171749	LOC255087	2234	ACCTCATGCAAACCTTCACGTC
XM_171720	LOC253188	2235	ACTCAGGAGGAACGATCTGTC

XM_171749	LOC255087	2235	ACTCAGGAGGAACGATCTGTC
XM_172164	LOC253355	2236	ACTACCATATTTCAGCAGCTGC
SK112	DMPK2	2237	ACACCTCAGGCAGTCACAGTC
SK112	DMPK2	2238	ACGCATCTTTAGGGTGACAAC
NM_024876	FLJ12229	2239	ACCTCTTCCAGGACACCTACC
SK013	ADCK4	2239	ACCTCTTCCAGGACACCTACC
SK015	BRSK2	2240	ACTCCATCAAGAACAGCTTTC
XM_113646	STK29	2240	ACTCCATCAAGAACAGCTTTC
SK016	Wnk2	2241	ACCTTCCTGAACAAGCTGCTC
NM_000051	ATM	2242	ACCTAACTGTGAGCTGTCTCC
SK038	ATM	2242	ACCTAACTGTGAGCTGTCTCC
SK060	CaMK2g	2243	ACCAGATGCTGACCATAAACC
NM_006482	DYRK2	2244	ACACGATTGGCGGCAGTAAGC
SK115	DYRK2	2244	ACACGATTGGCGGCAGTAAGC
NM_003583	DYRK2	2245	ACAGTGTTTAGAGTGGGATCC
NM_006482	DYRK2	2245	ACAGTGTTTAGAGTGGGATCC
SK115	DYRK2	2245	ACAGTGTTTAGAGTGGGATCC
NM_005233	EPHA3	2246	ACATTACACACCCATCAGGAC
SK123	EphA3	2246	ACATTACACACCCATCAGGAC
NM_005233	EPHA3	2247	ACTCACCAACACCACGGTGAC
SK123	EphA3	2247	ACTCACCAACACCACGGTGAC
SK125	EphA5	2248	ACAGAACTTGATCTTGGTGAC
X95425	HSEHK1	2248	ACAGAACTTGATCTTGGTGAC
XM_046083	LOC201771	2248	ACAGAACTTGATCTTGGTGAC
SK125	EphA5	2249	ACTGTGATTTCAGCTTGTTGGC
X95425	HSEHK1	2249	ACTGTGATTTCAGCTTGTTGGC
XM_046083	LOC201771	2249	ACTGTGATTTCAGCTTGTTGGC
SK125	EphA5	2250	ACAGATCAGTAGGTGAATGGC
X95425	HSEHK1	2250	ACAGATCAGTAGGTGAATGGC
XM_046083	LOC201771	2250	ACAGATCAGTAGGTGAATGGC
SK183	IRR	2251	ACTGGTCATCTTTGAGATGCC
XM_043563	INSRR	2251	ACTGGTCATCTTTGAGATGCC
SK200	PIM3	2252	ACGGTCTACACCGACTTCGAC
SK205	KSR1	2253	ACTGACAAAGAAGGAGCACCC
XM_034172	KSR	2253	ACTGACAAAGAAGGAGCACCC
SK250	NEK1	2254	ACATAAACAGGCCCATCAAAC
XM_048605	LOC257463	2254	ACATAAACAGGCCCATCAAAC
NM_000323	RET	2255	ACCGTCTACCTCAAGGTCTTC
NM_020629	RET	2255	ACCGTCTACCTCAAGGTCTTC
NM_020630	RET	2255	ACCGTCTACCTCAAGGTCTTC
NM_020975	RET	2255	ACCGTCTACCTCAAGGTCTTC
SK326	RET	2255	ACCGTCTACCTCAAGGTCTTC
NM_000323	RET	2256	ACCAGGAACTTCTCCACCTGC
NM_020629	RET	2256	ACCAGGAACTTCTCCACCTGC
NM_020630	RET	2256	ACCAGGAACTTCTCCACCTGC
NM_020975	RET	2256	ACCAGGAACTTCTCCACCTGC

SK326	RET	2256	ACCAGGAACCTTCTCCACCTGC
NM_000323	RET	2257	ACCTCATCTCATTTCCTGGC
NM_020629	RET	2257	ACCTCATCTCATTTCCTGGC
NM_020630	RET	2257	ACCTCATCTCATTTCCTGGC
NM_020975	RET	2257	ACCTCATCTCATTTCCTGGC
SK326	RET	2257	ACCTCATCTCATTTCCTGGC
SK345	MAST1	2258	ACAAACAGGTGTGTGGGACCC
XM_032034	SAST	2258	ACAAACAGGTGTGTGGGACCC
SK345	MAST1	2259	ACACGGATGTCTATAGTGTCC
XM_032034	SAST	2259	ACACGGATGTCTATAGTGTCC
NM_003137	SRPK1	2260	ACCAAGTGCCGTATCATCCAC
SK358	SRPK1	2260	ACCAAGTGCCGTATCATCCAC
NM_018571	ALS2CR2	2261	ACTTGTTGATGAGCCAACCC
SK434	STLK6	2261	ACTTGTTGATGAGCCAACCC
NM_018571	ALS2CR2	2262	ACAGGAGTATTAAAGCCAGCC
SK434	STLK6	2262	ACAGGAGTATTAAAGCCAGCC
SK440	ZC4/NRK	2263	ACTTCATGAGAAGACTGGTGC
SK443	CDK11	2264	ACCCTAATGTGATTGCATTGC
XM_166324	KIAA1028	2264	ACCCTAATGTGATTGCATTGC
SK443	CDK11	2265	ACTCCTGACCATGGATCCAAC
XM_166324	KIAA1028	2265	ACTCCTGACCATGGATCCAAC
SK450	ULK3	2266	ACTGAGCTCCTTGGAGAAGCC
XM_044630	DKFZP434C131	2266	ACTGAGCTCCTTGGAGAAGCC
SK450	ULK3	2267	ACTTCTTTGTACCTGCCCTGC
XM_044630	DKFZP434C131	2267	ACTTCTTTGTACCTGCCCTGC
SK450	ULK3	2268	ACACCCTGGACAAAAGAGGGAC
XM_044630	DKFZP434C131	2268	ACACCCTGGACAAAAGAGGGAC
SK453	TTBK2	2269	ACTATGTGGTCATGCAGTTGC
SK453	TTBK2	2270	ACTCAGCTACTACTGAACCTC
SK458	MLKL	2271	ACCAAGGAAAGAGGAGCGTGC
XM_113849	LOC197259	2271	ACCAAGGAAAGAGGAGCGTGC
SK459	DCAMKL3	2272	ACAAGAAAGAGGACAGAGGCC
XM_047355	KIAA1765	2272	ACAAGAAAGAGGACAGAGGCC
SK459	DCAMKL3	2273	ACCTGATCCTGGAGTACGTGC
XM_047355	KIAA1765	2273	ACCTGATCCTGGAGTACGTGC
SK460	SgK493	2274	ACTGGATGGAGCCAAGTGGTC
XM_038576	LOC91461	2274	ACTGGATGGAGCCAAGTGGTC
NM_139158	ALS2CR7	2275	ACTCTTCAGAAGTCGTGACCC
SK462	PFTAIRES	2275	ACTCTTCAGAAGTCGTGACCC
NM_139158	ALS2CR7	2276	ACAATCCAGAATGGTTCCAC
SK462	PFTAIRES	2276	ACAATCCAGAATGGTTCCAC
SK466	CDKL4	2277	ACTCAGTATGGTTCTTCAGTC
XM_065861	LOC130736	2277	ACTCAGTATGGTTCTTCAGTC
BC015792	BC015792	2278	ACATGTTTCATGGTCGTGGACC
ENSG00000165752	ENSG00000165752	2278	ACATGTTTCATGGTCGTGGACC
SK469	YANK3	2278	ACATGTTTCATGGTCGTGGACC

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BC015792	BC015792	2279	ACATGGCTCCGGAGATCTTCC
SK469	YANK3	2279	ACATGGCTCCGGAGATCTTCC
NM_017988	FLJ10074	2280	ACTTTCTGTGAGCTGTGAAAC
SK475	SCYL2	2280	ACTTTCTGTGAGCTGTGAAAC
SK476	NEK8	2281	ACCTTTGCACCTATCTCTGAC
SK476	NEK8	2282	ACTGAGCGAGAACTATTTGCC
SK476	NEK8	2283	ACACCCTTACACGGTGACTTC
NM_033266	ERN2	2284	ACCACAGATGAGGTGACACTC
SK498	IRE2	2284	ACCACAGATGAGGTGACACTC
NM_033266	ERN2	2285	ACTTCGGCCTCTGCAAGAAGC
SK498	IRE2	2285	ACTTCGGCCTCTGCAAGAAGC
SK500	NDR2	2286	ACCAGACTTGGCTTGGATGAC
SK500	NDR2	2287	ACACACAACCCACCAAGTGAC
SK510	PAK5	2288	ACCTTCTAGAACTGCAGGGAC
XM_045653	PAK7	2288	ACCTTCTAGAACTGCAGGGAC
SK510	PAK5	2289	ACTTGATGTTGGTGAGGGAGC
XM_045653	PAK7	2289	ACTTGATGTTGGTGAGGGAGC
AL137662	HSM801974	2290	ACCTGGCAGGAGAAACAGACC
SK520	NRBP2	2290	ACCTGGCAGGAGAAACAGACC
SK558	NEK5	2291	ACTTTGGTATAGCAAGAGTCC
XM_166970	LOC220435	2291	ACTTTGGTATAGCAAGAGTCC
SK581	SgK069	2292	ACATGATGACGCTGAGTGCTC
XM_064914	LOC126030	2292	ACATGATGACGCTGAGTGCTC
SK581	SgK069	2293	ACTGAAGCAGCTCCCGAAACC
XM_064914	LOC126030	2293	ACTGAAGCAGCTCCCGAAACC
SK581	SgK069	2294	ACCTCATGGCCTTCATCCAGC
XM_064914	LOC126030	2294	ACCTCATGGCCTTCATCCAGC
SK592	SgK110	2295	ACAACGTGCTGGTCTTCGACC
XM_064914	LOC126030	2295	ACAACGTGCTGGTCTTCGACC
SK592	SgK110	2296	ACTGCCTGTTTCCCTTGGGAC
XM_064914	LOC126030	2296	ACTGCCTGTTTCCCTTGGGAC
SK627	EphA10	2297	ACCGCCGAGGAAGTTATCCTC
SK627	EphA10	2298	ACGGAGTACGAGATCCGATAC
SK641	Wnk3	2299	ACCGTCCTTCAGGTATCAACC
XM_029183	PRKWINK3	2299	ACCGTCCTTCAGGTATCAACC
SK643	SgK223	2300	ACAGGCCAAGATAGAACATGC
SK643	SgK223	2301	ACTGGCTTTGCTGCCAGTACC
SK645	NEK10	2302	ACAAGGAGAAGAGGATTGTCC
XM_171056	LOC256519	2302	ACAAGGAGAAGAGGATTGTCC
SK646	EphA6	2303	ACCATTCCAAGGGTTGATTCC
XM_114973	LOC203806	2303	ACCATTCCAAGGGTTGATTCC
SK650	SBK	2304	ACCTGTTTGACATCATCCCTC
XM_171786	LOC254078	2304	ACCTGTTTGACATCATCCCTC
SK658	SgK288	2305	ACGGAGTACGCCATCAAGTGC
XM_171494	LOC255239	2305	ACGGAGTACGCCATCAAGTGC
SK690	LRRK2	2306	ACAGCCAGATCATCAGCTTGC

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SK695	CR1K	2307	ACAGTGACAAGAATCGGCTGC
NM_052853	MGC20727	2308	ACCTCAGGCCCCAACCTACATC
SK712	ADCK2	2308	ACCTCAGGCCCCAACCTACATC
NM_014299	BRD4	2309	ACCAAACACAACCTCAAGCATC
NM_058243	BRD4	2309	ACCAAACACAACCTCAAGCATC
SK763	BRD4	2309	ACCAAACACAACCTCAAGCATC
NM_014299	BRD4	2310	ACGGTCTTCAGTTCCAGATTC
SK763	BRD4	2310	ACGGTCTTCAGTTCCAGATTC
SK765	AlphaK1	2311	ACAGCAAGCCCATTCTTCTC
XM_057651	MIDORI	2311	ACAGCAAGCCCATTCTTCTC
SK765	AlphaK1	2312	ACACCTGAAGAAAGGGAGAGC
XM_057651	MIDORI	2312	ACACCTGAAGAAAGGGAGAGC
SK765	AlphaK1	2313	ACGTGCATCATCAAGGTGTCC
XM_057651	MIDORI	2313	ACGTGCATCATCAAGGTGTCC
SK780	ADCK5	2314	ACTGGGACAAGTCCAGCAAGC
SK780	ADCK5	2315	ACCCACATCCTGGCAACGTTT
XM_114612	LOC203054	2315	ACCCACATCCTGGCAACGTTT
NM_005762	TRIM28	2316	ACTGTCCCCTGTGCAAGCAAC
SK784	TIF1b	2316	ACTGTCCCCTGTGCAAGCAAC
ENSG00000139908	ENSG00000139908	2317	ACTCCCTCCTCAATATCTAGC
NM_000020	ACVRL1	2318	ACGTGTGAGAGCCCACATTGC
NM_000020	ACVRL1	2319	ACCGAGTTCGTCAACCACTAC
NM_000180	GUCY2D	2320	ACATGCAAATGGTCTCCGGCC
NM_000906	NPR1	2321	ACCCAGCATGCAACCAAGATC
NM_001184	ATR	2322	ACCCAGAATTCTTACAGAGCC
NM_001211	BUB1B	2323	ACAACAGCCAGTTATGACACC
NM_001211	BUB1B	2324	ACATTCCAAAGTCACCTGAAC
NM_001433	ERN1	2325	ACTTTGGCCTCTGCAAGAAGC
NM_001522	GUCY2F	2326	ACATGGAAATGGAGCTGCTAC
NM_001654	ARAF1	2327	ACTGCTGTGTGGTCTACCGAC
NM_001654	ARAF1	2328	ACTCCCAACGTCCATATGGTC
NM_001654	ARAF1	2329	ACGAGCTTATGACTGGCTCAC
NM_001726	BRDT	2330	ACAGGGAGCTTCAGTCAACTC
NM_002005	FES	2331	ACAGGGAGTATGCAGGACTGC
NM_002005	FES	2332	ACCTCAGCAATCAGCAGACAC
NM_002037	FYN	2333	ACATTACTCAGAGAGAGCTGC
NM_002037	FYN	2334	ACCAAAGGAAGAGTGCCATAC
NM_002648	PIM1	2335	ACTTGCCGGTGGCCATCAAAC
NM_002648	PIM1	2336	ACATCCTTATCGACCTCAATC
NM_002648	PIM1	2337	ACCTTCGAAGAAATCCAGAAC
NM_003390	WEE1	2338	ACAAGACCTTCCGCAAGCTGC
NM_003390	WEE1	2339	ACTCTTCACTGACCGGATGGC
NM_003496	TRRAP	2340	ACTACGTTGTGACCGAGGTTC
SK380	TRRAP	2340	ACTACGTTGTGACCGAGGTTC
NM_003503	CDC7L1	2341	ACTTCAGTGCCTAACAGTGGC
NM_003718	CDC2L5	2342	ACATCCAGCAGCAGTAGCAGC

NM_031267	CDC2L5	2342	ACATCCAGCAGCAGTAGCAGC
NM_000907	NPR2	2343	ACCTCAAGCTGTACCATGACC
NM_003995	NPR2	2343	ACCTCAAGCTGTACCATGACC
NM_000907	NPR2	2344	ACCAGCATATTGGACAACCTC
NM_003995	NPR2	2344	ACCAGCATATTGGACAACCTC
NM_000907	NPR2	2345	ACACAGTGAACACTGCTTCTC
NM_003995	NPR2	2345	ACACAGTGAACACTGCTTCTC
NM_004302	ACVR1B	2346	ACCCACTGCTGCTACACTGAC
NM_020327	ACVR1B	2346	ACCCACTGCTGCTACACTGAC
NM_020328	ACVR1B	2346	ACCCACTGCTGCTACACTGAC
NM_004302	ACVR1B	2347	ACGGTCTTGGTTTCAGGGAAGC
NM_020327	ACVR1B	2347	ACGGTCTTGGTTTCAGGGAAGC
NM_020328	ACVR1B	2347	ACGGTCTTGGTTTCAGGGAAGC
NM_004302	ACVR1B	2348	ACTGACACCATTGACATTGCC
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NM_004329	BMPR1A	2349	ACTGGGATGAAATCAGACTCC
NM_004329	BMPR1A	2350	ACAATAGAATGTTGTGCGGACC
NM_004329	BMPR1A	2351	ACCTTTATTGGTTTCAGCGAAC
NM_004336	BUB1	2352	ACAACCATGGGATTGGAACCC
NM_004336	BUB1	2353	ACGCTGCCATTGCAGAAGATC
NM_004438	EPHA4	2354	ACAGATATCAAAGGCCTGAAC
NM_004440	EPHA7	2355	ACTACTGCTGGATTCTAAAGC
NM_004440	EPHA7	2356	ACACTTGTGAACCCTGTGGCC
NM_004440	EPHA7	2357	ACCTACATTGACCCTGAAACC
NM_004443	EPHB3	2358	ACAACGTGGAGTTTGTGCCTC
NM_004670	PAPSS2	2359	ACCGTGTGGCTAACAGGTCTC
NM_004670	PAPSS2	2360	ACAGTGAGTGACTGTGTCCAC
NM_004817	TJP2	2361	ACATGTCTTTAACGGATGCTC
NM_004817	TJP2	2362	ACCTGACTGGTTTCAAACCTGC
NM_004958	FRAP1	2363	ACACCCCTCCATCCACCTCATC
NM_004958	FRAP1	2364	ACGTCAGCACCATCAACCTCC
NM_004963	GUCY2C	2365	ACCATGGTGCTTCTGTATACC
NM_005104	BRD2	2366	ACACAAGGTAGTGATGAAAGC
NM_005104	BRD2	2367	ACCACTGTCCTCAACATTCCC
NM_005104	BRD2	2368	ACTAGAACCAGGGCCTTTACC
NM_005157	ABL1	2369	ACACTGCTTCTGATGGCAAGC
NM_007313	ABL1	2369	ACACTGCTTCTGATGGCAAGC
NM_005157	ABL1	2370	ACGACAAGTGGGAGATGGAAC
NM_007313	ABL1	2370	ACGACAAGTGGGAGATGGAAC
NM_005158	ABL2	2371	ACTTCCTTCCAAGACTCGGAC
NM_007314	ABL2	2371	ACTTCCTTCCAAGACTCGGAC
NM_005158	ABL2	2372	ACAGCATGCTGATGGGTTCCTC
NM_007314	ABL2	2372	ACAGCATGCTGATGGGTTCCTC
NM_005211	CSF1R	2373	ACAACGAGAAGTGGGAGTTCC
NM_005211	CSF1R	2374	ACTTCTCCAGCCAAGTAGCCC

NM_005248	FGR	2375	ACTACAGCAACTTCTCCTCTC
NM_005248	FGR	2376	ACTACTTCACCTCCGCTGAAC
NM_005372	MOS	2377	ACTCTCTGGCAAATGACTACC
NM_005433	YES1	2378	ACAGCTGGTTGATATGGCTGC
NM_006182	DDR2	2379	ACCATGAAGGTCCACTGCAAC
NM_006182	DDR2	2380	ACTGGAGAGTTCTTCCGAGAC
NM_006875	PIM2	2381	ACTGCTATGGAAAGTGGGTGC
NM_006875	PIM2	2382	ACATCCTGATAGACCTACGCC
NM_007118	TRIO	2383	ACATCCTAGCTAAGAAGGAGC
NM_007118	TRIO	2384	ACCAAGGGCAAGATCTTCTGC
NM_007284	PTK9L	2385	ACAAGTGCAGCATCAAGGAGC
NM_013392	NRBP	2386	ACCTCCTGTGACCTCCACAAC
NM_013392	NRBP	2387	ACAGGAAGCCATCAGCAGTGC
NM_013392	NRBP	2388	ACATGATCCCAGAGAACGCTC
NM_014572	LATS2	2389	ACTTCCCTGGATGCCAAAGTC
NM_014572	LATS2	2390	ACCAACTCCTTCAACAGCCAC
NM_014840	KIAA0537	2391	ACCACAAGCACAACTTGAAGC
NM_014840	KIAA0537	2392	ACAATGCCCTTCGATGGTTTC
NM_014916	KIAA1079	2393	ACAGTGCGTAGAAGCGATTCC
NM_014916	KIAA1079	2394	ACTTGGAGCTTGATTACCCAC
NM_015906	TRIM33	2395	ACACAACACCACAATCAACCC
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NM_017433	MYO3A	2396	ACTAGCCCATTACAACTGCC
NM_018343	FLJ11159	2397	ACACCATGTTGAAGATCCTGC
NM_018423	DKFZp761P1010	2398	ACTTTCTGGGAGCTACCACAC
NM_020198	GK001	2399	ACTCTGTTACTGAATCTCCTC
NM_020198	GK001	2400	ACTTACTGAATGTCCTGGCCC
NM_020547	AMHR2	2401	ACCAGAGCTCTTGGACAAGAC
NM_020547	AMHR2	2402	ACTGTACTTCAATTCTGCCC
NM_020629	RET	2403	ACTCTATGATGCACAACACTC
NM_021120	DLG3	2404	ACATAAGCCATAATTCCAGCC
NM_021120	DLG3	2405	ACAAATCATTGAGGACCAGTC
NM_021133	RNASEL	2406	ACTTGTCCTGTGGATACACCC
NM_021158	C20orf97	2407	ACCTACTGCTCCAGATCGTGC
NM_021158	C20orf97	2408	ACAGGCACTGAGTATACCTGC
NM_021643	GS3955	2409	ACTCCGAACCTTGTGCGATTGC
NM_021643	GS3955	2410	ACTGTTCTACCAGATTGCCTC
NM_021643	GS3955	2411	ACCTCGCAGGAAATTCTGGAC
NM_000142	FGFR3	2412	ACTGTCTGGGTCAAGGATGGC
NM_022965	FGFR3	2412	ACTGTCTGGGTCAAGGATGGC
NM_000142	FGFR3	2413	ACAAGTTTGGCAGCATCCGGC
NM_022965	FGFR3	2413	ACAAGTTTGGCAGCATCCGGC
NM_000142	FGFR3	2414	ACTGACAAGGACCTGTGCGGAC
NM_022965	FGFR3	2414	ACTGACAAGGACCTGTGCGGAC
NM_024776	FLJ21140	2415	ACAGGGAAGGTGGAATCAGCC
NM_025052	FLJ23074	2416	ACCAGGTAAGAACTGAAAGC

NM_030952	DKFZP434J037	2417	ACCAGCTGGACTTGCCTGAAC
SK472	Nuak2	2417	ACCAGCTGGACTTGCCTGAAC
NM_031272	TEX14	2418	ACGGGCAACAATGACTGTGAC
NM_031272	TEX14	2419	ACTAGGTTGGTCCGAATCATC
NM_031965	GSG2	2420	ACTGATGTGTCAGAGGTCTGC
NM_031965	GSG2	2421	ACAATTGCTGATCACACACCC
NM_031965	GSG2	2422	ACGACCAGCTCTTCATTGTGC
NM_032237	FLJ23356	2423	ACTCTACTCTACCTCTGCCTC
NM_032237	FLJ23356	2424	ACCTGGAAGAAACACTAAACC
NG_000013	NG_000013	2425	ACGAAGGAGGTTGACACCAAC
NM_004197	STK19	2425	ACGAAGGAGGTTGACACCAAC
NM_032454	STK19	2425	ACGAAGGAGGTTGACACCAAC
NG_000013	NG_000013	2426	ACCTTAGTTTCCAGCAGGACC
NM_004197	STK19	2426	ACCTTAGTTTCCAGCAGGACC
NM_032454	STK19	2426	ACCTTAGTTTCCAGCAGGACC
NG_000013	NG_000013	2427	ACCTACCATGTGCACGACCTC
NM_004197	STK19	2427	ACCTACCATGTGCACGACCTC
NM_032454	STK19	2427	ACCTACCATGTGCACGACCTC
NM_032844	FLJ14813	2428	ACCATCCAGAATGAACATGAC
NM_032844	FLJ14813	2429	ACCAGGAATACTGCTCAGCAC
NM_033550	C20orf64	2430	ACTTAGCCAAGACAATTGGGC
NM_080823	C20orf148	2431	ACTGGAAGCTGATCCAGAACC
NM_080823	C20orf148	2432	ACATCGTCACGGAATCATGC
NM_138995	MYO3B	2433	ACATCGCCAATGAGCAAATCC
XM_027237	MAP3K9	2434	ACCTCTGTATCCCATTCCCTC
XM_027237	MAP3K9	2435	ACCCTTGGTGGTTTGTGTCCC
XM_034551	DYRK4	2436	ACGGAGCTGACACTGTTTCAGC
XM_042066	MAP3K1	2437	ACCTTCTTGAAGCATCTATGC
XM_042066	MAP3K1	2438	ACAGTTACTCCGTGGCCTTTC
XM_043865	PIK3R1	2439	ACCTCATCAGTATTGGCTTAC
XM_043865	PIK3R1	2440	ACGACTCCCTCAATGTCACAC
XM_047620	PIP5K1C	2441	ACATTGGCATCATCGACATCC
NM_006213	PHKG1	2442	ACAAACTCAACATCGTGCACC
XM_054871	LOC154966	2442	ACAAACTCAACATCGTGCACC
NM_006213	PHKG1	2443	ACGCTTTCCGAATCTATGGCC
XM_054871	LOC154966	2443	ACGCTTTCCGAATCTATGGCC
XM_061691	LOC119794	2443	ACGCTTTCCGAATCTATGGCC
SK134	Erk1	2444	ACGCAGTTGCAGTACATCGGC
XM_055766	MAPK3	2444	ACGCAGTTGCAGTACATCGGC
SK134	Erk1	2445	ACTATGACCCGACGGATGAGC
XM_055766	MAPK3	2445	ACTATGACCCGACGGATGAGC
XM_055866	KIAA1883	2446	ACGCAAGTTCATCTCGGAAGC
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XM_059051	LOC126520	2448	ACACAGGGTTTCACTCCAGAC
XM_059368	LOC129607	2449	ACCTCCTTTATTCTGAAGCC
XM_060051	LOC139728	2450	ACATGCTGCTGCTGAAGAAAC

XM_060051	LOC139728	2451	ACCTCTACCTGGCCATGGAAC
XM_061154	LOC118800	2452	ACTTTCATCAAGCCAAAGGAC
XM_062445	LOC121064	2453	ACATCTCCCTCACTTGTCATC
XM_062445	LOC121064	2454	ACCCAGGTGGCTGTGAATGTC
XM_062850	LOC121908	2455	ACCCACCTTCAGGATAGACAC
XM_062966	LOC122134	2456	ACATCCTACTGCATGAAGAAC
XM_064804	LOC125806	2457	ACACGGCAGCAGAAGAACTTC
XM_064804	LOC125806	2458	ACCTTCACCAAGCTCATGGAC
XM_064914	LOC126030	2459	ACTAGATCCAAATCCAAGACC
XM_064914	LOC126030	2460	ACAGGTCACACTAGGCCTCAC
XM_064914	LOC126030	2461	ACCTTCCACGACCTCTAAGCC
XM_065311	LOC129602	2462	ACATTCTGGAAGTTACAGGGC
XM_066264	LOC128968	2463	ACTTCCCACACTCCAAGAACC
XM_066534	LOC139189	2464	ACCTGCAAGGCATTGTAGTGC
XM_066968	LOC139932	2465	ACTATACTCATCCTACTCCAC
XM_066977	LOC139952	2466	ACCTTATACTGTGGAAATGCC
XM_066977	LOC139952	2467	ACACACAGAATGCTGGACACC
XM_069683	LOC136062	2468	ACCAGAACTCTTGGACTTTGC
XM_069722	LOC136126	2469	ACGTACAAAGCAGCTGCCAAC
XM_069722	LOC136126	2470	ACAACACACTATTTGGTGGAC
XM_070335	LOC137298	2471	ACAATGCTGAAGCTGAGGACC
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XM_070869	LOC138342	2473	ACCTGAGTGCACCTTCATCAC
XM_071218	LOC138961	2474	ACTTTGAGCTGAAGGGATTCC
XM_071218	LOC138961	2475	ACCTGAAAGACTGTCCATTCC
XM_071218	LOC138961	2476	ACAAGAGGTGGACACAGCAGC
XM_086946	LOC150537	2477	ACGTCAATGTCCTCAGTGACC
XM_090535	LOC160848	2478	ACTTGTCTAAAGTGCTGGAGC
NM_002748	MAPK6	2479	ACATGACTGAGCCACACAAAC
XM_090535	LOC160848	2479	ACATGACTGAGCCACACAAAC
SK340	RYK	2480	ACCTAGAATAGTGCTATGCAC
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XM_095399	LOC168921	2481	ACACCAACACAGAAGAAAGGC
XM_095455	LOC169014	2482	ACTTGAATAGCTCGGTGTCCC
XM_095455	LOC169014	2483	ACCAATCATCTTGGGACAGCC
SK169	HIPK1	2484	ACACAAGGGCAAGCCAACCTCC
XM_114728	LOC204851	2484	ACACAAGGGCAAGCCAACCTCC
XM_166672	LOC220231	2485	ACCTCAAACCAGGGAATATTC
XM_167020	LOC222521	2486	ACCAGGAAACACAGAAGAAGC
NM_002654	PKM2	2487	ACGGAAAGCTTTGCTTCTGAC
XM_167220	LOC222816	2487	ACGGAAAGCTTTGCTTCTGAC
SK709	SgK085	2488	ACCTGAAGCCTGAGAATATCC
XM_167231	LOC221757	2488	ACCTGAAGCCTGAGAATATCC
XM_169341	LOC222456	2489	ACGTCACTGAACCCAAAGAAC
XM_170826	LOC255185	2490	ACACAGATCTCCTGGCTTCCC
XM_171030	LOC256356	2491	ACAGTTCTTGCCGAGTGCTTC

XM_171030	LOC256356	2492	ACAGCCAGTTTGTTCACTTTC
XM_171520	LOC255376	2493	ACTTCTTGAGCTGGCTTCAC
XM_171744	LOC256238	2494	ACCTTTCTCTGAGCACAGGAC
XM_171744	LOC256238	2495	ACACAGTTCTAGGCACAGAGC
XM_171862	LOC253603	2496	ACTAATTTGCCCTCCCTACCTC
XM_171862	LOC253603	2497	ACCTGCGTATGAATCTATGCC
XM_172116	LOC254665	2498	ACCAGCACCTTAGAACAATGC
XM_172246	LOC256595	2499	ACCATAGATCACCTCATCTCC
XM_172550	LOC256248	2500	ACTTAAAGATCCTCTCCTAGC
XM_172605	LOC255992	2501	ACACTGAAGGAGGTTGACATC
XM_172741	LOC253939	2502	ACAAAGACATGGTGATCCAGC
ENSG00000172441	ENSG00000172441	2503	ACTTCCTGATAACCTGGTAGC
NM_000066	C8B	2504	ACAGGAAGGTGTGTAAACCGC
NM_000066	C8B	2505	ACATCACCACCCTGGCATAAC
NM_000121	EPOR	2506	ACATCAATGAAGTAGTGCTCC
NM_000121	EPOR	2507	ACCACCCACAAGGGTAACTTC
NM_000206	IL2RG	2508	ACACCACAGCTGATTTCTTCC
NM_000206	IL2RG	2509	ACTGCAGAATCTGGTGATCCC
NM_000206	IL2RG	2510	ACTACAGTGAACGACTCTGCC
NM_000264	PTCH	2511	ACCGTTCACGTTGCTTTGGCC
NM_000352	ABCC8	2512	ACGTCTTCCAGCCCAAGACAC
NM_000352	ABCC8	2513	ACTGTCTATGCCATGGTGTTT
NM_000416	IFNGR1	2514	ACCAGATCATGCCACAGGTCC
NM_000416	IFNGR1	2515	ACTCATCACGTCATACCAGCC
NM_000527	LDLR	2516	ACCAACGAATGCTTGGACAAC
NM_000527	LDLR	2517	ACCCTAGATCTCCTCAGTGGC
NM_000562	C8A	2518	ACCATCTGCAGTGGTGACATC
NM_000562	C8A	2519	ACAGAACAGGAGCACCATTAC
NM_000565	IL6R	2520	ACAACATGGATGGTCAAGGAC
NM_000565	IL6R	2521	ACAATACCTCGAGCCACAACC
NM_000577	IL1RN	2522	ACCTGAGCGAGAACAGAAAGC
NM_000587	C7	2523	ACTTGAGGTTGCTTGAACCAC
NM_000629	IFNAR1	2524	ACCTTTCAAGTTCAGTGGCTC
NM_000629	IFNAR1	2525	ACAAGCTTTCTACTTCCTCC
NM_000640	IL13RA2	2526	ACTGGTATGAGGGCTTGGATC
NM_000760	CSF3R	2527	ACTCCCTTGTACCAGGACACC
NM_000760	CSF3R	2528	ACGACTGTGTCTTTGGGCCAC
NM_000804	FOLR3	2529	ACGGACCTGCTCAATGTCTGC
NM_000833	GRIN2A	2530	ACCTCTTCTACTGGAAGCTGC
NM_000834	GRIN2B	2531	ACCTTCTGCCTTCTTAGAGCC
NM_000835	GRIN2C	2532	ACAAGAAGTTTCAGCGGCCCTC
NM_000835	GRIN2C	2533	ACGAGATCAGCAGTGTAGCCC
NM_000836	GRIN2D	2534	ACCTTCACCATTGGGAAATCC
NM_000874	IFNAR2	2535	ACCACTCCATTGTACCAACTC
NM_000874	IFNAR2	2536	ACAGGTGCAGTCATAATGCAC
NM_000876	IGF2R	2537	ACTGCAGCCTGCAAGAAAGAC

NM_000876	IGF2R	2538	ACCTACTTCTTCACATGGGAC
NM_000876	IGF2R	2539	ACCTACAACTTCCGGTGGTAC
NM_000877	IL1R1	2540	ACAAGGCCTGTGATTGTGAGC
NM_000878	IL2RB	2541	ACTTCCCAGTTCACATGCTTC
NM_000908	NPR3	2542	ACAGCAGACTTGGAAACAGAAC
NM_000908	NPR3	2543	ACAGAATAACCATTGAGAGGC
NM_000949	PRLR	2544	ACAGATGGAGGACTTCCTACC
NM_001263	CDS1	2545	ACTGGTGGATACGTGGAATTC
NM_001263	CDS1	2546	ACTCAGTCACACCTTGTCATC
NM_001263	CDS1	2547	ACTTCCACCCTTTCTAAAGGC
NM_001381	DOK1	2548	ACTCTGTTGCGTCGCTATGGC
NM_001381	DOK1	2549	ACTTGATGAGCATGCGCAGC
NM_001381	DOK1	2550	ACAACCTCAGCCCTGTACAGCC
NM_001495	GFRA2	2551	ACCGAGGGTGAGGAGTTCTAC
NM_001495	GFRA2	2552	ACAAGGAGAAGCCCAACTGCC
NM_001495	GFRA2	2553	ACAGAGCTCACGACAAATATC
NM_001496	GFRA3	2554	ACAGAAAGCCGACTCATGAAC
NM_001510	GRID2	2555	ACTGAATCGCTATCGAGACAC
NM_001510	GRID2	2556	ACATTGACACTTTGCCAACAC
NM_001558	IL10RA	2557	ACTCCATCTCCAAGTGTAGCC
NM_001558	IL10RA	2558	ACCGTGACCAACGTCATCATC
NM_001559	IL12RB2	2559	ACGAGACACCCACTTATACAC
NM_001559	IL12RB2	2560	ACAGCTGCTGGTGAAAGTTCC
NM_001560	IL13RA1	2561	ACCATCCTTCAATATAGTGCC
NM_001560	IL13RA1	2562	ACTCTGCACTGGAAGAAGTAC
NM_001737	C9	2563	ACATAGACTGCAGAATGAGCC
NM_001737	C9	2564	ACAGCAGGCTATGGGATCAAC
NM_001737	C9	2565	ACTACAGTAGCTCTGGGTCTC
NM_001842	CNTFR	2566	ACCATCACAGATGCCTACGCC
NM_147164	CNTFR	2566	ACCATCACAGATGCCTACGCC
NM_001842	CNTFR	2567	ACTGCCAGCAGTCTCTTGATC
NM_147164	CNTFR	2567	ACTGCCAGCAGTCTCTTGATC
NM_002183	IL3RA	2568	ACTTGAACGTTGCCAACAGGC
NM_002183	IL3RA	2569	ACACAGTACAAATAAGAGCCC
NM_002184	IL6ST	2570	ACTCGTGTGGAAGACATTGCC
NM_002184	IL6ST	2571	ACACATCTGGCCTAATGTTCC
NM_002185	IL7R	2572	ACACTCCTGCAGAGAAAGCTC
NM_002185	IL7R	2573	ACCAGTGAAGTGTAAGAAACC
NM_002186	IL9R	2574	ACCATCACTTTCCACCACTGC
NM_002186	IL9R	2575	ACCCTTGTTGCTGTGTCCATC
NM_002187	IL12B	2576	ACACTCTCTGCAGAGAGAGTC
NM_002303	LEPR	2577	ACTGTTGCTTTCGGAGTGAGC
NM_002303	LEPR	2578	ACCTATGATGCAGTGACTGC
NM_002303	LEPR	2579	ACAAGTCAAGGGTATCGTGCC
NM_002332	LRP1	2580	ACCACCAGCTACCTCATTGGC
NM_002332	LRP1	2581	ACCAACAAATGCCGGGTGAAC

NM_002332	LRP1	2582	ACCTGCCAGATCCAGAGCTAC
NM_002333	LRP3	2583	ACATCTTTCTCACC GGGAGAC
NM_002333	LRP3	2584	ACCAGGTGAAGGGCTATTGCC
NM_002335	LRP5	2585	ACCACCTTCTTGCTGTTTCAGC
NM_002336	LRP6	2586	ACCGCATGGTGATTGATGAAC
NM_002445	MSR1	2587	ACATGGAGAAGAGAATCCAGC
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NM_138716	MSR1	2587	ACATGGAGAAGAGAATCCAGC
NM_003105	SORL1	2588	ACTGGCTCAGTGGGAAAGAAC
NM_003353	UCN	2589	ACCCTTCTCTGTCCATTGACC
NM_003353	UCN	2590	ACCTCACCTTTCACCTGCTGC
NM_003383	VLDLR	2591	ACTGTGCAGCTGGGTTTGAAC
NM_003604	IRS4	2592	ACCTTGCCAGAGGTGATAACC
NM_003738	PTCH2	2593	ACACCTCTCAGATGCTGATAC
NM_003818	CDS2	2594	ACCGGTTTCATTTCTTTACTC
NM_003818	CDS2	2595	ACCAACAGCTTCACTGTGGAC
NM_003974	DOK2	2596	ACGACTGGCCCTACAGGTTTC
NM_003974	DOK2	2597	ACCCGGCAAGGCAATGAGATC
NM_003974	DOK2	2598	ACAGCATTGAGGAGACCCTGC
NM_003999	OSMR	2599	ACATTGACATCCCCTCCTTC
NM_004512	IL11RA	2600	ACTCTGGGCTAGGGCATGAAC
NM_147162	IL11RA	2600	ACTCTGGGCTAGGGCATGAAC
NM_004512	IL11RA	2601	ACTTGAGTCCCAGCCAGATC
NM_147162	IL11RA	2601	ACTTGAGTCCCAGCCAGATC
NM_004512	IL11RA	2602	ACAGTCCTAGGAGCTGATAGC
NM_147162	IL11RA	2602	ACAGTCCTAGGAGCTGATAGC
NM_004525	LRP2	2603	ACGATTGTACTGGGTAGATGC
NM_004631	LRP8	2604	ACAGATCCACCTACCAGAACC
NM_033300	LRP8	2604	ACAGATCCACCTACCAGAACC
NM_004633	IL1R2	2605	ACAGATGCTTTCTGCGCTTC
NM_004750	CRLF1	2606	ACCAACTACTCCCTCAAGTAC
NM_005137	DGCR2	2607	ACTTGCGAGGATGAGAGCGAC
NM_005174	ATP5C1	2608	ACCAGGAGACTAAAGTCCATC
NM_005174	ATP5C1	2609	ACTGTGTGGTGCTATTTCATTC
NM_005264	GFRA1	2610	ACTGGAGCATGTACCAGAGCC
NM_145793	GFRA1	2610	ACTGGAGCATGTACCAGAGCC
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NM_005515	HLXB9	2612	ACCGGCGGATGAAATGGAAAC
NM_005529	HSPG2	2613	ACAGCATCTCAGGAGACGACC
NM_005535	IL12RB1	2614	ACAGCCTCAGGTGAGATTCTC
NM_005535	IL12RB1	2615	ACAGAGACCCAAGTTACCCTC
NM_005544	IRS1	2616	ACGAGAACGAGAAGAAGTGGC
NM_005755	EBI3	2617	ACGGATGTCCAGCTGTTCTCC
NM_005755	EBI3	2618	ACATCATCAAGCCGACCCTC
NM_005755	EBI3	2619	ACTGGATCCGTTACAAGCGTC
NM_006140	CSF2RA	2620	ACGATGAATTTAAGCTGGGAC

NM_006653	SNT-2	2621	ACCCAATGCTCTAGGCTACAC
NM_006654	SNT-1	2622	ACCGCACAAGTGTGCATGTTT
NM_006654	SNT-1	2623	ACTGCCACGAGATGATGGTAC
NM_012275	IL1F5	2624	ACACTAGAGCCAGTGAACATC
NM_014138	PRO0659	2625	ACAGAAGTCAGAATCGATTCC
NM_014138	PRO0659	2626	ACTCTCAGCCTAGGCACCAAC
NM_014439	IL1F7	2627	ACTGTGACAAGGATAAAGGAC
NM_014779	KIAA0669	2628	ACAGGCCAATCCTGGTAGCAC
NM_016579	8D6A	2629	ACTGACAAGAACTGCGCAAC
NM_016579	8D6A	2630	ACTGGTGGCCATGAAGGAGTC
NM_000802	FOLR1	2631	ACTGAGCTTCTCAATGTCTGC
NM_016724	FOLR1	2631	ACTGAGCTTCTCAATGTCTGC
NM_016725	FOLR1	2631	ACTGAGCTTCTCAATGTCTGC
NM_016729	FOLR1	2631	ACTGAGCTTCTCAATGTCTGC
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NM_000802	FOLR1	2632	ACACCTGCAAGAGCAACTGGC
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NM_016729	FOLR1	2632	ACACCTGCAAGAGCAACTGGC
NM_016730	FOLR1	2632	ACACCTGCAAGAGCAACTGGC
NM_016731	FOLR1	2632	ACACCTGCAAGAGCAACTGGC
NM_017416	IL1RAPL2	2633	ACATGGCTTTGGCAGGTGAAC
NM_017522	LRP8	2634	ACACTCCGGATGGTGTATGAC
NM_018110	DOK4	2635	ACCTCTGGGACATCCACAACC
NM_018110	DOK4	2636	ACAGATTCATCCTGCTAAAGC
NM_018431	C20orf180	2637	ACACGGATCAATGACATCAGC
NM_018431	C20orf180	2638	ACGTGATACTACGTGGTTTAC
NM_018431	C20orf180	2639	ACACACTTGTGATGTGTCAGC
NM_018557	LRP1B	2640	ACGAGTCTTTAGATACCTGTC
NM_018557	LRP1B	2641	ACTACACTAATAGCAGGAGCC
NM_019618	IL1F9	2642	ACTTGGGAAGTCATACAACAC
NM_020526	EPHA8	2643	ACTGTGACCTCAGCTACTACC
NM_021258	IL22R	2644	ACCTACTTAGGGCAGCCAGAC
NM_022148	CRLF2	2645	ACGTGTTCTGACCTGTCTTAC
NM_024872	FLJ22570	2646	ACTCCATCTACTCCTCCTGGC
NM_024872	FLJ22570	2647	ACCAGTCCCATCTACCACAAC
NM_031429	RTBDN	2648	ACCTGGCAGGACCTTGTTGTC
NM_031429	RTBDN	2649	ACACAACAGAGACATCGGGCC
NM_031433	MFRP	2650	ACAGACCATGCAATACAGCTC
NM_031433	MFRP	2651	ACAACCTCAGCCTGGAGGCTC
NM_031433	MFRP	2652	ACAAGAGCCTGACAAGCCTGC
NM_032777	TEM5	2653	ACCCTGCTCTTGAGCAATAAC
NM_032777	TEM5	2654	ACATGGCCAGCAACCTGATGC
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NM_133445	GRIN3A	2658	ACGTACAAGATGCTATGGAGC
NM_133445	GRIN3A	2659	ACCAGCCCTTTCTCTCCACC
NM_139017	CRL3	2660	ACTGTGGAGAGTCCTGAAACC
XM_035037	LRP4	2661	ACTGGCAGACCAAGAGCATAC
XM_035037	LRP4	2662	ACAGGATCAGTCGTGCCAATC
XM_043613	GRID1	2663	ACTGTCATCGGCAACAGCATC
XM_043613	GRID1	2664	ACCTTTCTGCCAGAGCAGAGC
XM_060177	LOC126788	2665	ACCAGGTTCTCCTCAAACGGC
XM_060177	LOC126788	2666	ACTACAGCATCAGCAGCAGGC
XM_060177	LOC126788	2667	ACATGGAGTACGACCTGAAGC
XM_061180	LOC118851	2668	ACCACAGGCCATCAGTGGATC
XM_061852	LOC120086	2669	ACACATGCAAATCCAACTGGC
XM_064862	LOC125915	2670	ACCAGCTGGCTTGGAGTCTTC
XM_064862	LOC125915	2671	ACAGTGGTCTATGCCATCGCC
XM_069787	LOC136243	2672	ACTCCTGGATTGAGCTCCTTC
XM_069787	LOC136243	2673	ACCTTAGCTCAGGGAGCTTCC
XM_069787	LOC136243	2674	ACCTGTGTTGTGATCGGCTAC
XM_071152	LOC138883	2675	ACCATCTCCTATACGGGTTGC
M37712	HUMP58GTA	2676	ACCTGATTGGTGGTGGTATCC
XM_087511	LOC152715	2676	ACCTGATTGGTGGTGGTATCC
XM_088463	LOC158056	2677	ACGTGGCTCTGGATGATCTGC
XM_089078	LOC163702	2678	ACGCTGCTCTCCAGAACTTC
XM_089078	LOC163702	2679	ACCCTATTTCCAGTCACTCCC
XM_089078	LOC163702	2680	ACATTGAACCACCTTCTTTCC
XM_090812	LOC161327	2681	ACCATTGCAAGTGCCGAGAGC
XM_090812	LOC161327	2682	ACAGCCATGGACAACACCAGC
XM_116009	LOC205527	2683	ACTTCAGTGCATTCAAGGACC
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XM_166294	LOC220164	2685	ACGTGTATCTTATGCCTACAC
XM_166294	LOC220164	2686	ACAAGGGAAGGAGAAATGATC
XM_166723	LOC222361	2687	ACACACTCCAATGTGTCCCTC
XM_167059	LOC222582	2688	ACACGTTCCCATCATGGATTC
XM_167059	LOC222582	2689	ACTTGCCCTCAGTGTAAATTCGC
XM_169247	LOC245804	2690	ACAGACCTGCTCAATGTCTGC
XM_172034	LOC254337	2691	ACTGGGATCCTGGATAGAAAC
XM_172299	LOC256947	2692	ACACTTCCAGGGATGGAACAC
XM_172299	LOC256947	2693	ACTGTCAGTTAGCCTGCACAC
XM_174355	LOC254502	2694	ACCAGAATGCAAGTGTGGTGC
XM_174355	LOC254502	2695	ACATGTGTGCACCTTGAAGCC
NM_000033	ABCD1	2696	ACTCCAACCTGACCAAGCCAC
NM_000052	ATP7A	2697	ACTCTCCCTCCAGCTCATCTC
NM_000052	ATP7A	2698	ACAGTGTTGTTACCAGTGAAC
NM_000111	SLC26A3	2699	ACTGGAATGATGATCTTCCTC
NM_000112	SLC26A2	2700	ACTAATGGTGTGGGCTCACTC
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NM_000324	RHAG	2702	ACTGTTCTCGAGCAGCTCAAC
NM_000324	RHAG	2703	ACTGGGTTCCCTCTATCGGAAC
NM_000326	RLBP1	2704	ACCAAGGACCATGGACCTGTC
NM_000326	RLBP1	2705	ACATTGAGAACTGGCAAAGTC
NM_000326	RLBP1	2706	ACGCTGCCCCAAGTATGATGGC
NM_000339	SLC12A3	2707	ACGAAGAACAGAGTCAAGTCC
NM_000340	SLC2A2	2708	ACACTTGGAAGAATCAAAGCC
NM_000350	ABCA4	2709	ACCCTACAGTGGATAGAAGAC
NM_000370	TTPA	2710	ACAGAATCGCACACTGGGACC
NM_000392	ABCC2	2711	ACAGAAGACTCTGGACAAGCC
NM_000441	SLC26A4	2712	ACTGCCATTTTCATATGGAGCC
NM_000441	SLC26A4	2713	ACCTGAAAGGGATGTTTATGC
NM_000443	ABCB4	2714	ACTGGCCTTCTGGTATGGATC
NM_018849	ABCB4	2714	ACTGGCCTTCTGGTATGGATC
NM_018850	ABCB4	2714	ACTGGCCTTCTGGTATGGATC
NM_000443	ABCB4	2715	ACATGCAGACATCAGGAAGCC
NM_018849	ABCB4	2715	ACATGCAGACATCAGGAAGCC
NM_018850	ABCB4	2715	ACATGCAGACATCAGGAAGCC
NM_000593	TAP1	2716	ACTCTCATGTCCATTCTCACC
NM_000593	TAP1	2717	ACCCAGTGGTCTGTTGACTCC
NM_000927	ABCB1	2718	ACAGTTCGTAATGCTGACGTC
NM_001042	SLC2A4	2719	ACCATAGGAGCTGGTGTGGTC
NM_001042	SLC2A4	2720	ACCAGATCTCAGCTGCCTTCC
NM_001043	SLC6A2	2721	ACGTCATCATCGCCTGGTCAC
NM_001043	SLC6A2	2722	ACTTCCAGGTCTGAAGCGAC
NM_001044	SLC6A3	2723	ACTGAAAGGTGTGGGCTTCAC
NM_001044	SLC6A3	2724	ACCAACAACCTGCTACAGGGAC
NM_004211	SLC6A5	2724	ACCAACAACCTGCTACAGGGAC
NM_014229	SLC6A11	2724	ACCAACAACCTGCTACAGGGAC
NM_016615	SLC6A13	2724	ACCAACAACCTGCTACAGGGAC
NM_001045	SLC6A4	2725	ACGTATGCAGAAGCGATAGCC
NM_001089	ABCA3	2726	ACAACCTTCTGTTCAAGCTGC
NM_001089	ABCA3	2727	ACCAAGGCATGGTCCATTACC
NM_001171	ABCC6	2728	ACCCAGATCCTCATCTGGAC
NM_001606	ABCA2	2729	ACAGAAGAAGCCCACCATCTC
NM_001606	ABCA2	2730	ACCGCATTGCCATCATCTCCC
NM_002858	ABCD3	2731	ACTTCATCGCTGCCATGCCTC
NM_002858	ABCD3	2732	ACTACCAAAGTGGAAGAATGC
NM_002940	ABCE1	2733	ACATGACTTCATCATGGCCAC
XM_029730	LOC222915	2733	ACATGACTTCATCATGGCCAC
NM_002940	ABCE1	2734	ACACAGTTGCAAACAGTCCTC
XM_029730	LOC222915	2734	ACACAGTTGCAAACAGTCCTC
NM_003003	SEC14L1	2735	ACATCCTGCAGTGGAAATTCC
NM_003039	SLC2A5	2736	ACTGTTGGCATCCTTGTGGCC
NM_003042	SLC6A1	2737	ACAGCCCTGGTGGATGAGTAC
NM_003043	SLC6A6	2738	ACTCGTACAGGGACTGTATGC

NM_003044	SLC6A12	2739	ACGAGGACCAGGTGAAGGATC
NM_003044	SLC6A12	2740	ACAGCCTCCATAGACATGTTC
NM_003049	SLC10A1	2741	ACCATGGAGTTCAGCAAGATC
NM_003049	SLC10A1	2742	ACTCTTGATTGCCACCTCCTC
NM_003051	SLC16A1	2743	ACCATCTATGGGACTTGTAGC
NM_003057	SLC22A1	2744	ACCTTCCTCTTCTGCTCTAC
NM_003057	SLC22A1	2745	ACCATGAAGGACGCCGAGAAC
NM_003059	SLC22A4	2746	ACCTCCCTGTTCTTCGTAGGC
NM_003060	SLC22A5	2747	ACCATTGTGACCGAGTGGAAC
NM_003742	ABCB11	2748	ACGCATTGCTATTGCTCGGGC
NM_003786	ABCC3	2749	ACGTGGACCCAAACAATGTGC
NM_020037	ABCC3	2749	ACGTGGACCCAAACAATGTGC
NM_020038	ABCC3	2749	ACGTGGACCCAAACAATGTGC
NM_003786	ABCC3	2750	ACAGAGATTGGAGAGAAGGGC
NM_020037	ABCC3	2750	ACAGAGATTGGAGAGAAGGGC
NM_020038	ABCC3	2750	ACAGAGATTGGAGAGAAGGGC
NM_003786	ABCC3	2751	ACAGACAATGATCCAGTCACC
NM_020037	ABCC3	2751	ACAGACAATGATCCAGTCACC
NM_020038	ABCC3	2751	ACAGACAATGATCCAGTCACC
NM_003786	ABCC3	2752	ACATCATCTCCAACCGGTGGC
NM_004207	SLC16A3	2753	ACTGGCTTCTCCTACGCCTTC
NM_004212	SLC28A2	2754	ACAGAGGCACCTCTGCTCATC
NM_004212	SLC28A2	2755	ACTTTCACAGGTCATCTGCTCC
NM_004254	SLC22A8	2756	ACTGAAGGAGATGGCCCAGTC
NM_004256	ORCTL3	2757	ACTTCGGCCTGGACGTCTATC
NM_004299	ABCB7	2758	ACATTGAGGGCCAGAAAGTCC
NM_004299	ABCB7	2759	ACCATGGTTTGCTTGCTAACC
NM_004317	ASNA1	2760	ACAGACCCAGCACACAACATC
NM_004731	SLC16A7	2761	ACCCATGGCAAATGGATTGGC
NM_004803	ORCTL4	2762	ACCTTCCTGTGCCTTGGAATC
NM_004803	ORCTL4	2763	ACTGTCACGTGTGTTCTTCCTC
NM_004827	ABCG2	2764	ACTTACAGTTCTCAGCAGCTC
NM_004827	ABCG2	2765	ACCTCCTTCTGTCACTCAACTC
NM_004915	ABCG1	2766	ACATCATGCAGGATGACATGC
NM_016818	ABCG1	2766	ACATCATGCAGGATGACATGC
NM_004915	ABCG1	2767	ACCTGAACTACTGGTACAGCC
NM_016818	ABCG1	2767	ACCTGAACTACTGGTACAGCC
NM_004915	ABCG1	2768	ACAGTGGATGTCTTACATCTC
NM_016818	ABCG1	2768	ACAGTGGATGTCTTACATCTC
NM_005050	ABCD4	2769	ACTACACTTACCAGTGCTTCC
NM_020323	ABCD4	2769	ACTACACTTACCAGTGCTTCC
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NM_020326	ABCD4	2769	ACTACACTTACCAGTGCTTCC
NM_005050	ABCD4	2770	ACCTTTGACTATCTGGGCAGC
NM_020323	ABCD4	2770	ACCTTTGACTATCTGGGCAGC

NM_020324	ABCD4	2770	ACCTTTGACTATCTGGGCAGC
NM_020325	ABCD4	2770	ACCTTTGACTATCTGGGCAGC
NM_020326	ABCD4	2770	ACCTTTGACTATCTGGGCAGC
NM_005050	ABCD4	2771	ACCTCATCAGCTGCTTCACCC
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NM_005164	ABCD2	2772	ACCCTCTATCCCATCATTGGC
NM_005445	CSPG6	2773	ACTTCGAAGAGTTATTGGTGC
NM_005445	CSPG6	2774	ACGAGGAATTGCTAGATTGGC
NM_005495	SLC17A4	2775	ACTATGGCTCATTCTTGGCTC
NM_005495	SLC17A4	2776	ACATTGTGTGTTTATTGGCTC
NM_005495	SLC17A4	2777	ACATAGCTGGAGCCATCTCTC
NM_005502	ABCA1	2778	ACACCAGCATGAAGGACATGC
NM_005629	SLC6A8	2779	ACCACTTGGAGTACCGAGCTC
NM_005688	ABCC5	2780	ACCTGTTGCTGGGAGAGACAC
NM_005689	ABCB6	2781	ACGTCTTCCTCAAGTTCCTCC
NM_005689	ABCB6	2782	ACATCAGCTCTGGCTGCATCC
NM_005692	ABCF2	2783	ACAGAAGTAGATTTGCTGACC
NM_005692	ABCF2	2784	ACCATCTGACTCGAGAGATGC
XM_067219	LOC131136	2784	ACCATCTGACTCGAGAGATGC
NM_006444	SMC2L1	2785	ACTGGGCATCTCCAACCTGTC
NM_006444	SMC2L1	2786	ACAAAGGCAGATGCATCTAGC
NM_006444	SMC2L1	2787	ACTTAGTGTTGGTCAGAGGTC
NM_006516	SLC2A1	2788	ACCTTCGATGAGATCGCTTCC
NM_006672	SLC22A7	2789	ACTTCCTCCTGCCCATCTTCC
NM_006672	SLC22A7	2790	ACTAGACTGCTAGTGTCTCTCC
NM_006749	SLC20A2	2791	ACGTGAGTAATGCCATCGGTC
NM_006931	SLC2A3	2792	ACCCAGGATGTATCCCAAGAC
NM_006934	SLC6A9	2793	ACTTCTTCTCGTCCATGACGC
NM_006979	HKE4	2794	ACTCACATGAAGATTTCCACC
NM_007168	ABCA8	2795	ACCATCAGTACATATCCGAAC
NM_007168	ABCA8	2796	ACAGCCTCTCACAGTCTACCC
NM_080283	ABCA9	2796	ACAGCCTCTCACAGTCTACCC
NM_007188	ABCB8	2797	ACATTCTCAGCTGTCAGGTAC
NM_007256	SLC21A9	2798	ACTTCATCTCGGAGCCATACC
NM_007256	SLC21A9	2799	ACCAAAGAGAGCAGATCCAGC
NM_012089	ABCB10	2800	ACGATGTCCAGTGTTATCTCC
NM_012089	ABCB10	2801	ACTGGTTGGCCCCAAGTGGTTC
NM_012243	SLC35A3	2802	ACTCATGGCAGTTCTCACAGC
NM_012243	SLC35A3	2803	ACTTGGAGGCCTTGTAATAGC
NM_012244	SLC7A8	2804	ACATCTTCACAGCTGGGAAGC
NM_012244	SLC7A8	2805	ACGTGGGCTTCATCAACTACC
NM_012429	SEC14L2	2806	ACCCTTCCTGAGTGAGGACAC
NM_012429	SEC14L2	2807	ACCAAGTGGAGTATGAGATCC

NM_012434	SLC17A5	2808	ACGTGTGAATCTGAGTGTTGC
NM_012434	SLC17A5	2809	ACCACTCATTGTACTCAGAGC
NM_012434	SLC17A5	2810	ACTTTGGGCTATCGTAGTTGC
NM_013356	SLC16A8	2811	ACCAAGTTCCTGATGGCGCTC
NM_014229	SLC6A11	2812	ACATCATGCTGCTGATCCTCC
NM_014331	SLC7A11	2813	ACTCCTCATAATACGCCCTGC
NM_014331	SLC7A11	2814	ACAGGGATTGGCTTCGTCATC
NM_014437	SLC39A1	2815	ACCTTCTCGGAAATCCTGCCC
NM_014579	SLC39A2	2816	ACTCCTGGGCTGTATTTCTGC
NM_014579	SLC39A2	2817	ACCTTCCTGTATGTCACCTTC
NM_014580	SLC2A8	2818	ACATCTCCGAAATCGCCTACC
NM_014580	SLC2A8	2819	ACTCTGGAACAAATCACAGCC
NM_014713	LAPTM4A	2820	ACCTGGTACATGGTAGTAAAC
NM_014713	LAPTM4A	2821	ACATCAACAACCGAAACGTGC
NM_014848	SV2B	2822	ACCATCATGGATGAGTGTGGC
NM_014849	SV2	2823	ACGTTGGAGAATCAGATCCAC
NM_014849	SV2	2824	ACCCATCCTCTTTGCCTCAGC
NM_015559	SETBP1	2825	ACTTGTGGCGTCTTCACCAGC
NM_015559	SETBP1	2826	ACCCATATGGAATGCCTTACAC
NM_016124	RHD	2827	ACCTCGAGTTTCCGGAGACAC
NM_016225	RHD	2827	ACCTCGAGTTTCCGGAGACAC
NM_020485	RHCE	2827	ACCTCGAGTTTCCGGAGACAC
NM_138616	RHCE	2827	ACCTCGAGTTTCCGGAGACAC
NM_138617	RHCE	2827	ACCTCGAGTTTCCGGAGACAC
NM_138618	RHCE	2827	ACCTCGAGTTTCCGGAGACAC
NM_016124	RHD	2828	ACTCTGCTCTGCTGAGAAGTC
NM_016225	RHD	2828	ACTCTGCTCTGCTGAGAAGTC
NM_016321	RHCG	2829	ACGCACAAGAACTTGAGCGAC
NM_016321	RHCG	2830	ACCATCCACACATTTGGCGCC
NM_016609	LOC51310	2831	ACTGGGACTACAACGGACTGC
NM_016609	LOC51310	2832	ACTCTTCTCCTCCCAAGCTTC
NM_017585	SLC2A6	2833	ACCTGCATCTGACCAAATCCC
NM_017585	SLC2A6	2834	ACTGGGAGTTCGAGCAGATCC
NM_017585	SLC2A6	2835	ACCATGCTCTTCATCATGGGC
NM_017767	SLC39A4	2836	ACTACATCCTGCAGACCTTCC
NM_130849	SLC39A4	2836	ACTACATCCTGCAGACCTTCC
NM_017767	SLC39A4	2837	ACGTAGCACTCTGCGACATGC
NM_130849	SLC39A4	2837	ACGTAGCACTCTGCGACATGC
NM_017836	FLJ20473	2838	ACACTGGACAAATTGATGACC
NM_017836	FLJ20473	2839	ACCCAGACAACATTGCCACGC
NM_018057	NTT73	2840	ACTGGGCGGGATTGGATTTGC
NM_018375	FLJ11274	2841	ACACCACCAAGCAAGTGAAAC
NM_018407	LC27	2842	ACGCGGTTCTACTCCAACAGC
NM_018407	LC27	2843	ACCAGATCTTTGACTTTGCCC
NM_018484	SLC22A11	2844	ACCATAGAGGTGCTGATGTCC
NM_018484	SLC22A11	2845	ACTATCCAGGACCTGGAGAGC

NM_018672	ABCA5	2846	ACAAGCATCCATAGATGCTGC
NM_018672	ABCA5	2847	ACCGCCTTCAAAGAGAAATTC
NM_018672	ABCA5	2848	ACTGGAGAACCAAGAACGCAC
NM_019112	ABCA7	2849	ACTGTATGGCTGGTCGATCAC
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NM_033308	ABCA7	2850	ACCTCTTGGCCATGGTGATAC
NM_019112	ABCA7	2851	ACATCTCAAGGGCAGATTTCGC
NM_033308	ABCA7	2851	ACATCTCAAGGGCAGATTTCGC
NM_019624	ABCB9	2852	ACGGCAAGTACTACAAGAGGC
NM_019625	ABCB9	2852	ACGGCAAGTACTACAAGAGGC
NM_019624	ABCB9	2853	ACATCCTGGAGAACTTCTACC
NM_019625	ABCB9	2853	ACATCCTGGAGAACTTCTACC
NM_019624	ABCB9	2854	ACGGTACTCATCATCGCGCAC
NM_019625	ABCB9	2854	ACGGTACTCATCATCGCGCAC
NM_004996	ABCC1	2855	ACCTCATCCAGTCCACCATCC
NM_019862	ABCC1	2855	ACCTCATCCAGTCCACCATCC
NM_019898	ABCC1	2855	ACCTCATCCAGTCCACCATCC
NM_019899	ABCC1	2855	ACCTCATCCAGTCCACCATCC
NM_019901	ABCC1	2855	ACCTCATCCAGTCCACCATCC
NM_019902	ABCC1	2855	ACCTCATCCAGTCCACCATCC
NM_020041	SLC2A9	2856	ACCTGAGTATCGTGGGCATTTC
NM_020208	XT3	2857	ACTTCTTCATGCTGCTGATGC
NM_022405	XT3	2857	ACTTCTTCATGCTGCTGATGC
NM_020346	SLC17A6	2858	ACAGGGTGCTGGAGAAGAAGC
NM_020346	SLC17A6	2859	ACAGATGAAGAACGTAGGTAC
NM_020346	SLC17A6	2860	ACCACCAAGTCTTATGGTGCC
NM_020372	LOC57100	2861	ACTATAATGGCCTTCCTGTGC
NM_016609	LOC51310	2862	ACAGCGAATGATCACCGCTCC
NM_020372	LOC57100	2862	ACAGCGAATGATCACCGCTCC
NM_020407	RHBG	2863	ACTATCCACACCTTTGGTGCC
NM_020407	RHBG	2864	ACAAGTTCTTCACGCCCATCC
NM_020485	RHCE	2865	ACTCTCCTCTGCTGAGAAGTC
NM_138618	RHCE	2865	ACTCTCCTCTGCTGAGAAGTC
NM_020485	RHCE	2866	ACCTACTATGCTCTAGCAGTC
NM_138618	RHCE	2866	ACCTACTATGCTCTAGCAGTC
NM_020485	RHCE	2867	ACATTGTGCTGCTGGTGCTTC
NM_138616	RHCE	2867	ACATTGTGCTGCTGGTGCTTC
NM_138617	RHCE	2867	ACATTGTGCTGCTGGTGCTTC
NM_020708	SLC12A5	2868	ACCAAGACCAGAATGTGGTGC
NM_021082	SLC15A2	2869	ACAGTCCTATCATTGATCGGC
NM_021977	SLC22A3	2870	ACCTTCGCCTTCCTCTTCGTC
NM_021977	SLC22A3	2871	ACAGATCCTGAGACGCATTGC
NM_022042	SLC26A1	2872	ACGTCCTTCTTCGCCAACCTC
NM_134425	SLC26A1	2872	ACGTCCTTCTTCGCCAACCTC
NM_022042	SLC26A1	2873	ACTTCCTCATGGGCACCTCAC

NM_134425	SLC26A1	2873	ACTTCCTCATGGGCACCTCAC
NM_022127	SLC28A3	2874	ACTGTGATGTCCATGCTGTAC
NM_022127	SLC28A3	2875	ACCAAGGTGATAGCTTGTGTC
NM_022154	LOC64116	2876	ACCTGCCATCAATGGTGTGAC
NM_022154	LOC64116	2877	ACTCAATGCAGGGATGAGCAC
NM_022154	LOC64116	2878	ACAGCCATTCTACTCATTACC
NM_022169	ABCG4	2879	ACCTGAAGCTGAGTGAGAAGC
NM_022169	ABCG4	2880	ACAAGCTCTACATCCTGAGCC
NM_022436	ABCG5	2881	ACTGCTTCTCCTACGTCCTGC
NM_022437	ABCG8	2882	ACCTCTCTACGCCATCTACC
NM_022736	FLJ14153	2883	ACATGAACCTCATGGGATGGC
NM_022911	SLC26A6	2884	ACCTCTTGTCCGAGGCTATAC
NM_134263	SLC26A6	2884	ACCTCTTGTCCGAGGCTATAC
NM_134426	SLC26A6	2884	ACCTCTTGTCCGAGGCTATAC
NM_022911	SLC26A6	2885	ACATCCTGCCCAAGACTGCAC
NM_134263	SLC26A6	2885	ACATCCTGCCCAAGACTGCAC
NM_134426	SLC26A6	2885	ACATCCTGCCCAAGACTGCAC
NM_024331	C20orf121	2886	ACAGCTGTAGAAGAAGCTGGC
NM_024331	C20orf121	2887	ACTCTCTCCACACAAACCTTC
NM_030777	SLC2A10	2888	ACAGATGAGACTGCAACACAC
NM_030777	SLC2A10	2889	ACCAGCAGTTCCAGAAGAGAC
NM_032034	SLC4A11	2890	ACCATGTGCGAGAATGGATAC
NM_032034	SLC4A11	2891	ACCATGTTCTCGGATATCGCC
NM_032038	LOC83985	2892	ACCGCCATCTTCATTGAGGCC
NM_032038	LOC83985	2893	ACCTACCTGCACATCTGCCAC
NM_032148	DKFZP434K0427	2894	ACATTGGCATCCAGATTATCC
NM_032148	DKFZP434K0427	2895	ACAGCATTGGGTGATCTGCTC
NM_032718	MGC11332	2896	ACAGTTGCTGGAATAGTAGGC
NM_032718	MGC11332	2897	ACCATGGGTGCAGTTGTCTCTC
NM_032803	SLC7A3	2898	ACTTCGGCTATGGGATCCAGC
NM_033125	OKB1	2899	ACAGGATACTTGGTCAGGACC
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NM_145186	ABCC11	2900	ACCTATACTCTCCAAGATGGC
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NM_145186	ABCC11	2901	ACCTTGTCATGGCAACAGACC
NM_033226	ABCC12	2902	ACCCTGTGCAAGGTTAGCACC
NM_145187	ABCC12	2902	ACCCTGTGCAAGGTTAGCACC
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NM_145188	ABCC12	2903	ACACCGATGAGATGCTCTGGC
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NM_052832	SLC26A7	2904	ACAGGTGGCTTGTCTAATATC

NM_134266	SLC26A7	2904	ACAGGTGGCTTGTCTAATATC
NM_052885	SLC2A13	2905	ACTTGCAATATGGCTGGCTTC
NM_052934	SLC26A9	2906	ACATGCACAAGATTTCGCTTCC
NM_134325	SLC26A9	2906	ACATGCACAAGATTTCGCTTCC
NM_052934	SLC26A9	2907	ACGACTCAGAGGAGGACATTC
NM_134325	SLC26A9	2907	ACGACTCAGAGGAGGACATTC
NM_080282	ABCA10	2908	ACATCCCTTATTAAGCAGCAC
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NM_080283	ABCA9	2910	ACATCAGGTTTCAGTCACTGTC
NM_080284	ABCA6	2911	ACTTCTAGGACTGTGTATTGC
NM_020485	RHCE	2912	ACGTGTGTTGTAACCGAGTGC
NM_138616	RHCE	2912	ACGTGTGTTGTAACCGAGTGC
NM_138617	RHCE	2912	ACGTGTGTTGTAACCGAGTGC
NM_138617	RHCE	2913	ACGGCAATGGCATGATTGCTC
NM_138718	SLC26A8	2914	ACAGGTTCTTACGATGCATGC
NM_139177	C17orf26	2915	ACTTGGCTGACCTCCTGATGC
NM_139177	C17orf26	2916	ACTGCTCATCTTGGCCATCAC
XM_032693	KIAA0420	2917	ACCCACAAAGGCAAGATTCCC
XM_037173	LOC91252	2918	ACATCGCCTTGGTGAACGTGC
XM_046677	KIAA0062	2919	ACGTGCAAGGACACAGGAACC
XM_046677	KIAA0062	2920	ACCTGGACCACATGATTCCCTC
XM_047707	KIAA1265	2921	ACAGCTGTTGGTCACTATGCC
XM_051905	DKFZP564L0864	2922	ACTGGTTTTCAGCAACATTTGC
XM_051905	DKFZP564L0864	2923	ACCTTGGATGATGTGGGCTGC
XM_051905	DKFZP564L0864	2924	ACTGTGGCAGTCACAGCCATC
XM_060424	LOC127324	2925	ACCTCTCTGTGGTCAACACGC
XM_060424	LOC127324	2926	ACATTCCATTGGGCCCAGTCC
XM_060969	LOC118461	2927	ACCTGATTCTCAAGAGAAGCC
XM_063138	LOC122438	2928	ACAACGTGAGCAATTCTGCGC
XM_064152	LOC124470	2929	ACACCAGGCATCATCGAGAAC
XM_064152	LOC124470	2930	ACAAGAGTATAAGCCGGACAC
XM_066649	LOC139355	2931	ACGGAGATTCCAAGTTGGCTC
XM_067219	LOC131136	2932	ACATCCTGGCTTACAAGTTGC
XM_069204	LOC135143	2933	ACGCATGCCTTTAGACCACCC
XM_069204	LOC135143	2934	ACTGTATCAGAGGCAGGTGTC
XM_070474	LOC137518	2935	ACAGGAAAGGATACCAAAGGC
XM_086329	LOC148810	2936	ACATTGGACACATGGACACAC
XM_086329	LOC148810	2937	ACTGGGAACATGGCCCTCATC
XM_086889	LOC150287	2938	ACAACACCTACAGCCTGGTTC
XM_086889	LOC150287	2939	ACAGCCTGGTTTCATTCTAAAC
XM_087693	LOC153505	2940	ACATTTGGCGGTTCCCATACC
XM_087693	LOC153505	2941	ACCTCCTCAACTCCTTCCAGC
XM_091236	LOC161932	2942	ACTGGAAGTGGAGTCTCATGC
XM_092895	LOC164636	2943	ACCATATCCTTGATTGGCAGC
XM_092895	LOC164636	2944	ACCAAGTGGGAATACGAGATCC
XM_094956	LOC154664	2945	ACAGATCCTGAACTCTTCAGC

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XM_094956	LOC154664	2946	ACTGGAAGTGATCCACACTAC
XM_094956	LOC154664	2947	ACACTCCTTCATGGCATAACC
XM_099966	LOC159361	2948	ACCTGAGATCAGATGTCAAGC
XM_099966	LOC159361	2949	ACTGGAACCAGTCAGTCATGC
XM_115387	LOC204461	2950	ACACTGGGCCCTCACATTCTTC
XM_115387	LOC204461	2951	ACCTCATCTCCTTCCTCATTC
XM_167663	LOC221074	2952	ACTCTGGAGAAATACGGCTAC
XM_170932	LOC254428	2953	ACACCTGGTGTTCCCTCTACAC
XM_170932	LOC254428	2954	ACCCGGACAACCTTCTCCATCC
NM_016022	APH-1A	2955	ACAGGAGGTGTTCCGCTTTGC
NM_016022	APH-1A	2956	ACTTCCTGACTTCAGCCTTTTC
NM_031301	DKFZP564D0372	2957	ACCGAGCCGTTGCGTATCATC
NM_016022	APH-1A	2958	ACCCGCTTCGCGTTATCATCC
NM_031301	DKFZP564D0372	2959	ACAACCAGCGCTCCAGATAAC
NM_015331	NCSTN	2960	ACTCTACATGGACTGAGAGCC
NM_015331	NCSTN	2961	ACTTCCTAGAGCATCTGTCCC
NM_000015	NAT2	2962	ACATTCTTGAGCACCAGATCC
NM_000017	ACADS	2963	ACACCAGATGTTGCTCCAGAC
NM_000017	ACADS	2964	ACCGGAGTCATCATGAGTGTC
NM_000018	ACADVL	2965	ACCCACTTGGCTTCTGAATAC
NM_000030	AGXT	2966	ACGTGTTCCAGACCAGGAACC
NM_000030	AGXT	2967	ACGAAGCCCTTCTCCTTCTAC
NM_000030	AGXT	2968	ACATTGAGATCATGGGTGGCC
NM_000098	CPT2	2969	ACCATGCACTACCAGGACAGC
NM_000098	CPT2	2970	ACATTCTCTCAGACAGCAGCC
NM_000108	DLD	2971	ACTTGGTGCAGATGTGACAGC
NM_000108	DLD	2972	ACAAATGCTGACACAGATGGC
NM_000110	DPYD	2973	ACTTGGAGCTGGAGACACTGC
NM_000170	GLDC	2974	ACACATTCCGAGAGACAAGGC
NM_000170	GLDC	2975	ACATGGCAGGCATGAAGATTC
NM_000170	GLDC	2976	ACCAGAGAACAAATTCTGGCC
NM_000175	GPI	2977	ACAAGATGAAGTCTTTCTGCC
NM_000175	GPI	2978	ACTGAAGCCCTTAAGCCATAC
NM_000175	GPI	2979	ACTGGATGGACCAGCACTTCC
NM_000182	HADHA	2980	ACACAGATGGTGTCCAAGGGC
NM_000194	HPRT1	2981	ACGAAGTGTTGGATATAAGCC
NM_000196	HSD11B2	2982	ACACATTCAGCTGTGAACTCC
NM_000196	HSD11B2	2983	ACTTCATCCACTACTACCTGC
NM_000197	HSD17B3	2984	ACTATGTGGCATACTGAAGC
NM_000229	LCAT	2985	ACCACGTGTTTCATTTCCACAC
NM_000236	LIPC	2986	ACGCACAAGATTGGGAGAATC
NM_000236	LIPC	2987	ACCTACTACTTCGCCCAACCC
NM_000237	LPL	2988	ACTTTGAGTATGCAGAAGCCC
NM_000274	OAT	2989	ACAGTGCTGTCAACCAAGGGC
NM_000274	OAT	2990	ACAGACAGGATTGGCCAGAAC
NM_000300	PLA2G2A	2991	ACAGGAAAGGAAGCCGCACTC

NM_000300	PLA2G2A	2992	ACTGTGTGAGTGTGATAAGGC
NM_000320	QDPR	2993	ACTGTGACCTGATGTGGAAGC
NM_000348	SRD5A2	2994	ACGGTACTTCTGGGCCTCTTC
NM_000379	XDH	2995	ACCCTCACCCCTCAGCTTCTTC
NM_000379	XDH	2996	ACTGGTGGCAGACATCCCTTC
NM_000398	DIA1	2997	ACGCTTCAAGCTCTGGTACAC
NM_007326	DIA1	2997	ACGCTTCAAGCTCTGGTACAC
NM_000402	G6PD	2998	ACATCCGCAAACAGAGTGAGC
NM_000402	G6PD	2999	ACCGCATCATCGTGGAGAAGC
NM_000408	GPD2	3000	ACGGACAACATAACGATGCAC
NM_000414	HSD17B4	3001	ACTCTCTTCACCCAAATATGC
NM_000429	MAT1A	3002	ACCCGGATAAGATCTGTGACC
NM_000429	MAT1A	3003	ACTTCAAGACTTGCAACGTGC
NM_000429	MAT1A	3004	ACACCATCGTCATCTCTGTGC
NM_000436	OXCT	3005	ACCAGTGCTCATCGCCATACC
NM_000436	OXCT	3006	ACGACAACATGAAGCTGATGC
NM_000463	UGT1A1	3007	ACTGTCCAGGACCTATTGAGC
NM_000482	APOA4	3008	ACCTTCCAGATGAAGAAGAAC
NM_000485	APRT	3009	ACTCTGTGGGCCTCCTATTCC
NM_000485	APRT	3010	ACAGGGAACACATTCTTTTGC
NM_000531	OTC	3011	ACGCTCCAGGAACACTATAGC
NM_000531	OTC	3012	ACACTGCTTGCCCAGAAAGCC
NM_000662	NAT1	3013	ACCATTGATGGCAGGAACTAC
NM_000662	NAT1	3014	ACCCTCACCCATAGGAGATTC
NM_000663	ABAT	3015	ACCTGCTAAATAATGCAGCCC
NM_000673	ADH7	3016	ACCAGTACATTTACCGAGTAC
NM_000673	ADH7	3017	ACCCATCAGTGAGGTGCTGTC
NM_000689	ALDH1A1	3018	ACAGGATCAACAGAGGTTGGC
NM_000689	ALDH1A1	3019	ACTCAAGGCCCTCAGATTGAC
NM_000690	ALDH2	3020	ACTTCTTCAGCTACACACGCC
NM_000690	ALDH2	3021	ACAAGGCCAATTACCTGTCCC
NM_000691	ALDH3A1	3022	ACCTGGACAAGGATCTGTACC
NM_000693	ALDH1A3	3023	ACAGACAACATGCGGATTGCC
NM_000693	ALDH1A3	3024	ACTAGGTGAATACGCTTTGGC
NM_000694	ALDH3B1	3025	ACATCTTCTTCACAGGGAGCC
NM_000695	ALDH3B2	3025	ACATCTTCTTCACAGGGAGCC
NM_000694	ALDH3B1	3026	ACGGCTTCATGCACATGACCC
NM_000695	ALDH3B2	3027	ACTACCCATTGAACCTGACCC
NM_000696	ALDH9	3028	ACAGTGAGGCTGGTGTACCTC
NM_000696	ALDH9	3029	ACTAGCAGCTGGCGTCTTTAC
NM_000709	BCKDHA	3030	ACTTCGTCACTATCTCCTCTC
NM_000709	BCKDHA	3031	ACTGGGATAAACAGGACCACC
NM_000712	BLVRA	3032	ACTCTTGATGGAGGAATTCGC
NM_000791	DHFR	3033	ACTAAGTGCTTCTCCAAGACC
NM_000791	DHFR	3034	ACCCTTCAACTGAGCAGTTTC
NM_000819	GART	3035	ACTGCCCTTGCTCAATTCTGC

NM_000849	GSTM3	3036	ACTTGGAAGAGCTACCTGGAC
NM_000849	GSTM3	3037	ACCTGAAGGCTTTTCATGTGCC
NM_000853	GSTT1	3038	ACTTAAGCGATGCCTTTGCCC
NM_000853	GSTT1	3039	ACTACTGGTACCCTCAGGACC
NM_000854	GSTT2	3040	ACGCTCAAGGATGGTGATTTC
NM_000854	GSTT2	3041	ACGAACGTGTTTGAGGGACGGC
NM_000855	GUCY1A2	3042	ACTCCCATGCAAGTAATCAGC
NM_000857	GUCY1B3	3043	ACCCAAGAACTGGAAATCCTC
NM_000859	HMGCR	3044	ACTGACCATCTGCATGATGTC
NM_000859	HMGCR	3045	ACAGTCGCTGGATAGCTGATC
NM_000859	HMGCR	3046	ACAGAAGGTTGTCTTGTGGCC
NM_000883	IMPDH1	3047	ACATGGCCATTGCCATGGCTC
NM_000883	IMPDH1	3048	ACCCGTGAGGATGACAAATAC
XM_067688	LOC131961	3048	ACCCGTGAGGATGACAAATAC
XM_069825	LOC136307	3048	ACCCGTGAGGATGACAAATAC
NM_000883	IMPDH1	3049	ACCTCATAGCAGGCATCCAAC
NM_000884	IMPDH2	3050	ACATCGACTTCACTGCAGACC
NM_000884	IMPDH2	3051	ACAAGGTGTGAGAGTATGCAC
NM_000903	NQO1	3052	ACTTACGCTGCCATGTATGAC
NM_000904	NQO2	3053	ACTAGCGCTCCTTTCCGTAAAC
NM_000904	NQO2	3054	ACCATCTGGAAGGAAGAGCCC
NM_000904	NQO2	3055	ACTGGCACTTCGGGCAATAAC
NM_000918	P4HB	3056	ACTTCCAACAGTGACGTGTTTC
NM_000918	P4HB	3057	ACAGAGTTCTGCCACCGCTTC
NM_000929	PLA2G5	3058	ACTGCCTCAAGAGAAACCTAC
NM_000932	PLCB3	3059	ACGAAGAGCCCTTCGACTTCC
NM_000933	PLCB4	3060	ACGGTAGACCAATTAGTGAGC
NM_000933	PLCB4	3061	ACCATGCAGAAGTTACACTGC
NM_000942	PPIB	3062	ACAGGAGAGAAAGGATTTGGC
NM_001054	SULT1A2	3063	ACCTGCTCATCAGCACCTACC
NM_001055	SULT1A1	3063	ACCTGCTCATCAGCACCTACC
NM_001056	SULT1C1	3064	ACTGTATGGTTTCTACTACC
NM_001056	SULT1C1	3065	ACATAAAGAGGGACCCAAAGC
NM_001072	UGT1A6	3066	ACATTACAGCAGAAGCCCAGAC
NM_001080	ALDH5A1	3067	ACGGAGACATTATCCACACCC
NM_001080	ALDH5A1	3068	ACTGGACAGACTTGTGTTTGC
NM_001088	AANAT	3069	ACCCTATGTCCAGAGCTGTCC
NM_001088	AANAT	3070	ACATAGCCCACCTGCATGTGC
NM_001088	AANAT	3071	ACCTTCATGGAGCTCCACTGC
NM_001114	ADCY7	3072	ACCTACACTGTGAAGTGCATC
NM_001114	ADCY7	3073	ACTCGTACGATGACGAGATGC
NM_001115	ADCY8	3074	ACAATGAGGAGCTGTATTCTC
NM_001116	ADCY9	3075	ACCCTGGGAGACTGTTACTAC
NM_001116	ADCY9	3076	ACTACTGTAACCTTCTGCCAGC
NM_001179	ART3	3077	ACCCATCTATGTCTACAACCC
NM_001182	ALDH7A1	3078	ACGAGCCAATAGCAAGAGTCC

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NG_001082	NG_001082	3079	ACCCTAATGTTCTCTATGGGC
NM_001182	ALDH7A1	3079	ACCCTAATGTTCTCTATGGGC
NM_001236	CBR3	3080	ACATGTGCAACGAGTTACTGC
NM_001236	CBR3	3081	ACAGACATGGATGGGAAAGAC
NM_001303	COX10	3082	ACAGCTCTGGTTGTAAGTACC
NM_001303	COX10	3083	ACTGCATGATGTCGGTCACCC
NM_001360	DHCR7	3084	ACCTTCCAGGTGCTTCTGTAC
NM_001360	DHCR7	3085	ACCATTGACATCTGCCATGAC
NM_001360	DHCR7	3086	ACATCATCTACATGGCCATCC
NM_001361	DHODH	3087	ACTGGCTGTTGCTTCACCTC
NM_001379	DNMT1	3088	ACCAAGCTGGTCTACCAGATC
NM_001478	GALGT	3089	ACCAACACAGCAGACACAGTC
NM_001478	GALGT	3090	ACTGAAGCTGCCTTGACATC
NM_001482	GATM	3091	ACGCTTCTTTGAGTACCGAGC
NM_001497	B4GALT1	3092	ACCTCATTCCAATGAATGACC
NM_001497	B4GALT1	3093	ACTCACTCACCTACCAGGTGC
NM_001503	GPLD1	3094	ACTGTAACCTGGGCTGGACTC
NM_001512	GSTA4	3095	ACCTGCTGTTCCAACAAGTGC
NM_001527	HDAC2	3096	ACAGGGTCATCCCATGAAGCC
NM_001527	HDAC2	3097	ACCTGGTGTCCAGATGCAAGC
NM_001535	HRMT1L1	3098	ACAGCCAGAGGAGTTTGTGGC
NM_001535	HRMT1L1	3099	ACGGATAAAGTCATCCTGGAC
NM_001607	ACAA1	3100	ACGTGAATCTGAGGCCGGAAC
NM_001608	ACADL	3101	ACGTCTAGAACTCCTTCTGC
NM_001609	ACADSB	3102	ACCCTGTGGAGAAATACTTCC
NM_001618	ADPRT	3103	ACTGACATTAAGGTGGTTGAC
NM_001628	AKR1B1	3104	ACCTCTACCTTATTCACTGGC
NM_001628	AKR1B1	3105	ACCTGGCTTGAAGTATAAGCC
NM_001644	APOBEC1	3106	ACTGCCATTACCAAACGATTC
NM_005889	APOBEC1	3106	ACTGCCATTACCAAACGATTC
NM_001757	CBR1	3107	ACCAGCTGGACATCGACGATC
NM_001818	AKR1C4	3108	ACCACAGATGGTCCAACCAGC
NM_001876	CPT1A	3109	ACTTCAAGGTCTGGCTCTACC
NM_001889	CRYZ	3110	ACCACTCTTACCCTATACTCC
NM_001889	CRYZ	3111	ACTGCTTATCGAGCTCTGATC
NM_001922	DCT	3112	ACGGTGGACAGCCTAGTGAAC
NM_001922	DCT	3113	ACTACGTGATCACCACACAAC
NM_001922	DCT	3114	ACGATCCGACTCTGATTAGTC
NM_001966	EHHADH	3115	ACAATGGGCCGAGGCATTGTC
NM_002027	FNTA	3116	ACACCACTGGCTACAATGATC
NM_002028	FNTB	3117	ACCAACATCATCACTCCAGAC
NM_002028	FNTB	3118	ACTTTCTACAGAAGCCAGTCC
NM_002033	FUT4	3119	ACTACCACCACTGAGCCAAC
NM_002046	GAPD	3120	ACTCATGACCACAGTCCATGC
XM_069391	LOC135508	3120	ACTCATGACCACAGTCCATGC
XM_171437	LOC253659	3120	ACTCATGACCACAGTCCATGC

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NG_001038	NG_001038	3121	ACCCAGAAGACTGTGGATGGC
NM_002046	GAPD	3121	ACCCAGAAGACTGTGGATGGC
XM_060538	LOC127552	3121	ACCCAGAAGACTGTGGATGGC
XM_068131	LOC132990	3121	ACCCAGAAGACTGTGGATGGC
XM_069391	LOC135508	3121	ACCCAGAAGACTGTGGATGGC
NM_002064	GLRX	3122	ACAGCCACCAACCACACTAAC
NM_002153	HSD17B2	3123	ACAGCAAGGTTGCAGCAATGC
NM_002168	IDH2	3124	ACCAAGCCCATCACCATTGGC
NG_001155	NG_001155	3125	ACAAGTTGGTATGGCGTGTGC
NM_002300	LDHB	3125	ACAAGTTGGTATGGCGTGTGC
NM_002301	LDHC	3126	ACTTGCCCTTGTTGATGTTGC
NM_017448	LDHC	3126	ACTTGCCCTTGTTGATGTTGC
NM_002301	LDHC	3127	ACATGGTGATTCTAGTGTGCC
NM_017448	LDHC	3127	ACATGGTGATTCTAGTGTGCC
NM_002340	LSS	3128	ACTTGCTGGAGCTGCTGAACC
NM_002340	LSS	3129	ACGAGCTACAGGAACATCTTC
NM_002412	MGMT	3130	ACACACGTGTAACACTGCATC
NM_002454	MTRR	3131	ACAAGCCTCTCTGAATATTCC
NM_024010	MTRR	3131	ACAAGCCTCTCTGAATATTCC
NM_002454	MTRR	3132	ACCCAGACCATATTTCGTGTGC
NM_024010	MTRR	3132	ACCCAGACCATATTTCGTGTGC
NM_002454	MTRR	3133	ACAACATCCAGCTTCATGGCC
NM_024010	MTRR	3133	ACAACATCCAGCTTCATGGCC
NM_002541	OGDH	3134	ACTATTCATGGAGGGCTGAGC
NM_002541	OGDH	3135	ACTACGTGAAGCCAAGACTTC
NM_002660	PLCG1	3136	ACCGTCATGACTTTGTTCTAC
NM_002660	PLCG1	3137	ACAAGCCTATGCAGATGAACC
NM_002661	PLCG2	3138	ACATGCAGGACATGAACAACC
NM_002661	PLCG2	3139	ACGAGAAGCATTCACTCTACC
NM_002661	PLCG2	3140	ACGCTGACAGTCAAGGTTCTC
NM_002662	PLD1	3141	ACCAAAGAGGCCATAGTGCCC
NM_002663	PLD2	3142	ACCTGCACTCTGTATTCTGTC
NM_002663	PLD2	3143	ACTGGAGACTGGACATTATGC
NM_002663	PLD2	3144	ACTCCATCCTCAATGCCTACC
NM_002686	PNMT	3145	ACTGGAGCATGTACAGCCAAC
NM_002686	PNMT	3146	ACCTCCGCACCTATATCATGC
NM_002970	SAT	3147	ACTGCCTGGTTGCAGAAGTGC
NM_002970	SAT	3148	ACCTATGACCCGTGGATTGGC
NM_003000	SDHB	3149	ACAAGGCTGGAGACAAACCTC
NM_003000	SDHB	3150	ACCCGAAGGATTGACACCAAC
NM_003000	SDHB	3151	ACGGGCTCTACGAGTGCATTC
NM_003001	SDHC	3152	ACTCCCTGGGAACCTTTGAGTC
NM_003001	SDHC	3153	ACCTGGAATGGGATCCGACAC
NM_003032	SIAT1	3154	ACCAGGCATCAAGTTCAGTGC
NM_003033	SIAT4A	3155	ACCACCCACCATCTGGTGTAC
NM_003034	SIAT8A	3156	ACCACAGTTACATCTACATGC

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NM_003101	SOAT1	3157	ACTCCATCTTGCCAGGTGTGC
NM_003104	SORD	3158	ACCTTCCATCTTCTTCTGTGC
NM_003124	SPR	3159	ACTGCTGCTTATCAACAACGC
NM_003124	SPR	3160	ACAGACATGCAGCAGTTGGCC
NM_003167	SULT2A1	3161	ACAGTGGCCCAAGCTGAAGAC
NM_003330	TXNRD1	3162	ACATGTGTGAATGTGGGTTGC
NM_003330	TXNRD1	3163	ACTCAGAGTAGTAGCTCAGTC
NM_003330	TXNRD1	3164	ACAATTGGAATCCACCCTGTC
NM_003358	UGCG	3165	ACACCTCAACAAGAAGGCAAC
NM_003358	UGCG	3166	ACAAGATCATGATGATCCAGC
NM_003358	UGCG	3167	ACTGGTCGCTACAGATTACGC
NM_003477	PDX1	3168	ACCTCATGCATATGCTACTGC
NM_003477	PDX1	3169	ACAGTCACAATGTCAAGTGAC
NM_003491	ARD1	3170	ACCACAGAGAGCACAGATGTC
NM_003561	PLA2G10	3171	ACTCGCCCAAGTGTGACTGAC
NM_003578	SOAT2	3172	ACCTCTACTTCCTCTTCTGCC
NM_003578	SOAT2	3173	ACGTGCTGATGTGGACCATGC
NM_003595	TPST2	3174	ACCAACCACGTGGAATACCGC
NM_003596	TPST1	3175	ACCGGATAGAGGAACGTAGCC
NM_003635	NDST2	3176	ACTTCTTCTGAGCCTGCACC
NM_003706	PLA2G4C	3177	ACCTGGCTGACTGAGATGCTC
NM_003706	PLA2G4C	3178	ACACTCTAGATGTGGTGGTGTC
NM_003708	RODH-4	3179	ACAGGATCTGTCGTTGGTGAC
NM_003774	GALNT4	3180	ACATGTTCCAGAGGATAGACC
NM_003774	GALNT4	3181	ACCCACACTCAGGACTGTGTC
NM_003778	B4GALT4	3182	ACTACTTCGTGGGTGCCATTC
NM_003779	B4GALT3	3183	ACAGTAACCTCAGTCACCTGC
NM_003779	B4GALT3	3184	ACAAGTTTGGATACAGCCTCC
NM_003780	B4GALT2	3185	ACGGCGTCTATGTCATCAACC
NM_030587	B4GALT2	3185	ACGGCGTCTATGTCATCAACC
NM_003780	B4GALT2	3186	ACATCTTCAACCGGATCTCCC
NM_030587	B4GALT2	3186	ACATCTTCAACCGGATCTCCC
NM_003780	B4GALT2	3187	ACCACTCTTCACCAATATCAC
NM_030587	B4GALT2	3187	ACCACTCTTCACCAATATCAC
NM_003782	B3GALT4	3188	ACAGCGAGGAAGTGCCCTTTC
NM_003783	B3GALT2	3189	ACCCTGTGACATACACTTTCC
NM_003783	B3GALT2	3190	ACTGGGTGCAACATACTGTCT
NM_003783	B3GALT2	3191	ACAGCCACCTAATTACCTCTC
NM_003883	HDAC3	3192	ACAGGTGACATGTATGAAGTC
NM_003883	HDAC3	3193	ACCCGCATCGAGAATCAGAAC
NM_003888	ALDH1A2	3194	ACCATTCTGTAGATGGAGAC
NM_003888	ALDH1A2	3195	ACCAGGGTGTGTTCTTCAATC
NM_003896	SIAT9	3196	ACTTGAAAGCCAAGACCTGTC
NM_003896	SIAT9	3197	ACATCCTTCAGTACTCAGAGC
NG_000002	NG_000002	3198	ACTTCAACAAGGCCAAGTCCC
NM_003935	TOP3B	3198	ACTTCAACAAGGCCAAGTCCC

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NM_080925	LOC129020	3198	ACTTCAACAAGGCCAAGTCCC
NM_004036	ADCY3	3199	ACTCGGTGGAGAAGGAGAAGC
NM_004043	ASMT	3200	ACAGAGCTGTCCAGCGACTAC
NM_004043	ASMT	3201	ACCCACTACCACATGCTCCTC
NM_004044	ATIC	3202	ACTCAGTCTAACTCTGTGTGC
NM_004051	BDH	3203	ACGCCCCTATTGCTTGGTTC
NM_004059	CCBL1	3204	ACTTTGCCGTGGAAGCCTTTC
NM_004129	GUCY1B2	3205	ACTACTCGGATAGAAGTGGTC
NM_004129	GUCY1B2	3206	ACATCTGTACTGCCTGTGAAC
NM_004135	IDH3G	3207	ACAAACAATTCCCTCCGTCCGC
NM_004135	IDH3G	3208	ACGTCATCCACTGTAAGAGCC
NM_004168	SDHA	3209	ACGGTCTCTGCGATATGATAC
NM_004168	SDHA	3210	ACCGTGCATTATAACATGGGC
NM_004169	SHMT1	3211	ACCCATGGGTTCATGACAGAC
NM_004169	SHMT1	3212	ACAGAGGGATAGAGCTGACCC
NM_004190	LIPF	3213	ACAACAGCCTTGCCCTTCATTC
NM_004190	LIPF	3214	ACCTCCCTACTACAATGTGAC
NM_004192	ASMTL	3215	ACCTTCGAAGACCTCAGTGAC
NM_004267	CHST2	3216	ACTACAAGTGGCACAAGGAGC
NM_004267	CHST2	3217	ACATGCTGAGCGCTCTTTACC
NM_004285	H6PD	3218	ACTTATGGCAGGGACTGTTCC
NM_004285	H6PD	3219	ACCAGCTTCTATGAGGAGTAC
NM_004285	H6PD	3220	ACTTTGAGTTCAGTAGCGGCC
NM_004314	ART1	3221	ACCACTTCTCCTTCAAGACAC
NM_004314	ART1	3222	ACCTTCTTCGGCATCTGGACC
NM_004412	DNMT2	3223	ACTGATTCAAGGACGAATAGC
NM_004412	DNMT2	3224	ACACTGACGTGAACCAGTATC
NM_004412	DNMT2	3225	ACAGTGAAACAGCGTTATCGC
NM_004462	FDFT1	3226	ACCTCTGAACAGGAGTGGGAC
NM_004462	FDFT1	3227	ACCAATGCACTGCACCACATC
NM_004479	FUT7	3228	ACATCTTTGTGCCCTATGGCC
NM_004479	FUT7	3229	ACCAACGCTTCTTTGCCTGGC
NM_004482	GALNT3	3230	ACAGTGTGCTCTATTCTTCAC
NM_004493	HADH2	3231	ACCCATACCTTGGAAGACTTC
NM_004493	HADH2	3232	ACAGGCCATCATCGAGAACCC
NM_004544	NDUFA10	3233	ACCTGAAGTTCGATAAAGGGC
NM_004544	NDUFA10	3234	ACATCAGTTCAGAGAGCTGCC
NM_004550	NDUFS2	3235	ACCCAAGCAAAGAAACAGCCC
NM_004550	NDUFS2	3236	ACATCATGGCTGTGACCACAC
NM_004581	RABGGTA	3237	ACAAGCCAGATTCTGGGAGCC
NM_004581	RABGGTA	3238	ACTTTCACTGCTGGGACTATC
NM_004605	SULT2B1	3239	ACCACATTAAGGGCTGGCTTC
NM_004618	TOP3A	3240	ACCAAGCTCACCTCCCATTTC
NM_004618	TOP3A	3241	ACAGGAGACAGAGGAAGAACC
NM_004737	LARGE	3242	ACATCGTGTACAAGGAGGGCC
NM_133642	LARGE	3242	ACATCGTGTACAAGGAGGGCC

NM_004751	GCNT3	3243	ACCTGGAGGTCAAGAAGAAGC
NM_004775	B4GALT6	3244	ACTTCACATACTCACCATACC
NM_004775	B4GALT6	3245	ACAAGTCAATTCCCTCATCACC
NM_004776	B4GALT5	3246	ACCACAGTGAAACCTTCCTGC
NM_004776	B4GALT5	3247	ACCTCCCAGTCCTGTTTCAGAC
NM_004784	NDST3	3248	ACCTGTACAGTGGCTACAAAC
NM_004784	NDST3	3249	ACGTGGAACCTCTCAAAGCTGC
NM_004792	PPIG	3250	ACGAGAGTTTTCGCTGTTAAAC
NM_004832	GSTTLp28	3251	ACTGAAACTGTGGATGGCAGC
NM_004863	SPTLC2	3252	ACCAGGTATTTTCAGGAGACGC
NM_004881	PIG3	3253	ACTTAATGCAGAGACAAGGCC
NM_004881	PIG3	3254	ACAGCTGCTATCCAACCTCACC
NM_004905	AOP2	3255	ACCATCCCTGAAGAAGAAGCC
NM_004911	ERP70	3256	ACCCAGGAAGAAATTGTTGCC
NM_004964	HDAC1	3257	ACCTGGAGAAGATCAAACAGC
NM_005003	NDUFAB1	3258	ACGTTAGAGGGCATCCAGGAC
NM_005003	NDUFAB1	3259	ACAAGATTGACCCAGAGAAGC
NM_005006	NDUFS1	3260	ACCAGGGAGGTGAATGTGATC
NM_005006	NDUFS1	3261	ACTTGTTCCACCTCAGCTAAC
NM_005023	PGGT1B	3262	ACTCGAGACAAGCAGGTTGAC
NM_005023	PGGT1B	3263	ACCTAATAAGCCTGTAGACAC
NM_005038	PPID	3264	ACACGACTGGGAAACCTCTCC
NM_005084	PLA2G7	3265	ACTCCTGCAAACCTGGAATTCC
NM_005090	PLA2G4B	3266	ACGGTCAAGAACAGCAGTAGC
NM_005090	PLA2G4B	3267	ACCCAAGCTGCTTCACCAACC
NM_005090	PLA2G4B	3268	ACAAGCTGCTGCACCTGACAC
NM_005114	HS3ST1	3269	ACTGGGAGGAGCATTACAGCC
NM_005114	HS3ST1	3270	ACACCCAAGTGTTCTACAACC
NM_005114	HS3ST1	3271	ACGTGCACATGCAGAACTGGC
NM_005309	GPT	3272	ACTTCCGGATGACCATTCTGC
NM_005327	HADHSC	3273	ACACAGTAGTGTTGGTAGACC
NM_005327	HADHSC	3274	ACCTCATGGAAGCAATCAGGC
NM_005357	LIPE	3275	ACAGCCTCAAGGCTCATCCAC
NM_005357	LIPE	3276	ACAGCATGCTCAAGAGCCTGC
NM_005412	SHMT2	3277	ACAAGTACTCGGAGGGTTATC
NM_005412	SHMT2	3278	ACGGCTCATCATAGCTGGCAC
NM_005420	STE	3279	ACCAGATGATCTTGTCATTGC
NM_005484	ADPRTL2	3280	ACCAATCTCCAGTTCAACAAC
NM_005484	ADPRTL2	3281	ACCTTCATAACAGGATGCTTC
NM_005485	ADPRTL3	3282	ACCCTGAACCAGACCAACATC
NM_005485	ADPRTL3	3283	ACCTACTTAGAACAGACTGGC
NM_005485	ADPRTL3	3284	ACATTCTCCCAGAGCGAGTAC
NM_005530	IDH3A	3285	ACAAGATGGGCTTGAAAGGCC
NM_005530	IDH3A	3286	ACAATTAAGGACGGAAAGAGC
NM_005566	LDHA	3287	ACATCCTGGGCTATTGGACTC
NM_005589	ALDH6A1	3288	ACCTGGTATTTCAGCATCTTCC

NM_005589	ALDH6A1	3289	ACATGGACCTTTATTCTTACC
NM_005589	ALDH6A1	3290	ACATGGCAAGAGGGTTCAAGC
NM_005668	SIAT8D	3291	ACTATGTGCTTGACAGGCGCC
NM_005742	P5	3292	ACCAGAATGGGAAGAAAGCAGC
NM_005742	P5	3293	ACGGAGCGGAGGATACAGTTC
NM_005742	P5	3294	ACAAGATCCGACATCGTGTCC
NM_005771	RDHL	3295	ACTAAACATGCTTCTCTGACC
NM_005771	RDHL	3296	ACGCTCTAACAAGTCTCTTCC
NM_005794	DHRS2	3297	ACCAGTGAGCAGATCTGGGAC
NM_005794	DHRS2	3298	ACAATGTGAGCAAGACAGCGC
NM_005891	ACAT2	3299	ACAAGGTTGCAGTTCTGTCCC
NM_005896	IDH1	3300	ACACACCAAGTGACGGAACCC
NM_005911	MAT2A	3301	ACCCAGATAAGATTTGTGACC
NM_005911	MAT2A	3302	ACTTTGGTAGGGACAGCTTCC
NM_005917	MDH1	3303	ACCATGCCAAGGTGAAATTGC
NM_005917	MDH1	3304	ACGTGAGAAGATGGATCTTAC
NM_005918	MDH2	3305	ACTTCTCCTGAAGAACAGCCC
NM_005956	MTHFD1	3306	ACCCAGACAGACAAGGCTCTC
NM_005957	MTHFR	3307	ACATCTGTGTGGCAGGTTACC
NM_005989	AKR1D1	3308	ACTCAGAACCTAAATCGACCC
NM_005989	AKR1D1	3309	ACGCTGGCTTGGTGAAATCCC
NM_006011	SIAT8B	3310	ACAATCAGATCAGCTGTGAAC
NM_006011	SIAT8B	3311	ACTTGTGCCATCGTGGGCAAC
NM_006011	SIAT8B	3312	ACTGGCTGACCAACAAAGTCC
NM_006033	LIPG	3313	ACGGATGCGGTCAATAATACC
NM_006033	LIPG	3314	ACAGAAGACCCTGAGAACACC
NM_006037	HDAC4	3315	ACAAGCAGCAGTTCCAGCAGC
NM_006041	HS3ST3B1	3316	ACCTTCGAGAGCTTGACGTTT
NM_006042	HS3ST3A1	3316	ACCTTCGAGAGCTTGACGTTT
NM_006041	HS3ST3B1	3317	ACCCGGGCTATGTACCTTACC
NM_006042	HS3ST3A1	3318	ACGTCCCTTTACGTCTTCTAC
NM_006043	HS3ST2	3319	ACTTACCTGTGTTACAGCTTC
NM_006043	HS3ST2	3320	ACTTCCCGCTAGCTCAGATTC
NM_006044	HDAC6	3321	ACTACATTGCTGCTTTCTGCTG
NM_006044	HDAC6	3322	ACTACTGTGAGGCCTATGTCC
NM_006044	HDAC6	3323	ACGATAGACCAGCTGTAGCTC
NM_006066	AKR1A1	3324	ACTGGCCTTATGCCTTTGAGC
NM_006090	CEPT1	3325	ACACCACCATTGTCAAGACAC
NM_006090	CEPT1	3326	ACTGCCCTACAGCTACAGAGC
NM_006090	CEPT1	3327	ACAATAGCAGGAACAAGTGTC
NM_006100	ST3GALVI	3328	ACCCTAATACGACAGTGATTC
NM_006100	ST3GALVI	3329	ACATATGTGACGAAGTTCAAC
NM_006111	ACAA2	3330	ACCTGGTTTACGAATTAAGGC
NM_006112	PPIE	3331	ACATCAAGATTGGGAACAAGC
NM_006112	LOC256719	3331	ACATCAAGATTGGGAACAAGC
NM_006112	PPIE	3332	ACCAGGTCTACTATCCATGGC

NM_006169	NNMT	3333	ACTCTGCAGAAAGCCAGATTC
NM_006225	PLCD1	3334	ACTGGATTCACTCCTGCTTGC
NM_006225	PLCD1	3335	ACCAGGAACCAATCATCTACC
NM_006225	PLCD1	3336	ACAGACTCCTCCAACCTACAGC
NM_006226	PLCL1	3337	ACCCAGCCATTATCTCACTAC
NM_006278	SIAT4C	3338	ACAGATTCCGATTCTCAACCC
NM_006279	SIAT6	3339	ACCCATGTTCTCTGGATGACTC
NM_006279	SIAT6	3340	ACGACACTGCGCATCACCTAC
NG_001063	NG_001063	3341	ACCTATGAAGGTATGATGCAC
NM_006330	LYPLA1	3341	ACCTATGAAGGTATGATGCAC
NM_006347	PPIH	3342	ACTGGAGTCGCCAGTATTTAC
NM_006412	AGPAT2	3343	ACGGTGGAGAACATGAGCATC
NM_006412	AGPAT2	3344	ACCACCTTCCTCCACATCTCC
NM_006437	ADPRTL1	3345	ACCTGATGAGTCAGGATGCTC
NM_006456	STHM	3346	ACTTCCGTGGCCTGTTCAATC
NM_006456	STHM	3347	ACATCCGCGACTATGTGATGC
NM_006581	FUT9	3348	ACTGTACAACAAATCCCATGC
NM_006588	SULT1C2	3349	ACTTGCTGCCACCATCCTTGC
NM_006588	SULT1C2	3350	ACATGAAGAAGAACCCAAAGC
NM_006636	MTHFD2	3351	ACAAGGATGTTGATGGCTTTC
XM_068588	LOC133883	3351	ACAAGGATGTTGATGGCTTTC
NM_006774	INMT	3352	ACTCTCTCCGACTTTACCGAC
NM_006774	INMT	3353	ACCTTGCCCTCACTGCTCAAGC
NM_006798	UGT2A1	3354	ACCCACTACGTTATGTGAGAC
NM_006877	GMPR	3355	ACCTACTCAGGGATTCCCATC
NM_006877	GMPR	3356	ACCAGGTTCTGTGTGCCACCAC
NM_006892	DNMT3B	3357	ACCTTCAATAAGCTCGTCTCC
NM_006892	DNMT3B	3358	ACAGACGTGTCCAACATGGGC
NM_006895	HNMT	3359	ACAAGAGCCTGAATTTAGTGC
NM_006899	IDH3B	3360	ACTCGGCACAACAATCTAGAC
NM_006907	PYCR1	3361	ACAAGATAATGGCTAGCTCCC
NM_006907	PYCR1	3362	ACACATTGTGGTGTCTGCGC
NM_006927	SIAT4B	3363	ACCACCCACCATTTCATGTAC
NM_006927	SIAT4B	3364	ACGACAGGTGGACAGAGCATC
NM_007101	SARDH	3365	ACAGGTCATTGAGAACTGCCC
NM_007101	SARDH	3366	ACACGATCAAGAAGGAGTGCC
NM_007101	SARDH	3367	ACCATCGCCTACGGTTACATC
NM_007103	NDUFV1	3368	ACAAGACAAAGGAGATCCTGC
NM_007103	NDUFV1	3369	ACAATGAGGCCCTCCAATCTGC
NM_007103	NDUFV1	3370	ACATCTCTGGCCATGTCAACC
NM_007210	GALNT6	3371	ACACAACCTCAGAGGGACCTTC
NM_007283	MGLL	3372	ACCATGTTCTCCACAAGGAGC
NM_012079	DGAT1	3373	ACTGGTTGAGTCTATCACTCC
NM_012079	DGAT1	3374	ACGTCCACGACTACTACGTGC
NM_012190	FTHFD	3375	ACCAAAGCAGGACTCATCCTC
NM_144776	FTHFD	3375	ACCAAAGCAGGACTCATCCTC

NM_012203	GRHPR	3376	ACAGCTGTGTTTCATCAACATC
NM_012331	MSRA	3377	ACTATGCGGAAGACTACCACC
NM_013240	N6AMT1	3378	ACTCTTTTCAGTCTCTCAAGTTC
NM_013305	SIAT8E	3379	ACTCCACAAGATGCCTGGAGC
NM_013328	P5CR2	3380	ACAAGATAATAGCCAGCTCCC
NM_013328	P5CR2	3381	ACACATCGTGGTCTCCTGTGC
NM_013328	P5CR2	3382	ACTGAGGTGGAAGAGGACCTC
NM_013391	DMGDH	3383	ACTGGATCCTGCATGGAGAAC
NM_013443	VI	3384	ACATCCAGAATGAGCACAGTC
NM_014234	HSD17B8	3385	ACATGGGATCCGCTGTAACTC
NM_014236	GNPAT	3386	ACCTGCTGAAGAAGTTGTCCC
NM_014256	B3GNT3	3387	ACATCCTGCAGTGGGACTTCC
NM_014256	B3GNT3	3388	ACAACATGGTCTTCTACCTGC
NM_014291	GCAT	3389	ACTATCTCGGGAGCCAGTCAC
NM_014317	TPT	3390	ACATTCAAGAAGACCGCCAGC
NM_014337	PPIL2	3391	ACCATCTTCCACAGATCCATC
NM_014351	SULT4A1	3392	ACGTGTGGATCGTCACTTACC
NM_014364	GAPDS	3393	ACCAGTGCAAGAGCCCCAAAC
NM_014364	GAPDS	3394	ACCAAAGTCATCCCAGAGCTC
NM_014364	GAPDS	3395	ACGAATATGGCTACAGTCACC
NM_014384	ACAD8	3396	ACCCGAGACCACCTCAATGTC
NM_014384	ACAD8	3397	ACTCCAGGGTCCACCAGATTC
NM_014403	SIAT7D	3398	ACCGGCTGGTTCAACATGATC
NM_014403	SIAT7D	3399	ACCACTACTTTTGAGAAGGGCC
NM_014403	SIAT7D	3400	ACTGAGAAGGCGGTCTTCTCC
NM_014434	NR1	3401	ACTCCTACCCGGTGGTGAATC
NM_014465	SULT1B1	3402	ACCAGATGACATTGTGATAGC
NM_014473	HSA9761	3403	ACCCAAGGCTAGTAGCTGAAC
NM_014473	HSA9761	3404	ACAGAATTCACTGTTTCAGTCC
NM_014475	DHDH	3405	ACCAAGGGCATGGTACAGCTC
NM_014589	PLA2G2E	3406	ACCTACAACCGCAAATATGCC
NM_014762	DHCR24	3407	ACAGGCATCGAGTCATCATCC
NM_014762	DHCR24	3408	ACCTCTTTGGCTGGATGGTGC
NM_014762	DHCR24	3409	ACCACAAGCTGCGAGAGAAGC
NM_015192	PLCB1	3410	ACAGAGCTACTGGATCTCAGC
NM_015192	PLCB1	3411	ACCCAATCCGATATGTGAACC
NM_015725	PRRDH	3412	ACTACTTCCGGGACCTCTATC
NM_015725	PRRDH	3413	ACAGACCAACATCCGCTACTC
NM_015879	SIAT8C	3414	ACCAATCTTACCACCTTCAAC
NM_015879	SIAT8C	3415	ACCAGCTGCCTGCTGAGTTTC
NM_015900	PS-PLA1	3416	ACTGATGGCCTTTCCCTGTGC
NM_015917	LOC51064	3417	ACATCAACCTGCAGTTGCGGC
NM_015917	LOC51064	3418	ACATGTTATTGCTCTGACC
NM_015922	H105E3	3419	ACTGAAGACCTTCCCTATGCC
NM_015922	H105E3	3420	ACATTCCACTACTACAGCTGC
NM_016026	ARSDR1	3421	ACAGGAGCTAATACAGGTATC

NM_016026	ARSDR1	3422	ACGTATTCTGTACACCCTGGC
NM_016059	PPIL1	3423	ACTTTGCTGAGTTGGCTCGTC
NM_016142	HSD17B12	3424	ACACAATTGGTACTGCCTGGC
NM_016229	LOC51700	3425	ACGGAATCTTGGGAATCAGACC
NM_016229	LOC51700	3426	ACATGATCAAGGAGCACCTTC
NM_016243	LOC51706	3427	ACGACTGCTAGACAAGACGAC
NM_016245	LOC51170	3428	ACCTTTGTGGTAGACTGCAGC
NM_016245	LOC51170	3429	ACTGGCTGCCTTACAAATAAC
NM_016246	LOC51171	3430	ACGTACACCTTGACCAAGCTC
NM_016246	LOC51171	3431	ACTTCTGCACGGGCATTGAAC
NM_016286	DCXR	3432	ACTCAGGCGGATCTTGACAGC
NM_016286	DCXR	3433	ACAGATCCTTTGAGGTGAACC
NM_016341	PLCE1	3434	ACTGGGTAGCATGTTCTGTGTC
NM_016576	LOC51292	3435	ACTATAGCCTCGTTCAGTGGC
NM_016591	LOC51301	3436	ACCTTCTGAAGTCTTCAATCC
NM_017417	GALNT8	3437	ACACGCGAGACTACAGATGTC
NM_017417	GALNT8	3438	ACCGCACTGTGATTGTGTCTC
NM_017417	GALNT8	3439	ACTTGGCCTGGAACATACCTC
NM_017421	COQ3	3440	ACTTCCCAAACCACTGTGCGAC
NM_017423	GALNT7	3441	ACAGATTCAAACCTGTGGTAC
NM_017423	GALNT7	3442	ACAGAACCATTGTGCACTGTGC
NM_018137	PRMT6	3443	ACCGGCATTCTGAGCATCTTC
NM_018137	PRMT6	3444	ACTCACTGGAAACAGGCGCTC
NM_018396	METL	3445	ACAAGTGTCTCTCGAAGAGCC
NM_018441	HSA250303	3446	ACCAGATCATGACAACCTGGCC
NM_018446	AD-017	3447	ACAGCATTCAAGCACAACACTC
NM_018446	AD-017	3448	ACCTCAGTTTGTAAGGCTGC
NM_018960	GNMT	3449	ACACTGTCTGGCATCCTTCAC
NM_019109	HMT-1	3450	ACGGAGTCAAAGTTGTACTTC
NM_019109	HMT-1	3451	ACCAATGCTATGCGAGAAGAC
NM_019109	HMT-1	3452	ACAGAGGACGAAGACTTCTCC
NM_019854	HRMT1L3	3453	ACCTGGAGGGCTTATGTTTCC
NM_020121	UGCGL2	3454	ACAGTGCACAGCAACTGTGAC
NM_020132	LPAAT-gamma1	3455	ACCTTGAACCTTCAGAGGAAAC
NM_020132	LPAAT-gamma1	3456	ACCTCCTGAACTTCCTGTCC
NM_020133	LPAAT-delta	3457	ACACCATTCAGCTCTTCACTC
NM_020133	LPAAT-delta	3458	ACGGAGAAGAAGCATGAGATC
NM_020133	LPAAT-delta	3459	ACCAGGAGAAGGATGCCTTTC
NM_020156	C1GALT1	3460	ACCTCGTTTATCATCTTCGTC
NM_020244	CHPT1	3461	ACGCTCGTGCTCATCTCCTAC
NM_020244	CHPT1	3462	ACTTTAGTGCTTTGTGCCTGC
NM_020474	GALNT1	3463	ACCCAGTGAAATTAACCTGC
NM_020549	CHAT	3464	ACATGTATCTCAACAACCGCC
NM_020984	CHAT	3464	ACATGTATCTCAACAACCGCC
NM_020985	CHAT	3464	ACATGTATCTCAACAACCGCC
NM_020986	CHAT	3464	ACATGTATCTCAACAACCGCC

NM_020549	CHAT	3465	ACTGAGCATCTGCTCAAGCAC
NM_020984	CHAT	3465	ACTGAGCATCTGCTCAAGCAC
NM_020985	CHAT	3465	ACTGAGCATCTGCTCAAGCAC
NM_020986	CHAT	3465	ACTGAGCATCTGCTCAAGCAC
NM_020549	CHAT	3466	ACATGAGAGACCTCTGCAGTC
NM_020984	CHAT	3466	ACATGAGAGACCTCTGCAGTC
NM_020985	CHAT	3466	ACATGAGAGACCTCTGCAGTC
NM_020986	CHAT	3466	ACATGAGAGACCTCTGCAGTC
NM_020981	B3GALT1	3467	ACTCGCCCTACTTCTTCTTAC
NM_020981	B3GALT1	3468	ACAGTTTGTGTAGGTATCGCC
NM_021004	humNRDR	3469	ACTAGCTTCAGCAGGATGCTC
NM_021071	ART4	3470	ACACTACTACCTCACCTCAGC
NM_021071	ART4	3471	ACAGGAGTTTGGGAACCAGAC
NG_001161	NG_001161	3472	ACAGCATACTGGAGGCCATTC
NM_021074	NDUFV2	3472	ACAGCATACTGGAGGCCATTC
NM_021079	NMT1	3473	ACCATCCAACCCACAAGAGTC
NM_021079	NMT1	3474	ACGGCAACCTGCAGTATTACC
NM_021139	UGT2B4	3475	ACAATCCTGGATGAACTTGTC
NM_021151	CROT	3476	ACTGAGAGTGAAGGGCGTTCC
NM_021151	CROT	3477	ACCTGGGATTGCAGCATTAAAC
NM_021151	CROT	3478	ACATCAACCAAGCTAAAGCCC
NM_021199	SQRDL	3479	ACGACGAGAAGATCTCCTACC
NM_021199	SQRDL	3480	ACATCATGTCCACTGGTGACC
NM_021232	PRODH2	3481	ACTCAGCCTGACTATGAGGCC
NM_022120	OXCT2	3482	ACAGGAAGAAAGAGCTGACGC
NM_022167	XT2	3483	ACTTCAAGCCACAGGACTTCC
NM_022167	XT2	3484	ACCTCTCAGGAAAGATGATGC
NM_022552	DNMT3A	3485	ACAACAAGCAGCCCATGTACC
NM_022552	DNMT3A	3486	ACTTGGGCATTTCAGGTGGACC
NM_022552	DNMT3A	3487	ACTGACGTCTCCAACATGAGC
NM_022569	NDST4	3488	ACTCGGTCAAGATATCATAGC
NM_022569	NDST4	3489	ACAATAGCATCATGGTCCTCC
NM_022569	NDST4	3490	ACTCTTGGTACCAGCACCAAC
NM_022819	PLA2G2F	3491	ACTGAGATAGTCTGCAGTGAC
NM_022819	PLA2G2F	3492	ACTGCAGCATCTATGAACCGC
NM_024827	HDAC11	3493	ACCATCATTGATCTTGATGCC
NM_024827	HDAC11	3494	ACAATGCAGGCACCGACATCC
NM_025193	C(27)-3BETA-HSD	3495	ACTTCTGCTACGATGGATCAC
NM_030765	B3GNT4	3496	ACAGCTTGGCTGTGCTGTTGC
NM_030765	B3GNT4	3497	ACCTTCTTGCTCCTGGCCATC
NM_030765	B3GNT4	3498	ACGATGTCTTTGTCCACGTCC
NM_030821	PLA2G12	3499	ACCCTGAAGACCATCCGGAAC
NM_031279	AGXT2L1	3500	ACCATGCTTACCATGGTCACC
NM_031279	AGXT2L1	3501	ACCAAAGAAATTGCAGAAGCC
NM_031302	LOC83468	3502	ACTGTATGACACCACCTTGGC
NM_031302	LOC83468	3503	ACATAAACCTTGGGACTTCCC

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NM_031463	LOC83693	3504	ACCTTCCAATTCGAGAAGCCC
NM_031463	LOC83693	3505	ACCACTTCAGCAGAGCCCTTGC
NM_031900	AGXT2	3506	ACTTCCCGGACATCAGTAACC
NM_031900	AGXT2	3507	ACAAGCACCGTCTTCTTCCAC
NM_032047	B3GNT5	3508	ACTTATGCAGTTCAGTTGGGC
NM_032047	B3GNT5	3509	ACTTAGAAGATCTCCAGGACC
NM_032664	FUT10	3510	ACCATCAACCGGACCTACCTC
NM_032664	FUT10	3511	ACTTACATCGAGGTCGATTCC
NM_006411	AGPAT1	3512	ACCAGAGCTCTCTCGATCTGC
NM_032741	AGPAT1	3512	ACCAGAGCTCTCTCGATCTGC
NM_006411	AGPAT1	3513	ACCACAATGGCTCCATGCTGC
NM_032741	AGPAT1	3513	ACCACAATGGCTCCATGCTGC
NM_003781	B3GALT3	3514	ACACTTCGAGAGCATTCAAAC
NM_033167	B3GALT3	3514	ACACTTCGAGAGCATTCAAAC
NM_033168	B3GALT3	3514	ACACTTCGAGAGCATTCAAAC
NM_033169	B3GALT3	3514	ACACTTCGAGAGCATTCAAAC
NM_003781	B3GALT3	3515	ACTGAGACGTGTGATTGCAGC
NM_033167	B3GALT3	3515	ACTGAGACGTGTGATTGCAGC
NM_033168	B3GALT3	3515	ACTGAGACGTGTGATTGCAGC
NM_033169	B3GALT3	3515	ACTGAGACGTGTGATTGCAGC
NM_006057	B3GALT5	3516	ACAAGAAAGACGGGAACTTCC
NM_033170	B3GALT5	3516	ACAAGAAAGACGGGAACTTCC
NM_033171	B3GALT5	3516	ACAAGAAAGACGGGAACTTCC
NM_033172	B3GALT5	3516	ACAAGAAAGACGGGAACTTCC
NM_033173	B3GALT5	3516	ACAAGAAAGACGGGAACTTCC
NM_006057	B3GALT5	3517	ACTATCTGACTGAACTGCTTC
NM_033170	B3GALT5	3517	ACTATCTGACTGAACTGCTTC
NM_033171	B3GALT5	3517	ACTATCTGACTGAACTGCTTC
NM_033172	B3GALT5	3517	ACTATCTGACTGAACTGCTTC
NM_033173	B3GALT5	3517	ACTATCTGACTGAACTGCTTC
NM_006057	B3GALT5	3518	ACTTCATCAAGCCTCGGACTC
NM_033170	B3GALT5	3518	ACTTCATCAAGCCTCGGACTC
NM_033171	B3GALT5	3518	ACTTCATCAAGCCTCGGACTC
NM_033172	B3GALT5	3518	ACTTCATCAAGCCTCGGACTC
NM_033173	B3GALT5	3518	ACTTCATCAAGCCTCGGACTC
NM_006577	B3GNT1	3519	ACATCTGCTCCTATGTAGATC
NM_033252	B3GNT1	3519	ACATCTGCTCCTATGTAGATC
NM_052968	APOA5	3520	ACCTACCTGCAGATAGCTGCC
NM_053017	ART5	3521	ACTTTCCCTTCAAGGCCCTGC
NM_053017	ART5	3522	ACAGGCCTTCTCTGTCTTTCC
NM_054110	GALNT7	3523	ACACTGGAGCGTATGACTCTC
NM_054110	GALNT7	3524	ACCAGCAGGAAGGAGATTTCAC
NM_080605	B3GALT6	3525	ACTTTTCCTTTCAAGGCTTCCC
NM_133373	LOC113026	3526	ACCCTCACCTCCAAGATTCTC
NM_133491	SSAT2	3527	ACTGTTTGGTAGCAGAGATTTC
NM_133491	SSAT2	3528	ACAGACACTGATGCTGAGGCC

NM_138706	IMAGE:4907098	3529	ACCTTCCTCAACCTCACGCTC
NM_138706	IMAGE:4907098	3530	ACGCCTACATGGGCATGTGTC
NM_138969	RDH-E2	3531	ACAAGAGTGCACGCCTATACC
NM_139126	PPIL4	3532	ACAGGAGAGTCCCTCTGTAC
XM_032719	CARM1	3533	ACTTCAAGGACAAGATCGTTC
XM_032719	CARM1	3534	ACACATTTGACATCCGGATCC
XM_032719	CARM1	3535	ACATGTCTGCTTATTGCCAAC
XM_036383	ADCY2	3536	ACAGAAGCAATGGCTCAAGTC
XM_036383	ADCY2	3537	ACCTGTGAGGAATAATCAAC
XM_042836	PLCL2	3538	ACACCAGGACTGATGATGGAC
XM_047025	OATL1	3539	ACCACCTATGCCGTTACCCAC
XM_047025	OATL1	3540	ACCTTTGAAGATGCTGTTGAC
XM_047025	OATL1	3541	ACCACATCATGCGCAATGGGC
XM_050509	GALNT5	3542	ACCTCATCAAGGAGATTCTGC
XM_050509	GALNT5	3543	ACAGTCATTCTGGAAGACTGC
XM_051264	TR2	3544	ACAGTTGGAGAAAGGTTCAAC
XM_051896	PLA2G4A	3545	ACAGTGGGCTCACATTTAACC
XM_051896	PLA2G4A	3546	ACAGAATCCATCTCGTTGCTC
XM_055342	LOC115154	3547	ACACACCTGAATGAAGAAGGC
XM_056254	HS3ST4	3548	ACCAGGGCCATCTCTGACTAC
XM_056254	HS3ST4	3549	ACCCAGATGTCATCCACAGAC
XM_058395	LOC119391	3550	ACCAGCCAATGTCAACTGATC
XM_058395	LOC119391	3551	ACCCTTATGAACGAGCTCGCC
XM_058395	LOC119391	3552	ACCACCTTCTTTGGTGGAAACC
XM_058404	LOC119548	3553	ACTCAGTGGGAAGCGAAGTCAC
XM_058856	LOC124872	3554	ACGATGGAATCTGGCTGTTCC
XM_058992	LOC126129	3555	ACTTTCTCACCGGTGTGTTTC
XM_059366	LOC129644	3556	ACCTGAAGTCCGTGGACATCC
XM_059665	LOC133688	3557	ACACTGGGTGGAAGCCATTAC
XM_059665	LOC133688	3558	ACACCATCAAGGAGCATTTC
XM_060166	LOC126766	3559	ACTTCCTCACACGGATATCC
XM_060166	LOC126766	3560	ACCATGGCCTGTGCAATTATC
XM_060331	LOC127107	3561	ACACTGAGAGCAGTGGCTGTC
XM_060331	LOC127107	3562	ACAAGAGAGCACAGGCAGAAC
XM_060822	LOC128096	3563	ACATTCTGGATCAGTCATGCC
XM_060822	LOC128096	3564	ACCAACCCAGTCTATGTGGGC
NM_172341	PEN-2	3565	ACCTCCTGGATCACCATCTTC
NM_172341	PEN-2	3566	ACTACCTCTCCTTCACCATAC
XM_060828	LOC128103	3567	ACTAGCATGGCATTCCAGGTC
NM_001168	BIRC5	3568	ACCACTTCAGGGTTTATTCC
NM_000888	ITGB6	3569	ACTGTGGGCAGTGTATCTGCC
NM_000888	ITGB6	3570	ACGGGAACCAATCCACTCTAC
XM_060863	LOC128183	3571	ACACCACAGTGCAAGACAAGC
XM_060871	LOC128189	3572	ACTACCTTATTACAGCCACC
XM_060871	LOC128189	3573	ACTTACAGGTATGCCTTCCTC
XM_060976	LOC118478	3574	ACTGCAGTGGAAATGGTTTCTC

XM_060976	LOC118478	3575	ACCCTGATTGCTCTGTGCTAC
XM_060976	LOC118478	3576	ACATGAAAGCCATTGACAGCC
XM_061221	LOC118933	3577	ACTCCTTGTC AACAGAATTCC
XM_061221	LOC118933	3578	ACAGATGAGAAATTCTGGGGCC
XM_061221	LOC118933	3579	ACCTGACTGCCATGAAAGTGC
XM_061222	LOC118934	3580	ACTGGACAGAAGCGACTCTAC
XM_061222	LOC118934	3581	ACAGGACATTGTGGCTGATCC
XM_062367	LOC120943	3582	ACAGTGGGAAGGATACAGCAAC
XM_062367	LOC120943	3583	ACATGGGCTTATATTGTGAGC
XM_062519	LOC121214	3584	ACATCCCTCTGGCTAAGTTGC
XM_062862	LOC121927	3585	ACTACATGGTCTCCATGTTCC
XM_062862	LOC121927	3586	ACAATCCCATCACCATCTCGC
XM_063084	LOC122335	3587	ACTGCTAAGACCGAGTGGTTC
XM_063293	LOC122718	3588	ACAGGATCTACAAACAGGTTT
XM_063293	LOC122718	3589	ACACATCCAGAGCTGATCCTC
XM_063293	LOC122718	3590	ACACGGAGAAGATGGGTTCCC
XM_063593	LOC123326	3591	ACCTGATGAAGGCCTTCGACC
XM_063826	LOC123745	3592	ACATCGAAGACGAGCCGATCC
XM_064820	LOC125836	3593	ACTGTATACCGCCACATCGAC
XM_064820	LOC125836	3594	ACATCTGTGACACTGGATCGC
XM_064820	LOC125836	3595	ACCTCCTTACTCAGCTGCAAC
XM_064999	LOC126242	3596	ACCTGGCTTAAAGTATAAGCC
XM_064999	LOC126242	3597	ACTGAACAGCCAGGATATGAC
XM_089195	LOC163862	3597	ACTGAACAGCCAGGATATGAC
XM_064999	LOC126242	3598	ACCGCCTTACTCAGCTACAAC
XM_065242	LOC129440	3599	ACGACGACTTCCTGATTCTCC
XM_065541	LOC130040	3600	ACACGAGGATCCTGGAGGTAC
XM_065541	LOC130040	3601	ACATTGCCATTGACAGCGAGC
XM_065756	LOC130516	3602	ACCAGCATTATGGACCACTCC
XM_065789	LOC130585	3603	ACTGGCCTCAACTACATGGTC
XM_065943	LOC130896	3604	ACGCAGTGATAAGCGCAGAAC
XM_065961	LOC130946	3605	ACAAAGGCAAGTACAACCTGAC
XM_066634	LOC139334	3606	ACAGATGCCGACATGGCCATC
XM_066753	LOC139543	3607	ACCTATGGCAAGTTCCATGGC
XM_066753	LOC139543	3608	ACATCAAGAAAGTGGAGGGCC
XM_066916	LOC139835	3609	ACCAGAGGGTGAGTTTGTGTC
XM_067020	LOC140028	3610	ACCACTTCCAGGAGCGAGATC
XM_067020	LOC140028	3611	ACTGAGTATGTTGTGGAATCC
XM_067020	LOC140028	3612	ACTGAGCACCAAGTTGCCCTCC
XM_067531	LOC131748	3613	ACTGGTGGCACATCCATCTAC
XM_067584	LOC131872	3614	ACGCATCTGGTTCTGAAGGCC
XM_067584	LOC131872	3615	ACTCAGGGAAGAAGCTGTTGC
XM_067688	LOC131961	3616	ACAACTGTACCGCAGAGTTCC
XM_067765	LOC132281	3617	ACAGCAAATTCTGTACCCAAC
XM_068075	LOC132869	3618	ACTCTCTGTGGCAGATTTGGC
NG_000914	NG_000914	3619	ACTGGTGGCAAGTCCATCTAC

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NG_001025	NG_001025	3619	ACTGGTGGCAAGTCCATCTAC
XM_063182	LOC122552	3619	ACTGGTGGCAAGTCCATCTAC
XM_066617	LOC139318	3619	ACTGGTGGCAAGTCCATCTAC
XM_068341	LOC133419	3619	ACTGGTGGCAAGTCCATCTAC
XM_089755	LOC159692	3619	ACTGGTGGCAAGTCCATCTAC
XM_092514	LOC165317	3619	ACTGGTGGCAAGTCCATCTAC
XM_167261	LOC222940	3619	ACTGGTGGCAAGTCCATCTAC
XM_068376	LOC133486	3620	ACACCTGGTAACCAAGCCTGC
XM_068376	LOC133486	3621	ACGTCATCCACAACTTTGGGC
XM_068926	LOC134602	3622	ACTGGTAAAGAAGGCTCCACC
XM_068926	LOC134602	3623	ACTGACACGATTAAGCTCAAC
XM_069334	LOC135399	3624	ACAATGTCTCCGGTACATCGC
XM_069782	LOC136234	3625	ACATTGTAGGTGCCTGCGGAC
XM_069782	LOC136234	3626	ACAGACCTCAACATCTACATC
XM_069782	LOC136234	3627	ACTCTTCTCTGTGAACATACC
XM_069825	LOC136307	3628	ACAAATACCGCCTGGACCTGC
XM_069833	LOC136330	3629	ACCAGTGACTAACCAGAACTC
XM_069833	LOC136330	3630	ACCACAGCCCAGGTTCTGATC
XM_070277	LOC137202	3631	ACCATCAGCCACAACAGCAGC
XM_070717	LOC138031	3632	ACTGCTTGGTGGGCTTCACTC
XM_085058	LOC145226	3633	ACGGGTGGTTAATGTGTCTC
XM_085058	LOC145226	3634	ACAGCAAGCTGGCCAATGTGC
XM_085119	FLJ10607	3635	ACAGAGACTGGAGTTGTTCAGC
XM_085119	FLJ10607	3636	ACAGATTGTTGCTACGGCAAC
XM_085119	FLJ10607	3637	ACTACATGTGTCTCGGAGGTTTC
XM_087088	LOC151056	3638	ACCAACTGATTGAGAGTGGGC
XM_087088	LOC151056	3639	ACATCCAAGTTGTGGCTGCTC
XM_087136	LOC151234	3640	ACACTGTGGGATTGACCAGGC
XM_087136	LOC151234	3641	ACCCACTTTCTTGAGGTCATC
XM_089195	LOC163862	3642	ACTGCCTACAGCTCCTTCAGC
XM_089555	LOC159373	3643	ACAAGACACTCTCCATAGACC
XM_089555	LOC159373	3644	ACTTCTGGGTGGATTCAACAC
XM_090294	LOC160428	3645	ACTGAATAGCTCTGTGCCTCC
XM_090294	LOC160428	3646	ACTATTCCAATCAACCAGGCC
XM_090294	LOC160428	3647	ACATCGATGGAGTGTTGCAGC
XM_090320	LOC160469	3648	ACAACATCTCATGGTCAGAGC
XM_090320	LOC160469	3649	ACGATGTAGATACCACAAGGC
XM_090901	LOC145538	3650	ACAGAGATGAGGTCTCCACTC
XM_091291	LOC162024	3651	ACTGATGTCTCTGGGCAGTGC
XM_091633	LOC147116	3652	ACCCTAAACACACACTCTCCC
XM_091633	LOC147116	3653	ACCATATTAGTCTTTGCTGCC
XM_092624	LOC165492	3654	ACAAAGGAAGCAAGAAGCAGC
XM_092624	LOC165492	3655	ACGGAATTATTCCAGGGTTTC
XM_092624	LOC165492	3656	ACATGTGGTCTTGGAAGCTC
XM_093062	LOC170027	3657	ACCAGCCAATTAGGCACAAGC
XM_093062	LOC170027	3658	ACAATCAAGCACGAGCCAAGC

XM_093255	LOC170327	3659	ACAGTCCTTTACATCACTGCC
XM_093255	LOC170327	3660	ACTTTCAAGGGCATCCTAGGC
XM_093255	LOC170327	3661	ACCTTATTGTTACATTGGCC
XM_093615	LOC166039	3662	ACCAGGGAGCTGCAAGTGATC
XM_093702	LOC166161	3663	ACTATAGGCTGGCTCCTCAAC
XM_093702	LOC166161	3664	ACCAAGGATGAAGCACTTCCC
XM_093702	LOC166161	3665	ACCCTTGTTGGCCAATGATTC
XM_093980	LOC166624	3666	ACCTCACCTGGTTTCAGTACC
XM_094098	LOC166794	3667	ACTGAAGAGGACCATGATGAC
XM_094300	LOC167127	3668	ACCTTGGGCTCCATGGTGAAC
XM_094300	LOC167127	3669	ACGCACCTCAAGCCCTATGTC
XM_094687	LOC167821	3670	ACCATCTTCCAGGACATCTTC
XM_094687	LOC167821	3671	ACTCTGGTGTGGTCGTGGAC
XM_095086	LOC168415	3672	ACCCTAGCATTACATAATACCC
XM_172596	LOC256726	3672	ACCCTAGCATTACATAATACCC
XM_095705	LOC169445	3673	ACAGTTCCTGAGAACCAACCC
XM_095861	LOC169681	3674	ACACCGCACTATCCAGGATCC
XM_095861	LOC169681	3675	ACACCTAGAGATGGACACTGC
XM_095884	LOC158284	3676	ACAAGAACAGCAGCTCTTCCC
XM_095884	LOC158284	3677	ACATAGTGAGTGTGAACTCCC
XM_095921	LOC169760	3678	ACCTGGATCTGCCTTATGATC
XM_172777	LOC253554	3678	ACCTGGATCTGCCTTATGATC
XM_095921	LOC169760	3679	ACTGTGTACCTCAAGCCCAGC
XM_172777	LOC253554	3679	ACTGTGTACCTCAAGCCCAGC
NM_002014	FKBP4	3680	ACAGCAACAACGAGAAGGGCC
XM_095921	LOC169760	3680	ACAGCAACAACGAGAAGGGCC
XM_114786	LOC199971	3681	ACCCTGAAGACTGTGGATGAC
XM_115401	LOC204474	3682	ACGCAGTCTTCTAGTGCTAAC
XM_115401	LOC204474	3683	ACGTATCCAAGCTGGAAGAGC
XM_115853	LOC205093	3684	ACAGAGGCCACAAGATCCCAC
XM_116260	LOC205983	3685	ACCAAGGATGAAGAGATTACC
XM_116260	LOC205983	3686	ACAGAGGTCTGACATCAGAAC
XM_116285	LOC206030	3687	ACCCTGACCAACTGCTTATGC
XM_116493	LOC202432	3688	ACCCAGAAGACTGTGAATGGC
XM_116529	LOC206469	3689	ACCTGCCAAATATGGTAACAC
XM_166248	LOC220027	3690	ACATGCTGTTTGATGCTGTTT
XM_166248	LOC220027	3691	ACTACTGTGCCTTGATGGTAC
XM_166504	LOC221893	3692	ACAATGCTGCCCACCACTATC
XM_166593	ADCY1	3693	ACGATTTCAGATTCGCACTGTC
XM_166593	ADCY1	3694	ACTTCCTCATGTCCAACCCTC
XM_166722	LOC222360	3695	ACCAAAGAACCCTTACCGCCC
XM_167104	LOC222593	3696	ACTAGTCCAGTGATCTCACC
XM_167105	LOC222594	3697	ACATGATTATGTTCCAGCCAC
XM_167105	LOC222594	3698	ACACAGCAACCTGAAGTCATC
XM_167188	LOC221654	3699	ACTCAAGTGTATCAGATCGCC
XM_167201	LOC222789	3700	ACCTGGCCTGCATGAGAGATC

XM_167201	LOC222789	3701	ACTCCAGCGGTCTCAAGATAC
XM_168454	POR	3702	ACCTACGAGCACTTCAATGCC
XM_168454	POR	3703	ACAAGGTCTACGTCCAGCACC
XM_169007	ST8SIA-VI	3704	ACTTGCTTCCTGCTGTGATGC
XM_170778	LOC255195	3705	ACGCCTTGGCTTTGACCTCTC
XM_170778	LOC255195	3706	ACCTGGTGCATCTCCACACTC
XM_171048	LOC255218	3707	ACCAGTTCCTGCTGAAGCAGC
XM_171289	LOC254592	3708	ACTACATCTGCTGTCACTGCC
XM_171635	LOC254885	3709	ACATTGCTGAGCCCTTAAGCC
XM_171635	LOC254885	3710	ACACGCCATCATGACACTGGC
XM_171659	LOC256896	3711	ACTACTACCTTGTTCACTGGC
XM_171663	LOC254927	3712	ACCCTTCAGCTAGTATTACTC
XM_171939	LOC255993	3713	ACTCATGGTATGACCACACTC
XM_171939	LOC255993	3714	ACTGCATCAGGACATAAGAGC
XM_171939	LOC255993	3715	ACTGGGCAAGAACTAAGCCC
XM_171955	LOC256129	3716	ACGATGCCTTTGTACACACCC
XM_171955	LOC256129	3717	ACCCTTCTATGTGCCCGAGTC
XM_171955	LOC256129	3718	ACTGTGCTTTCCGCAACCTGC
XM_172177	LOC255139	3719	ACGTGGCTTAAAGTATCAGCC
XM_172181	LOC255782	3720	ACAGTTCACACCATCACTTCC
XM_172235	LOC255412	3721	ACCGAGGACCTGTTTCACTTCC
XM_172242	LOC254652	3722	ACTCTGTGATGAGAACACTGC
XM_172244	LOC253533	3723	ACGATAGTGACAGTGAAGGCC
XM_172281	LOC257047	3724	ACAGGTCCCTGGCATGTTGTCC
XM_172351	LOC254325	3725	ACTCTGAAGCATACAAGTCCC
XM_172351	LOC254325	3726	ACAAGTCCCGGCATCTTGTCC
XM_172380	LOC254420	3727	ACAACACCTACCAATGGTGGC
XM_172380	LOC254420	3728	ACCAGCATCCTCTCGGTCAATC
XM_172516	LOC255961	3729	ACTCTCACACTATGCCTAGGC
XM_172522	LOC255256	3730	ACTGGGTTGTGGTGTCAAC
XM_172522	LOC255256	3731	ACTACGACAAACCAATCCAGC
XM_172522	LOC255256	3732	ACGATGGGCTTGGATCAGATC
XM_172596	LOC256726	3733	ACGCACACACATTCCACTTAC
NM_000043	TNFRSF6	3734	ACCAAGGTTCTCATGAATCTC
NM_000210	ITGA6	3735	ACTCCTAACAGAATTGACCTC
NM_000210	ITGA6	3736	ACCCGAGAAGGAAATCAAGAC
NM_000213	ITGB4	3737	ACCATGAATCCCAGGTGCAC
NM_000230	LEP	3738	ACCCTCATCAAGACAATTGTC
NM_000230	LEP	3739	ACCAGACACTGGCAGTCTACC
NM_000315	PTH	3740	ACAATGTCTTGGTTGAGAGCC
NM_000315	PTH	3741	ACATGTAATCCATCACTAGCC
NM_000460	THPO	3742	ACCTCCGAGTCCTCAGTAAAC
NM_000460	THPO	3743	ACCTCCAGCCTGGATATTCTC
NM_000479	AMH	3744	ACCTACCAGGCCAACAATTGC
NM_000546	TP53	3745	ACAATGGTTCACTGAAGACCC
NM_000546	TP53	3746	ACTAAGCGAGCACTGCCCAAC

NM_000549	TSHB	3747	ACTGTAGAAATACCAGGATGC
NM_000557	GDF5	3748	ACAGCCCAAGAAGGATGAACC
NM_000557	GDF5	3749	ACCATCACCAGCTTTATTGAC
NM_000557	GDF5	3750	ACCCTGATGAACTCCATGGAC
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NM_000576	IL1B	3752	ACTGGTACATCAGCACCTCTC
NM_000585	IL15	3753	ACTGAAGCTGGCATTTCATGTC
NM_000585	IL15	3754	ACAGCAATGAAGTGCTTTCTC
NM_000585	IL15	3755	ACATCACTCTGCTGCTTAGAC
NM_000589	IL4	3756	ACAGAGCAGAAGACTCTGTGC
NM_000589	IL4	3757	ACCGAGTTGACCGTAACAGAC
NM_000589	IL4	3758	ACAAGCAGCTGATCCGATTCC
NM_000590	IL9	3759	ACTTCCTCATCAACAAGATGC
NM_000590	IL9	3760	ACCACCATGCAAACAAGATAC
NM_000595	LTA	3761	ACTGCTCTGGAGAGCAAACAC
NM_000598	IGFBP3	3762	ACAGATACCCAGAACTTCTCC
NM_000598	IGFBP3	3763	ACCTGAAGTTCCTCAATGTGC
NM_000599	IGFBP5	3764	ACCTGAGATGAGACAGGAGTC
NM_000600	IL6	3765	ACACAGACAGCCACTCACCTC
NM_000600	IL6	3766	ACCCAACCACAAATGCCAGCC
NM_000600	IL6	3767	ACAACATCATCTCATTCTGCGC
NM_000605	IFNA2	3768	ACACTGAACTCTACCAGCAGC
NM_000605	IFNA2	3769	ACTCATGTTTTCTGCTATGACC
NM_000609	SDF1	3770	ACACTCCAACTGTGCCCTTC
NM_000609	SDF1	3771	ACAGACAAGTGTGCATTGACC
NM_000614	CNTF	3772	ACTCCTGGAATACAAGATCCC
NM_000614	CNTF	3773	ACAGTAAGGTCCATCCATGAC
NM_000632	ITGAM	3774	ACTCAGACAGGAAGTAGCAGC
NM_000632	ITGAM	3775	ACAACATCTGCCAGGATGACC
NM_000632	ITGAM	3776	ACAAGCTCGGCTTCTTCAAGC
NM_000639	TNFSF6	3777	ACAGTCTTCCCTGTCCAACC
NM_000660	TGFB1	3778	ACCCACAACGAAATCTATGAC
NM_000660	TGFB1	3779	ACAGCAGGGATAACACACTGC
NM_000735	CGA	3780	ACCAAGTGCTGTCTTGATGAC
NM_000758	CSF2	3781	ACTACAAGCAGCACTGCCCTC
NM_000799	EPO	3782	ACACTTCCGCAAACCTCTTCC
NM_000800	FGF1	3783	ACAGTGGATGGGACAAGGGAC
NM_033136	FGF1	3783	ACAGTGGATGGGACAAGGGAC
NM_033137	FGF1	3783	ACAGTGGATGGGACAAGGGAC
NM_000800	FGF1	3784	ACCAGCACATTTCAGCTGCAGC
NM_000825	GNRH1	3785	ACCCAACGCTTCGAATGCACC
NM_000879	IL5	3786	ACCAATTCCCTAGACTACCTGC
NM_000880	IL7	3787	ACACGAACTTTAGCTGCATCC
NM_000880	IL7	3788	ACAATGGAACTGAATGCTCC
NM_000882	IL12A	3789	ACTCCAGACCCAGGAATGTTT
NM_000885	ITGA4	3790	ACTTGTTTGGGAAGAGAGAGAC

NM_000885	ITGA4	3791	ACGTGATTACAGGAAGCATAC
NM_000887	ITGAX	3792	ACTGAAGGAGAAGATCTTTGC
NM_000939	POMC	3793	ACCTCACCACGGAAAGCAACC
NM_001200	BMP2	3794	ACAGCTGGTCACAGATAAGGC
NM_001200	BMP2	3795	ACGTTGGTCAACTCTGTTAAC
NM_001201	BMP3	3796	ACAAGGTCTCTGAACACATGC
NM_001242	TNFRSF7	3797	ACTACTGGGCTCAGGGAAAGC
NM_001244	TNFSF8	3798	ACCACGAGCCGCAGCTATTTTC
NM_001250	TNFRSF5	3799	ACACCTGGAACAGAGAGACAC
NG_001334	NG_001334	3800	ACCAGAAGTATTCATTTCCTGC
NM_000515	GH1	3800	ACCAGAAGTATTCATTTCCTGC
NM_001317	CSH1	3800	ACCAGAAGTATTCATTTCCTGC
NM_001318	CSHL1	3800	ACCAGAAGTATTCATTTCCTGC
NM_002059	GH2	3800	ACCAGAAGTATTCATTTCCTGC
NM_020991	CSH2	3800	ACCAGAAGTATTCATTTCCTGC
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NM_022579	CSHL1	3800	ACCAGAAGTATTCATTTCCTGC
NM_022640	CSH1	3800	ACCAGAAGTATTCATTTCCTGC
NM_022644	CSH2	3800	ACCAGAAGTATTCATTTCCTGC
NG_001334	NG_001334	3801	ACCTCCTTCTGCTTCTCAGAC
NM_001317	CSH1	3801	ACCTCCTTCTGCTTCTCAGAC
NM_001318	CSHL1	3801	ACCTCCTTCTGCTTCTCAGAC
NM_020991	CSH2	3801	ACCTCCTTCTGCTTCTCAGAC
NM_022579	CSHL1	3801	ACCTCCTTCTGCTTCTCAGAC
NM_022640	CSH1	3801	ACCTCCTTCTGCTTCTCAGAC
NM_022644	CSH2	3801	ACCTCCTTCTGCTTCTCAGAC
NG_001334	NG_001334	3802	ACAGCGATGACTATCACCTCC
NM_001317	CSH1	3802	ACAGCGATGACTATCACCTCC
NM_001318	CSHL1	3802	ACAGCGATGACTATCACCTCC
NM_020991	CSH2	3802	ACAGCGATGACTATCACCTCC
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NM_022581	CSHL1	3802	ACAGCGATGACTATCACCTCC
NM_022640	CSH1	3802	ACAGCGATGACTATCACCTCC
NM_022644	CSH2	3802	ACAGCGATGACTATCACCTCC
NG_001334	NG_001334	3803	ACAAGGTCGAGACATTCCTGC
NM_000515	GH1	3803	ACAAGGTCGAGACATTCCTGC
NM_001317	CSH1	3803	ACAAGGTCGAGACATTCCTGC
NM_001318	CSHL1	3803	ACAAGGTCGAGACATTCCTGC
NM_002059	GH2	3803	ACAAGGTCGAGACATTCCTGC
NM_020991	CSH2	3803	ACAAGGTCGAGACATTCCTGC
NM_022556	GH2	3803	ACAAGGTCGAGACATTCCTGC
NM_022557	GH2	3803	ACAAGGTCGAGACATTCCTGC
NM_022558	GH2	3803	ACAAGGTCGAGACATTCCTGC
NM_022559	GH1	3803	ACAAGGTCGAGACATTCCTGC

NM_022560	GH1	3803	ACAAGGTCGAGACATTCCTGC
NM_022561	GH1	3803	ACAAGGTCGAGACATTCCTGC
NM_022562	GH1	3803	ACAAGGTCGAGACATTCCTGC
NM_022578	CSHL1	3803	ACAAGGTCGAGACATTCCTGC
NM_022579	CSHL1	3803	ACAAGGTCGAGACATTCCTGC
NM_022580	CSHL1	3803	ACAAGGTCGAGACATTCCTGC
NM_022581	CSHL1	3803	ACAAGGTCGAGACATTCCTGC
NM_022640	CSH1	3803	ACAAGGTCGAGACATTCCTGC
NM_022641	CSH1	3803	ACAAGGTCGAGACATTCCTGC
NM_022642	CSH1	3803	ACAAGGTCGAGACATTCCTGC
NM_022644	CSH2	3803	ACAAGGTCGAGACATTCCTGC
NM_022645	CSH2	3803	ACAAGGTCGAGACATTCCTGC
NM_022646	CSH2	3803	ACAAGGTCGAGACATTCCTGC
NG_001334	NG_001334	3804	ACCCTCAAGCAGACCTACAGC
NM_001317	CSH1	3804	ACCCTCAAGCAGACCTACAGC
NM_001318	CSHL1	3804	ACCCTCAAGCAGACCTACAGC
NM_020991	CSH2	3804	ACCCTCAAGCAGACCTACAGC
NM_022578	CSHL1	3804	ACCCTCAAGCAGACCTACAGC
NM_022579	CSHL1	3804	ACCCTCAAGCAGACCTACAGC
NM_022580	CSHL1	3804	ACCCTCAAGCAGACCTACAGC
NM_022581	CSHL1	3804	ACCCTCAAGCAGACCTACAGC
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NM_022642	CSH1	3804	ACCCTCAAGCAGACCTACAGC
NM_022644	CSH2	3804	ACCCTCAAGCAGACCTACAGC
NM_022645	CSH2	3804	ACCCTCAAGCAGACCTACAGC
NM_022646	CSH2	3804	ACCCTCAAGCAGACCTACAGC
NM_001552	IGFBP4	3805	ACCCACGAGGACCTCTACTTC
NM_001552	IGFBP4	3806	ACGAGGACCTCTACTTCATCC
NM_001552	IGFBP4	3807	ACCAGCTGGCTGACAGCTTTC
NM_001561	TNFRSF9	3808	ACCAGCAATGCAGAGTGTGAC
NM_001561	TNFRSF9	3809	ACGTGGTCTGTGGACCATCTC
NM_001665	ARHG	3810	ACCGTGTTTCGACAATTACAGC
NM_001665	ARHG	3811	ACCAAGAAGGACCTGAGAGCC
NM_001666	ARHGAP4	3812	ACCAAAGCTTCCGGAAGGAGC
NM_001666	ARHGAP4	3813	ACCTCTTCACCTTCCTCAACC
NM_001719	BMP7	3814	ACAAGGCCGTCTTCAGTACCC
NM_001719	BMP7	3815	ACATCACAGCCACCAGCAACC
NM_001720	BMP8	3816	ACCCTCCACGTCAGCATGTTC
NM_001720	BMP8	3817	ACTCCGCCTCTATGTGGAGAC
NM_001720	BMP8	3818	ACCTCTGTGCTCTACTATGAC
NM_001901	CTGF	3819	ACCTGTGCCTGCCATTACAAC
NM_002006	FGF2	3820	ACTTACCGGTCAAGGAAATAC
NM_002006	FGF2	3821	ACACCAGTTGGTATGTGGCAC
NM_002007	FGF4	3822	ACTACCTGCTGGGCATCAAGC
NM_002007	FGF4	3823	ACCATGAAGGTCACCCACTTC

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NM_002053	GBP1	3824	ACAGAATCAGGAAGCATCATC
NM_002170	IFNA8	3825	ACCTGGAAGTCCTGTGTGATC
NM_002176	IFNB1	3826	ACCTCCTGGCTAATGTCTATC
NM_002177	IFNW1	3827	ACATGACCCTCCTAGACCAAC
NM_002177	IFNW1	3828	ACCAACTCCACACTGGACTTC
XM_071038	LOC138685	3828	ACCAACTCCACACTGGACTTC
XM_095763	LOC158017	3828	ACCAACTCCACACTGGACTTC
NM_002178	IGFBP6	3829	ACAGAGGAATCCAGGCACCTC
NM_002178	IGFBP6	3830	ACTCAGTGTGTCAGCAACTCC
NM_002203	ITGA2	3831	ACGGGTGTGTGTTCTGACATC
NM_002205	ITGA5	3832	ACTTCTTTGGCTCTGCCCTTC
NM_002205	ITGA5	3833	ACTGTGGATCATCATCCTAGC
NM_002206	ITGA7	3834	ACTGTGTGGTGTTCAGCTGCC
NM_002208	ITGAE	3835	ACTAAGATCACTGTCGTCTTC
NM_002208	ITGAE	3836	ACCCAGCATCCTTTGCATTAC
NM_002209	ITGAL	3837	ACAGCACAGGAAGCCTCTATC
NM_002209	ITGAL	3838	ACCAGCATGTTCATGCACTGAC
NM_002309	LIF	3839	ACCTGGACAAGCTATGTGGCC
NM_002309	LIF	3840	ACCTCGGGTAAGGATGTCTTC
NM_002342	LTBR	3841	ACTACCTGACCATCTGCCAGC
NM_002342	LTBR	3842	ACTGGCAACATCTACATCTAC
NM_002416	MIG	3843	ACCAACCAAGGGACTATCCAC
NM_002507	NGFR	3844	ACAGGCCTGTACACACACAGC
NM_002507	NGFR	3845	ACGTATTCCGACGAGGCCAAC
NM_002546	TNFRSF11B	3846	ACGAAGAAACCTCTCATCAGC
NM_002546	TNFRSF11B	3847	ACGCCTAACTGGCTTAGTGTC
NM_002546	TNFRSF11B	3848	ACCAAGACACCTTGAAGGGCC
NM_002632	PGF	3849	ACCATGCAGCTCCTAAAGATC
NM_002632	PGF	3850	ACGTGGAGCTGACGTTCTCTC
NM_002632	PGF	3851	ACGTTCTCTCAGCACGTTTCGC
NM_002820	PTHLH	3852	ACTAACAAGGTGGAGACGTAC
NM_002891	RASGRF1	3853	ACTTCCTCAACACCTTCCTGC
NM_003238	TGFB2	3854	ACACTCGATATGGACCAGTTC
NM_003238	TGFB2	3855	ACATCTCCAACCCAGCGCTAC
NM_003239	TGFB3	3856	ACCGAGTCGGAATACTATGCC
NM_003239	TGFB3	3857	ACTGTCCATGTACACCTTTC
NM_003239	TGFB3	3858	ACTGTACAACACTCTGAACCC
NM_003243	TGFBR3	3859	ACTCCATTGTGATACAGGTTTC
NM_003243	TGFBR3	3860	ACAGCAGGAAGGCAGCAAGTC
NM_003327	TNFRSF4	3861	ACCTCAGAAGTGGGAGTGAGC
NM_003376	VEGF	3862	ACTGAGGAGTCCAACATCACC
NM_003377	VEGFB	3863	ACCAAGTCCGGATGCAGATCC
NM_003377	VEGFB	3864	ACAGCCAGTGTGAATGCAGAC
NM_003637	ITGA10	3865	ACATGAGGTTCAACGCATCAC
NM_003637	ITGA10	3866	ACAAACAGACTGAATGGGAGC
NM_003790	TNFRSF12	3867	ACTTCCACAAGAAGATTGGTC

NM_003790	TNFRSF12	3868	ACCGTCCAGTTGGTGGGTAAC
NM_003807	TNFSF14	3869	ACCAAAGCTGGCTACTACTAC
NM_003807	TNFSF14	3870	ACTACATCTACTCCAAGGTGC
NM_003807	TNFSF14	3871	ACATCTACTCCAAGGTGCAGC
NM_003809	TNFSF12	3872	ACTTGCTGGTGGATGGTGTGC
NM_003809	TNFSF12	3873	ACTTCGGACTCTTCCAGGTTT
NM_003810	TNFSF10	3874	ACGTGTACTTTACCAACGAGC
NM_003810	TNFSF10	3875	ACATTGTCTTCTCCAACTCC
NM_003811	TNFSF9	3876	ACAAAGAGGACACGAAGGAGC
NM_003811	TNFSF9	3877	ACCTGGACAGAGTCCGAATCC
NM_003820	TNFRSF14	3878	ACATTGCCCCACCTCAATGGCC
NM_003820	TNFRSF14	3879	ACCCTGGAGGAATGTCAGCAC
NM_003841	TNFRSF10C	3880	ACTCCTGCCTCTTCTCATTAC
NM_003844	TNFRSF10A	3881	ACAATTCTGCTGAGATGTGCC
NM_003844	TNFRSF10A	3882	ACAGGTGTCACTGTACAGTCC
NM_003867	FGF17	3883	ACGGAGATCGTGCTGGAGAAC
NM_003867	FGF17	3884	ACTTCATCAAGCGCCTCTACC
NM_004115	FGF14	3885	ACTCATCCATGTTGTACAGAC
NM_004115	FGF14	3886	ACCCAAGCCATTGGAAGTTGC
NM_004120	GBP2	3887	ACAGAGCTGACAGATCGAATC
NM_004195	TNFRSF18	3888	ACTGCACCCAGTTTCGGGTTTC
NM_004308	ARHGAP1	3889	ACGTGGAGAGTGACTACACAC
NM_004308	ARHGAP1	3890	ACACCTTCACCAAGTTCCTTC
NM_004469	FIGF	3891	ACAGCAGATCAGGGCTGCTTC
NM_004469	FIGF	3892	ACAGCATGTGCAAAGCATTCG
NM_004490	GRB14	3893	ACGAAGTGGTGATTGAAGTGC
NM_004490	GRB14	3894	ACTCAATAAGGGCGTTCTTCC
NM_004658	RASAL1	3895	ACAGCTACTGTCTGGAGGAGC
NM_004706	ARHGEF1	3896	ACTAGGGCTGACCTCATCTCC
NM_004706	ARHGEF1	3897	ACCGATCACAAAGCCTTCTAC
NM_004723	ARHGEF2	3898	ACAACCGCTGTAAAGACACCC
NM_004723	ARHGEF2	3899	ACCAAGTACCCGTTACTCATC
NM_004723	ARHGEF2	3900	ACTTCTACATGGCCTACAGGC
NM_004761	RAB2L	3901	ACGGATGTCTTGGTGTTCCTC
NM_004815	PARG1	3902	ACAGAAGATCTTCGATGGGTC
NM_004815	PARG1	3903	ACTCTGAGGAGCTTGGCTTGC
NM_004962	GDF10	3904	ACATGGTTCGCTGTCCACATGC
NM_004962	GDF10	3905	ACGCACAGCACTTCCACAAGC
NM_005117	FGF19	3906	ACAAGAACAGAGGCTTTCTTC
NM_005118	TNFSF15	3907	ACCTCTGAGTGCAGTGAAATC
NM_005118	TNFSF15	3908	ACTGGTTCCAGCCCCTTACC
NM_005167	ARHC	3909	ACCACAGCAGGTATACAGCTC
NM_005247	FGF3	3910	ACACAGAAGTCCCTCCCTGTTC
NM_005259	GDF8	3911	ACCCAGGCACTGGTATTTGGC
NM_005260	GDF9	3912	ACAAGTGCTCAGGCTTATCAC
NM_005260	GDF9	3913	ACCATGGTACAGAACATCATC

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NM_005311	GRB10	3914	ACGTGCTGGATGACAGCGTTC
NM_005311	GRB10	3915	ACCAGCTGAACAAAGGAGTCC
NM_005429	VEGFC	3916	ACTACCACAGTGTCAGGCAGC
NM_005435	ARHGEF5	3917	ACAATGTCCAGAGTATGCGAC
NM_005448	BMP15	3918	ACTCGCTTCAATCTCTCCTGC
NM_005448	BMP15	3919	ACTTCATCCTTGGACATTGCC
NM_005448	BMP15	3920	ACTACGCGATGGTCTCAATTC
NM_005614	RHEB2	3921	ACAAGGCAAGTCTTCATGCTC
NM_005614	RHEB2	3922	ACCTGAAGAAGCAAAGTCCCC
NM_005618	DLL1	3923	ACCCAGAAAGACTCATCAGCC
NM_005811	GDF11	3924	ACCACCGAGACCGTCATTAGC
NM_005811	GDF11	3925	ACTGGATCATCGCACCTAAGC
NM_006116	MAP3K7IP1	3926	ACGGACATTGACCTTCTCAGC
NM_006270	RRAS	3927	ACTTCGTGTCTGACTACGACC
NM_006325	RAN	3928	ACTGGCATAGAGATCTGGTAC
NM_006506	RASA2	3929	ACAGCCTGTTGACTCCAATTC
NM_006506	RASA2	3930	ACAAGCAGAGAGCTCACCTAC
NM_006573	TNFSF13B	3931	ACTGCTGTCTTGCTGCCTCAC
NM_006573	TNFSF13B	3932	ACGCCATGGGACATCTAATTC
NM_006850	IL24	3933	ACAGTTGGACGTAGAAGCAGC
NM_007182	RASSF1	3934	ACGCCTTCAGCATGCCTGAAC
NM_007368	GAP1IP4BP	3935	ACATGTTCCAGGTCATCCAGC
NM_012211	ITGA11	3936	ACAAGATATGCGGTGGCCGTC
NM_012219	MRAS	3937	ACCGCTTCCACCAGCTTATCC
NM_012452	TNFRSF13B	3938	ACAGAGGCTCAGAAGCAAGTC
NM_013371	IL19	3939	ACGCTGCTGCCATTAAATCCC
NM_014438	IL1F8	3940	ACAATCTTTGAGTGGGTTTGC
NM_014440	IL1F6	3941	ACCAGACGCTCATAGCAGTCC
NM_014448	ARHGEF16	3942	ACGCTGAGAAGTACTTCCACC
NM_014448	ARHGEF16	3943	ACTTCAGCAAGGTCAAGTCCC
NM_014452	TNFRSF21	3944	ACAGACACATCCTGAAGCTGC
NM_014482	BMP10	3945	ACGGTGTGCGACTTTAACACAC
NM_014737	RASSF2	3946	ACAACCTTGTAATATGAAGGCC
NM_014784	ARHGEF11	3947	ACAACAGGTCTCGTTCAACGC
NM_014784	ARHGEF11	3948	ACTCTGGGACAGAACGCTTTC
NM_014958	ARHGEF15	3949	ACGAAAGGAGGAGGCACCTTC
NM_015313	ARHGEF12	3950	ACTGGCAGCAGCTTGTAGTC
NM_015313	ARHGEF12	3951	ACCTGCCTGTCTCAGAAGAAC
NM_015318	P114-RHO-GEF	3952	ACAGGAGAGATGGATGAAGCC
NM_015647	TNFRSF6B	3953	ACAGCCTATAAGCAAGACGAC
NM_016434	TNFRSF6B	3953	ACAGCCTATAAGCAAGACGAC
NM_032957	TNFRSF6B	3953	ACAGCCTATAAGCAAGACGAC
NM_015647	TNFRSF6B	3954	ACCCAGAGCAAGATCTCGTCC
NM_016434	TNFRSF6B	3954	ACCCAGAGCAAGATCTCGTCC
NM_032945	TNFRSF6B	3954	ACCCAGAGCAAGATCTCGTCC
NM_032957	TNFRSF6B	3954	ACCCAGAGCAAGATCTCGTCC

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NM_016084	RASD1	3955	ACCAAGTCTTGCCTCAAGAAC
NM_016084	RASD1	3956	ACAGCGACCTCATGTACATCC
NM_016204	GDF2	3957	ACACGCTGGACATCAGTGTCC
NM_016204	GDF2	3958	ACCCTGGTGCATCTCAAGTTC
NM_016205	PDGFC	3959	ACAAGGAACAGAACGGAGTAC
NM_016205	PDGFC	3960	ACGAGGTCCTTCAGTTGAGAC
NM_018402	IL26	3961	ACATTGTCCCAAGCTGTTGAC
NM_018647	TNFRSF19	3962	ACCCTCCTCCTCCTTACGAAC
NM_018647	TNFRSF19	3963	ACCTCAGCTCCACGAATATGC
NM_018647	TNFRSF19	3964	ACTGGTAGAATCAGCATCAAC
NM_019074	DLL4	3965	ACCTACTGTGAACTCCACGTC
NM_019113	FGF21	3966	ACCTCTACACAGATGATGCCC
NM_019555	ARHGEF3	3967	ACGTCGCTAGCAAACCTCATC
NM_019851	FGF20	3968	ACTTAACAAAGACGGAACCTCC
NM_019851	FGF20	3969	ACTGATGTACACTTGAAGTGC
NM_020525	IL22	3970	ACAAGTCCAACTTCCAGCAGC
NM_020525	IL22	3971	ACCCTTGAAGAAGTGCTGTTC
NM_020634	GDF3	3972	ACTCTCAACCCTGATCAGTGC
NM_020634	GDF3	3973	ACCAAGCTGTCTCCCATTTCC
NM_020637	FGF22	3974	ACTTCTTCCTGCGCGTGGATC
NM_020637	FGF22	3975	ACAACACCTACGCCTCACAGC
NM_020638	FGF23	3976	ACTCTCCTCAGTATCACTTCC
NM_020996	FGF6	3977	ACTGTCACTCATTTCTTCCC
NM_022556	GH2	3978	ACACCTATCAGGAGTTTAACC
NM_022559	GH1	3979	ACACCTACCAGGAGTTTAACC
NM_022560	GH1	3979	ACACCTACCAGGAGTTTAACC
NG_001334	NG_001334	3980	ACAGCAACGTCTATGACCTCC
NM_000515	GH1	3980	ACAGCAACGTCTATGACCTCC
NM_022559	GH1	3980	ACAGCAACGTCTATGACCTCC
NM_022560	GH1	3980	ACAGCAACGTCTATGACCTCC
NM_022561	GH1	3981	ACACCTACCAGGAGTTTAGGC
NM_022641	CSH1	3981	ACACCTACCAGGAGTTTAGGC
NM_022645	CSH2	3981	ACACCTACCAGGAGTTTAGGC
NM_032496	ARHGAP9	3982	ACTGTAACCTGGTGGACCTTC
NM_032496	ARHGAP9	3983	ACCTGGGAATTGTGTTTGGAC
NM_003823	TNFRSF6B	3984	ACACGCAGTTCTGGAACCTACC
NM_032945	TNFRSF6B	3984	ACACGCAGTTCTGGAACCTACC
NM_032957	TNFRSF6B	3984	ACACGCAGTTCTGGAACCTACC
NM_003823	TNFRSF6B	3985	ACGCTGGTTTCTGCTTGGAGC
NM_032945	TNFRSF6B	3985	ACGCTGGTTTCTGCTTGGAGC
NM_032957	TNFRSF6B	3985	ACGCTGGTTTCTGCTTGGAGC
NM_052851	GT650	3986	ACAGCAAAGGCTTTGGACATC
NM_052949	RASGRP4	3987	ACCACATGCTCAACATGGTGC
NM_130769	GPHA2	3988	ACACAACATCACCTCCGTCTC
NM_130769	GPHA2	3989	ACAACATCACCTCCGTCTCTC
NM_001202	BMP4	3990	ACTGGTCCACCACAATGTGAC

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NM_130850	BMP4	3990	ACTGGTCCACCACAATGTGAC
NM_130851	BMP4	3990	ACTGGTCCACCACAATGTGAC
NM_133639	ARHV	3991	ACGTACTAATTCAGCTGGACC
XM_027943	RASGRF2	3992	ACTGGCTGTGTCCAGAACATC
XM_030185	LOC90230	3993	ACTCCTCTGATCGATCTGCCC
XM_032902	ITGA1	3994	ACAGCCTCGGTACAATCATAC
XM_032902	ITGA1	3995	ACCGTGTCAACCTAGATTAC
XM_035950	LOC56832	3996	ACTGTGCCTGGGAGATTGTCC
XM_047536	OBSCN	3997	ACACTAACCATCTCCCAGTGC
XM_054745	LOC257478	3998	ACGGCCAGCAGATGATCTTCC
XM_059223	LOC128239	3999	ACAGGATATTAGTGCATGCAC
XM_059223	LOC128239	4000	ACCTGGCCAAGCTGATCTTTC
XM_059223	LOC128239	4001	ACCAAATTCGATGTGCAAC
XM_059230	LOC128272	4002	ACTCATCTCTGGGTCAGGCAC
XM_059230	LOC128272	4003	ACTTCTTAGGCTCTGCCGAGC
XM_063142	LOC122460	4004	ACCCGAGAAGCTACAGGATTC
XM_063142	LOC122460	4005	ACTGTTACTACGATTGCTACC
XM_065455	LOC129896	4006	ACGAGGGATATGAACCTGCCC
XM_065455	LOC129896	4007	ACTCTGCCTGACATTATAAGC
XM_071038	LOC138685	4008	ACAGAAGAGACTTCAGGTTTC
XM_071048	LOC138684	4009	ACCTAGAAGCACTCATGGGAC
XM_071048	LOC138684	4010	ACTGAGCAAACAAGGAAGACC
XM_084665	LOC143872	4011	ACCCAAGCATTCCTCTTCTC
XM_084665	LOC143872	4012	ACCCAAAGCTTCACCAAACCC
XM_090404	LOC160629	4013	ACAGATGGAACCTCTGCAACC
XM_090404	LOC160629	4014	ACACAGCCTACAGGCAGAAGC
XM_092722	LOC164209	4015	ACTCCCAAGGTGGCAAAGATC
XM_094119	LOC166824	4016	ACATTCCGCTACTGCAGAGGC
XM_095759	LOC158011	4017	ACGACACACTGGCTGTTTGGC
XM_095759	LOC158011	4018	ACAGTCTGGAACGACTGCAGC
NG_001150	NG_001150	4019	ACATGACCCTCCTGGACCAAC
XM_095763	LOC158017	4019	ACATGACCCTCCTGGACCAAC
XM_095763	LOC158017	4020	ACACTGGACTTCATCTGCAGC
XM_113880	LOC197414	4021	ACAGCCCTCACAAATGGATGGC
XM_167711	ITGA8	4022	ACCTCCTCAGGAGGACATGAC
XM_167936	LOC221178	4023	ACACCAGTGCAGAAGATCTGC
XM_172762	LOC253347	4024	ACAGAAGTGACTTCAGATTCC
XM_172762	LOC253347	4025	ACAGCAGGTCTTCAACTTCTC
XM_172762	LOC253347	4026	ACATGACCTTCCTGGACCAAC
NM_032551	GPR54	4027	ACGCTGGTCATCTACGTCATC
NM_032551	GPR54	4028	ACTCACTGCATGTCCTACAGC
AB083611	AB083611	4029	ACTGTGTTGTGGAGGGTTCTC
AB083611	AB083611	4030	ACGTCTCTGTTGTGGAGAGTC
AF182273	AF182273	4031	ACAGCCTGTGCTGGCTATCAC
NG_000004	NG_000004	4031	ACAGCCTGTGCTGGCTATCAC
NM_000776	CYP3A3	4031	ACAGCCTGTGCTGGCTATCAC

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NM_017460	CYP3A4	4031	ACAGCCTGTGCTGGCTATCAC
AF182273	AF182273	4032	ACTGCAGGAGGAAATTGATGC
NG_000004	NG_000004	4032	ACTGCAGGAGGAAATTGATGC
NM_000776	CYP3A3	4032	ACTGCAGGAGGAAATTGATGC
NM_017460	CYP3A4	4032	ACTGCAGGAGGAAATTGATGC
AB083590	AB083590	4033	ACTCTGGATAGCCGCCCTTTCC
AF317653	GPR62	4033	ACTCTGGATAGCCGCCCTTTCC
AB083590	AB083590	4034	ACTTGCAATGCCTCCAGAGAC
AF317653	GPR62	4034	ACTTGCAATGCCTCCAGAGAC
AF380192	TA4	4035	ACCTGGTGATGATTTCAATCC
ENSG00000146383	ENSG00000146383	4035	ACCTGGTGATGATTTCAATCC
D86519	D86519	4036	ACTCCTTCTCCAGCTTTACTC
D86519	D86519	4037	ACACTTGTATTCACTGCTGTC
D86519	D86519	4038	ACTCTAGGCTTCATCCTCATC
ENSG00000124860	ENSG00000124860	4039	ACTGACTCCTCTGTGATCTCC
SK601	Obscn	4039	ACTGACTCCTCTGTGATCTCC
J02906	HUMCYP11F	4040	ACTTCCACATGGATACCCCTGC
NG_000008	NG_000008	4040	ACTTCCACATGGATACCCCTGC
NM_000774	CYP2F1	4040	ACTTCCACATGGATACCCCTGC
M33189	HUMCYP2DG	4041	ACATGGATGGTGGGTGAAACC
NM_000102	CYP17	4042	ACCCTGAGTTGAATGTCATAC
NM_000103	CYP19	4043	ACCATGTCTGTCTCTTTGTTT
NM_031226	CYP19	4043	ACCATGTCTGTCTCTTTGTTT
NM_000269	NME1	4044	ACATGCAAGCTTCCGAAGATC
NM_000269	NME1	4045	ACTGGTGAAATACATGCACTC
NM_000269	NME1	4046	ACCGTGAGACTTCTGCATAC
NM_000395	CSF2RB	4047	ACCTGTGACCTCAGTGATGAC
NM_000395	CSF2RB	4048	ACTATTCTACAAGCCCAGCCC
NM_000395	CSF2RB	4049	ACCGGTCTTGAGATCAAGAAC
NM_000498	CYP11B2	4050	ACCAGGAAGTGGCCTTCAACC
NM_000500	CYP21A2	4051	ACTTACCTACAAGCTGGTGTC
NG_000013	NG_000013	4052	ACCTGCAGCATCATCTGTTAC
NM_000500	CYP21A2	4052	ACCTGCAGCATCATCTGTTAC
NM_000534	PMS1	4053	ACAGATGTTTCCGCAGCTGAC
NM_000534	PMS1	4054	ACCAGCGCATGGAATTGGCC
NM_000534	PMS1	4055	ACCAGACAATTACCCATGTAC
NM_000535	PMS2	4056	ACAGTTGCAAAGCCTCATTC
NM_000535	PMS2	4057	ACACACAACAGAGAACAAGCC
NM_000535	PMS2	4058	ACCATGAGACACATCGCCAAC
NM_000756	CRH	4059	ACCCATCTCCCTGGATCTCAC
NM_000756	CRH	4060	ACACAGCAAGCTCACAGCAAC
NG_000008	NG_000008	4061	ACAAAGAGTTCTGTCACTGC
NM_000764	CYP2A7	4061	ACAAAGAGTTCTGTCACTGC
NM_030589	CYP2A7	4061	ACAAAGAGTTCTGTCACTGC
U22029	HSU22029	4061	ACAAAGAGTTCTGTCACTGC
NM_000765	CYP3A7	4062	ACTCTGAGACCCACAAAGCTC

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NM_000766	CYP2A13	4063	ACATGATGCCGTCAAGGAGGC
U22028	HSU22028	4063	ACATGATGCCGTCAAGGAGGC
NM_000769	CYP2C19	4064	ACCGTGTTCAAGAGGAAGCCC
NM_000771	CYP2C9	4064	ACCGTGTTCAAGAGGAAGCCC
NM_000772	CYP2C18	4064	ACCGTGTTCAAGAGGAAGCCC
NM_000769	CYP2C19	4065	ACATCAGGATTGTAAGCACCC
NM_000770	CYP2C8	4066	ACTTCCGTGCTACATGATGAC
NM_030878	CYP2C8	4066	ACTTCCGTGCTACATGATGAC
NM_000771	CYP2C9	4067	ACTCTCAAAGGTCTATGGCCC
NM_000771	CYP2C9	4068	ACCAGAGATACATTGACCTTC
NM_000773	CYP2E	4069	ACAACCTCTGAGATATGGGCTC
NM_000775	CYP2J2	4070	ACTCTGACAGCACTAAGGAAC
NM_000778	CYP4A11	4071	ACCATCATGAAGTGTGCCTTC
XM_089093	LOC163720	4071	ACCATCATGAAGTGTGCCTTC
NM_000779	CYP4B1	4072	ACGTTGGCTAAGGCTATGGAC
NM_000779	CYP4B1	4073	ACATCTTCTGCGATGTGGGTC
NM_000782	CYP24	4074	ACCGGTTAGAGAAGTATTCTC
NM_000782	CYP24	4075	ACAATGAGCCTGTTGAGATGC
NM_000783	CYP26A1	4076	ACAATGTGCGGCGCATCTTGC
NM_057157	CYP26A1	4076	ACAATGTGCGGCGCATCTTGC
NM_000783	CYP26A1	4077	ACTGGCAGCTTCTAAATGGAC
NM_057157	CYP26A1	4077	ACTGGCAGCTTCTAAATGGAC
NM_000784	CYP27A1	4078	ACATGGAGCTATGGAAGGAGC
NM_000784	CYP27A1	4079	ACTCACTCTATGCCACCTTCC
NM_000786	CYP51	4080	ACTCTTGCGCAGGGCAGCATAC
NM_000961	PTGIS	4081	ACAGAAGCCATGTATACCAAC
NM_000961	PTGIS	4082	ACAGAAGGTTCTAGACAGCAC
NM_001067	TOP2A	4083	ACCCAGCAAATGTGGGTTTAC
NM_001067	TOP2A	4084	ACCCAAGAGCTTTGGATCAAC
NM_001067	TOP2A	4085	ACTTCAAACGGAATGACAAGC
NM_001068	TOP2B	4086	ACCATCACAATTGGCCATCAC
NM_001068	TOP2B	4087	ACAGCATGATGATAGTTCTCTC
NM_001068	TOP2B	4088	ACCCTACTGAGCCACCTTCTC
NM_001082	CYP4F2	4089	ACCTACGCCTTCTATGACAAC
NM_001107	ACYP1	4090	ACTCCAAGGTGCGTCATATGC
NM_001107	ACYP1	4091	ACTTGAAACAAGAGGAAGTCC
NM_001108	ACYP2	4092	ACAATTCCATGAAGTCCTGGC
NM_138448	ACYP2	4092	ACAATTCCATGAAGTCCTGGC
NM_001334	CTSO	4093	ACAGATACTCAGCAGAAGTAC
NM_001334	CTSO	4094	ACAGCAGGTCATTGACTGTTTC
NM_001364	DLG2	4095	ACTGCTCCTATAATTGTCAAC
NM_001364	DLG2	4096	ACTTCTCCCAGGCACTATTCC
NM_001364	DLG2	4097	ACGAACCAATCAGAAACGCTC
NM_001648	KLK3	4098	ACTCAGAAGGTGACCAAGTTC
NM_001700	AZU1	4099	ACTGCTTCCAAAGCCAGAACC
NM_001700	AZU1	4100	ACCCAGGTTTGTCAACGTGAC

NM_001932	MPP3	4101	ACCACGTTGGAGATGAGCTCC
NM_001932	MPP3	4102	ACCTATGATCAGCCTTGTGAC
NM_001932	MPP3	4103	ACCTTCATAGACCGGCATTAC
NM_002431	MNAT1	4104	ACTGCCCTGAGTGTGGTACTC
NM_002431	MNAT1	4105	ACTGGAGAGTTCTGATCTCCC
NM_002431	MNAT1	4106	ACTTCTTCTCTTGCTTGTCAC
NM_002436	MPP1	4107	ACTGTGACCGAGGACATGTAC
NM_002436	MPP1	4108	ACCAGAATTCTTCATGGTGGC
NM_002436	MPP1	4109	ACTACAGATGTTTCATGAGAGC
NM_002461	MVD	4110	ACCACAACAGCCGTCATCAGC
NM_002461	MVD	4111	ACTGAGAAGAAGCTGACAGGC
NM_002461	MVD	4112	ACCAATGCCGTGATCTTCACC
NM_002512	NME2	4113	ACTTCGAGCAGAAGGGATTCC
NM_002512	NME2	4114	ACTGGTGAAGTACATGAAGTC
NM_002512	NME2	4115	ACTGAAGAAGTGGTTGACTAC
NM_002513	NME3	4116	ACGCCTTGTCAGTATATGGC
NM_002566	P2RY11	4117	ACCTATGTGCCCTACCACATC
NM_002566	P2RY11	4118	ACACCCCTCTACTCTACATGGC
NM_002793	PSMB1	4119	ACTTACCAGAGAGACTCCTTC
NM_002793	PSMB1	4120	ACAGAATGTGGAGCATGTTCC
NM_002794	PSMB2	4121	ACATATCATGTGAACCTCCTC
NM_002801	PSMB10	4122	ACGTCCAAGATGGAGCTACAC
NM_003299	TRA1	4123	ACCTTCCAAGCCGAAGTTAAC
NM_003299	TRA1	4124	ACACATCTGGGAGTCTGACTC
NM_003299	TRA1	4125	ACGACTTCCATGATATGATGC
NM_003353	UCN	4126	ACATTGACCTCACCTTTTACC
NM_004087	DLG1	4127	ACAGAGCAACCTCTTTTCAGGC
NM_004087	DLG1	4128	ACCACACATTGGAGATGACTC
NM_004087	DLG1	4129	ACACCACCTGATATCACCAAC
NM_004300	ACP1	4130	ACCGGGTATGAGATAGGGAAC
NM_004391	CYP8B1	4131	ACCAAGCAGTCCTTTGCCTTC
NM_004669	CLIC3	4132	ACCATCCTGCTCTATGACAGC
NM_004669	CLIC3	4133	ACTCCGCGTTCATCAAGAACC
NM_004742	BAIAP1	4134	ACAGTCTGGCTCTAAGCAGTC
NM_004742	BAIAP1	4135	ACAAGAGACCTATGATTCACC
NM_004742	BAIAP1	4136	ACAGCCAGAATAGTTCTCAGC
NM_004820	CYP7B1	4137	ACCAGAGAACAATTGGACAGC
NM_004820	CYP7B1	4138	ACTGTCCTCATATTCAACCAC
NM_004853	STX8	4139	ACAGAGCTTTGTTGCAGAACC
NM_004853	STX8	4140	ACAGCCTCTTGTTGGGATGATC
NM_005009	NME4	4141	ACTCATCCGCTACATGAGCTC
NM_005009	NME4	4142	ACCATGATTGGACACACCGAC
NM_005009	NME4	4143	ACATCAGCAGGAATGTCATCC
NM_005340	HINT1	4144	ACAGATGGTGGACAGTCTGTC
NM_005348	HSPCA	4145	ACAGGCTGGTGCAGATATCTC
XM_068004	LOC132731	4145	ACAGGCTGGTGCAGATATCTC

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NM_005348	HSPCA	4146	ACACCAAAGAAGGCCTGGAAC
NM_005348	HSPCA	4147	ACGACAAGTCTGTGAAGGATC
XM_068004	LOC132731	4147	ACGACAAGTCTGTGAAGGATC
NM_005374	MPP2	4148	ACAGTGTCACTCCTCAAGATCC
NM_005374	MPP2	4149	ACGAATGATGTATTTGACCAC
NM_005374	MPP2	4150	ACATTTATGAGGAGGTGGCCC
NM_005394	PMS2L8	4151	ACCTTGAGCGGAGCTGAGAAC
NM_005395	PMS2L9	4152	ACTATCAGCCACAGTCTCTGC
NM_005395	PMS2L9	4153	ACAACATAGTCCAGAACCTGC
NM_005395	PMS2L9	4154	ACAGTGGTACTGAGTCTAAGC
NM_005443	PAPSS1	4155	ACATGGTATTCCATGCTACAC
NM_005443	PAPSS1	4156	ACTTACACTCAGGATCGCAAC
NM_005443	PAPSS1	4157	ACAGGAACGGGATATTGTACC
NM_005515	HLXB9	4158	ACATGATCCTGCCTAAGATGC
NM_006668	CYP46	4159	ACCAAGTACAACAAGGACTCC
NM_006668	CYP46	4160	ACAAGGACTCCAAGATGTACC
NM_007079	PTP4A3	4161	ACAGCACCTTCATTGAGGACC
NM_032611	PTP4A3	4161	ACAGCACCTTCATTGAGGACC
NM_007079	PTP4A3	4162	ACAAGGTAGTGGAAAGACTGGC
NM_032611	PTP4A3	4162	ACAAGGTAGTGGAAAGACTGGC
NM_007253	CYP4F8	4163	ACCTATGCCTTCTATCACAAC
NM_007253	CYP4F8	4164	ACCTCAGATGCCATTACAGAC
NM_007355	HSPCB	4165	ACCAGAAACCCTGATGACATC
NM_007355	HSPCB	4166	ACACTGGTGAGAGCAAAGAGC
XM_055551	LOC220763	4166	ACACTGGTGAGAGCAAAGAGC
XM_172185	LOC254262	4166	ACACTGGTGAGAGCAAAGAGC
XM_172356	LOC256424	4166	ACACTGGTGAGAGCAAAGAGC
NM_007355	HSPCB	4167	ACCTGGAGATCAACCCTGACC
NM_012247	SPS	4168	ACATGCCAGACAATGCAGTGC
NM_012247	SPS	4169	ACTTCAGGCGGCCCTTCTGATC
NM_012248	SPS2	4170	ACCTTGGTAGAAGATCCCTAC
NM_012248	SPS2	4171	ACCACCAATGGCTGGATAATC
NM_012248	SPS2	4172	ACCAATAATTGCCAAGATGGC
NM_012283	KCNG2	4173	ACTGGTTCTCCTTCGAGTTCC
NM_012283	KCNG2	4174	ACGCCACTCAACATCATTGAC
NM_012301	KIAA0705	4175	ACCAGTCTGTTCCCTATTGGTC
NM_012301	KIAA0705	4176	ACTTGACATTCAGGGATGCCC
NM_012301	KIAA0705	4177	ACGAATGGATTCCCTCTGGTCC
NM_013330	NME7	4178	ACCAGATGCAATATCAAAGGC
NM_013330	NME7	4179	ACCTGTTGCATTGTTAAACCC
NM_013330	NME7	4180	ACAGAATGCTGTTCACTGTAC
NM_014045	DKFZP564C1940	4181	ACTTACGCCAGGATATGACTC
NM_014214	IMPA2	4182	ACCTTCACACAGGTTCAATTGC
NM_014214	IMPA2	4183	ACATTGGATTGCTGTTTCGAC
NM_014241	PTPLA	4184	ACCTTGCTTGAGATAGTTTAC
NM_014241	PTPLA	4185	ACATACTTCATTAAATGGGCC

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NM_014381	MLH3	4186	ACTGTTAATGGCATGGCTGCC
NM_014381	MLH3	4187	ACCAACATCAGATTCTGCCAC
NM_014381	MLH3	4188	ACAACCTGGAGCTACTCCAGAC
NM_014428	TJP3	4189	ACAGTTCCTGGTGAACATTCC
NM_014428	TJP3	4190	ACTCCTTCTACATCCGCACTC
NM_014428	TJP3	4191	ACAACATATGTGCAGTACTACC
NM_014471	SPINK4	4192	ACTCCCTTTCTCAAGAATGCC
NM_014471	SPINK4	4193	ACTTTCTCAAGAATGCCCATC
NM_015533	DKFZP586B1621	4194	ACGCTCCTTATCGTGAAGAAC
NM_015533	DKFZP586B1621	4195	ACATGTCAGCACTGGAGATGC
NM_015533	DKFZP586B1621	4196	ACTGGAGGAACACCTGAATGC
NM_016292	TRAP1	4197	ACACTCGATTATCAGCAGCAC
NM_016593	CYP39A1	4198	ACAGTCTTTGCTATGGGAAAC
NM_016593	CYP39A1	4199	ACATCTCCTTTATCCAGTCAC
NM_016602	GPR2	4200	ACACACTTGGTCTCCGTCATC
NM_016602	GPR2	4201	ACCAGCAAACGCAAGGATGTC
NM_016602	GPR2	4202	ACTCAATCCCGTTCTCTACGC
NM_016616	LOC51314	4203	ACCTTGCGAGCAATGCAACC
NM_017636	TRPM4	4204	ACACAGATGGCCATGTACTTC
NM_017636	TRPM4	4205	ACTGTCCTCTGCATCGACTTC
NM_017636	TRPM4	4206	ACATCCGCGAGTACGAACAGC
NM_017823	FLJ20442	4207	ACTGTTACCTGGTGAAGGAGC
NM_017823	FLJ20442	4208	ACATTGCTGAAATCCGACGAC
NM_017881	FLJ20559	4209	ACCAAATTGCAGTGTCTATATC
NM_017881	FLJ20559	4210	ACTCTGTGGTATCAACAGACC
NM_017881	FLJ20559	4211	ACAAGAAATGCAGGACATCAC
NM_018208	FLJ10761	4212	ACCTTCCAGAATGGGCTGTGC
NM_018208	FLJ10761	4213	ACAGCATCAAAGGTCACGTGC
NM_018208	FLJ10761	4214	ACTCACTTCTTCTGGGCTCTC
NM_018238	FLJ10842	4215	ACAACCTCATTCCTCCCAATGC
NM_018238	FLJ10842	4216	ACTTCGACGAACAGATGAGGC
NM_018238	FLJ10842	4217	ACACTTGATGTCTTGCAGATC
NM_018291	FLJ10986	4218	ACTGTGGAACGTCTTCTTGTC
NM_018291	FLJ10986	4219	ACAGCCATGGTACCTGGGTTC
NM_018339	FLJ11149	4220	ACAAGTGGTAGATAATCTTCC
NM_018339	FLJ11149	4221	ACTTCCAGCTGATATATCCAC
NM_018339	FLJ11149	4222	ACATTGTTGGCTACCTGAGAC
NM_019885	P450RAI-2	4223	ACGGTGTCCAATTCCATTGGC
NM_019885	P450RAI-2	4224	ACCATGCAGGAGCTGAAGGAC
NM_020421	LOC57143	4225	ACTAATGACTTTGGCGCTGTC
SK401	ADCK1	4225	ACTAATGACTTTGGCGCTGTC
NM_020421	LOC57143	4226	ACATTCTCCTGATGGAGGTGC
SK401	ADCK1	4226	ACATTCTCCTGATGGAGGTGC
NM_020421	LOC57143	4227	ACACTGAGGACTTAGAGATTC
SK401	ADCK1	4227	ACACTGAGGACTTAGAGATTC
NM_020674	CYP-M	4228	ACAGATGGTAATGGGTAGTAC

NM_021114	SPINK2	4229	ACCAATGAATGTACTCTGTGC
NM_021114	SPINK2	4230	ACTGCTGATGGAGCAGTTTAC
NM_021187	CYP4F11	4231	ACACCTTCTATGACAACCTGCC
NM_021187	CYP4F11	4232	ACAAGAGTGTGAACATCATGC
NM_022139	GFRA4	4233	ACTGCTTGGATGGTGCCATTC
NM_145762	GFRA4	4233	ACTGCTTGGATGGTGCCATTC
NM_145763	GFRA4	4233	ACTGCTTGGATGGTGCCATTC
NM_022358	KCNK15	4234	ACTTCTGCCACGTGCACAAGC
NM_022474	MPP5	4235	ACAGGAAATGCAGCTAGAGCC
NM_022474	MPP5	4236	ACTCAGATGACCCTTATGTTT
NM_022474	MPP5	4237	ACATAGAAGAAGATAAGGAGC
NM_022571	HUMNP11Y20	4238	ACTTCCTGGACCTCTTCACTC
NM_022571	HUMNP11Y20	4239	ACGTGCTTCGGCATCGTGTAC
NG_000004	NG_000004	4240	ACGAACATTGCTATCTCCAGC
NM_022820	CYP3A43	4240	ACGAACATTGCTATCTCCAGC
NM_057095	CYP3A43	4240	ACGAACATTGCTATCTCCAGC
NM_057096	CYP3A43	4240	ACGAACATTGCTATCTCCAGC
NM_022820	CYP3A43	4241	ACCCAATAAGGCACCTGTCAC
NM_057095	CYP3A43	4241	ACCCAATAAGGCACCTGTCAC
NM_057096	CYP3A43	4241	ACCCAATAAGGCACCTGTCAC
NM_023944	CYP4F12	4242	ACATCATGCTTGACAAGTGGC
NM_024110	CARD14	4243	ACAGGGAGAAGGTGAATGCGC
NM_052819	CARD14	4243	ACAGGGAGAAGGTGAATGCGC
NM_024110	CARD14	4244	ACGGTTATAAGAGGCTACTCC
NM_024110	CARD14	4245	ACAGAAGAAGGTGGTGTGGAC
NM_024594	FLJ12899	4246	ACTAACGTGGCATATGGATCC
NM_024594	FLJ12899	4247	ACTGCCTTGTAAGGGCTTGC
NM_024594	FLJ12899	4248	ACACAAGCTGACAAGCTGGTC
NM_024779	FLJ22055	4249	ACAAGAAGAAGCATTTCGTGC
NM_024779	FLJ22055	4250	ACTCGATCAATGAGCTCAGCC
NM_024779	FLJ22055	4251	ACAAGATCAAGGTCAACAATC
NM_024819	FLJ22955	4252	ACTTCGGCACTGAGGTCTTGC
NM_024819	FLJ22955	4253	ACTCAAGTACATGAAGCACAC
NM_024819	FLJ22955	4254	ACTTGCACTGAGCTGGAGC
NM_024960	C20orf48	4255	ACACAATAGGTGATCTTCAGC
NM_024960	C20orf48	4256	ACTTCTTACTGGCTGTACCAC
NM_024960	C20orf48	4257	ACAATAGCAAGAATGTGTGCC
NG_000008	NG_000008	4258	ACTCCATCATGAAGGTGTCCC
NM_030589	CYP2A7	4258	ACTCCATCATGAAGGTGTCCC
NM_030622	CYP2S1	4259	ACCTCCAACGTAGTCTGCTCC
NM_030622	CYP2S1	4260	ACCACCATCCTACAAGCCTTC
NM_032030	FKSG83	4261	ACTTAGATGTGATTCTCATGC
NM_032030	FKSG83	4262	ACCTTGTCATTCCAAGTGGGC
NM_032030	FKSG83	4263	ACACAGTATCAGTCTGTCTCC
NM_032787	FLJ14454	4264	ACTTAACCCAGATGCACAGAC
NM_032787	FLJ14454	4265	ACCATTAACATCCCGAATCCC

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NM_032787	FLJ14454	4266	ACAGGTCATTGCCAACCTTAC
NM_001230	CASP10	4267	ACTCTGCATAGGATTGGTCCC
NM_032974	CASP10	4267	ACTCTGCATAGGATTGGTCCC
NM_032976	CASP10	4267	ACTCTGCATAGGATTGGTCCC
NM_032977	CASP10	4267	ACTCTGCATAGGATTGGTCCC
NM_001229	CASP9	4268	ACCATATGATCGAGGACATCC
NM_032996	CASP9	4268	ACCATATGATCGAGGACATCC
NM_001229	CASP9	4269	ACCTGCTTAGAGGACACAGGC
NM_032996	CASP9	4269	ACCTGCTTAGAGGACACAGGC
NM_033115	MGC16169	4270	ACAAGGTCGAGATAGAAGCTC
SK664	TBCK	4270	ACAAGGTCGAGATAGAAGCTC
NM_033115	MGC16169	4271	ACCAGATCTCTATGCCATCCC
SK664	TBCK	4271	ACCAGATCTCTATGCCATCCC
NM_033115	MGC16169	4272	ACCATTTCAGTGCTGCCTTCAC
SK664	TBCK	4272	ACCATTTCAGTGCTGCCTTCAC
NM_033256	PPP1R14A	4273	ACAGACATGCCCCGATGAGATC
NM_033256	PPP1R14A	4274	ACAAAGCTTCAAGGCCTCCAC
NM_001223	CASP1	4275	ACCCACCACTGAAAGAGTGAC
NM_033292	CASP1	4275	ACCCACCACTGAAAGAGTGAC
NM_033293	CASP1	4275	ACCCACCACTGAAAGAGTGAC
NM_033294	CASP1	4275	ACCCACCACTGAAAGAGTGAC
NM_033295	CASP1	4275	ACCCACCACTGAAAGAGTGAC
NM_033347	KCNK7	4276	ACGCACTTCTTGTTACTTGC
NM_005714	KCNK7	4277	ACATCCTAGGGCAGGATGAAC
NM_033347	KCNK7	4277	ACATCCTAGGGCAGGATGAAC
NM_033348	KCNK7	4277	ACATCCTAGGGCAGGATGAAC
NM_033455	KCNK7	4277	ACATCCTAGGGCAGGATGAAC
NM_033456	KCNK7	4277	ACATCCTAGGGCAGGATGAAC
M37712	HUMP58GTA	4278	ACATGAGTATTTCCGCGAGAC
NM_001787	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_024011	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_033486	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_033487	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_033488	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_033489	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_033490	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_033491	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_033492	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_033493	CDC2L1	4278	ACATGAGTATTTCCGCGAGAC
NM_033527	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_033528	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_033529	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_033531	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_033532	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_033534	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_033536	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC

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NM_033537	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_033621	CDC2L2	4278	ACATGAGTATTTCCGCGAGAC
NM_000796	DRD3	4279	ACTGGATGTCATGATGTGTAC
NM_033658	DRD3	4279	ACTGGATGTCATGATGTGTAC
NM_033659	DRD3	4279	ACTGGATGTCATGATGTGTAC
NM_033660	DRD3	4279	ACTGGATGTCATGATGTGTAC
NM_033663	DRD3	4279	ACTGGATGTCATGATGTGTAC
NM_033660	DRD3	4280	ACTGCTCCATCTCCCTGAGTC
NM_000075	CDK4	4281	ACCCTCAAGAGTGTGAGAGTC
NM_032913	CDK4	4281	ACCCTCAAGAGTGTGAGAGTC
NM_052984	CDK4	4281	ACCCTCAAGAGTGTGAGAGTC
NM_053278	GPR102	4282	ACGGGTAATTCTGTACACGGC
NM_057163	GNRHR2	4283	ACTAATGGCCACGTATTCTGC
NM_057163	GNRHR2	4284	ACCGTTCAAGGTGTAAGGAAAC
NM_005105	RBM8A	4285	ACAGCTTCAAGGCTCAATGGC
NM_057163	GNRHR2	4285	ACAGCTTCAAGGCTCAATGGC
NM_078473	BLP1	4286	ACATCCTCTGCTCTTACCTAC
NM_031940	BLP1	4287	ACGATTCTGTTTGGGACACAC
NM_078473	BLP1	4287	ACGATTCTGTTTGGGACACAC
NM_080671	KCNE4	4288	ACCTGATGCTGAACATGCTGC
NM_005265	GGT1	4289	ACTACTTTGGCTCCAAGGTCC
NM_013421	GGT1	4289	ACTACTTTGGCTCCAAGGTCC
NM_013430	GGT1	4289	ACTACTTTGGCTCCAAGGTCC
NM_080839	GGTL4	4289	ACTACTTTGGCTCCAAGGTCC
XM_086868	LOC257456	4289	ACTACTTTGGCTCCAAGGTCC
NM_005265	GGT1	4290	ACACTGGCCATCATCTACAAC
NM_013421	GGT1	4290	ACACTGGCCATCATCTACAAC
NM_013430	GGT1	4290	ACACTGGCCATCATCTACAAC
NM_080839	GGTL4	4290	ACACTGGCCATCATCTACAAC
NM_080920	GGTLA4	4290	ACACTGGCCATCATCTACAAC
NM_080876	SKRP1	4291	ACAAGTTGGCGTTATTAAGCC
NM_080876	SKRP1	4292	ACCTGAAACCAACATCCTGTC
NM_080876	SKRP1	4293	ACCATATGTCCAAATTCTGGC
NM_004178	TARBP2	4294	ACAGTGAGCTCTCTGAGGAGC
NM_134323	TARBP2	4294	ACAGTGAGCTCTCTGAGGAGC
NM_134324	TARBP2	4294	ACAGTGAGCTCTCTGAGGAGC
NM_138327	Tar1	4295	ACTCATTCAATCCATGGCCAC
NM_138327	Tar1	4296	ACTACTATGCTGTGTGTGATC
NM_138327	Tar1	4297	ACACTGCAGAGGAGGTTGCTC
NM_138445	LOC115330	4298	ACACAGCAAGGCCAGCATGAC
NM_138445	LOC115330	4299	ACTACATCGAGCGTGCCTGTC
NM_138445	LOC115330	4300	ACGCTGGTGTTCATCGGCTAC
NM_138738	SPAP1	4301	ACCTCTGTGTCTGTGAGTTCC
NM_138739	SPAP1	4301	ACCTCTGTGTCTGTGAGTTCC
SK465	Erk7	4302	ACATGGGCTTCCTTCTTGCTC
SK465	Erk7	4303	ACCGCGTCTATCAGATGATCC

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SK537	SPEG	4304	ACAGAGACGGCTGAGGATGAC
NM_005876	APEG1	4305	ACAAGGTCTCATTATGGACC
SK537	SPEG	4305	ACAAGGTCTCATTATGGACC
SK537	SPEG	4306	ACTGTCTGACAGGAATCTCCC
NM_022048	CSNK1G1	4307	ACTACCTTCGATATGTCAGGC
SK647	CK1g1	4307	ACTACCTTCGATATGTCAGGC
SK709	SgK085	4308	ACCAGGATTCAAGATCTGGAC
SK709	SgK085	4309	ACGAATAAGTGCAAGCGAAGC
XM_167231	LOC221757	4309	ACGAATAAGTGCAAGCGAAGC
NM_003852	TIF1	4310	ACACCCAAGTTGGAGTCATTC
SK783	TIF1a	4310	ACACCCAAGTTGGAGTCATTC
NM_003852	TIF1	4311	ACAACAACAACAGGAAGTGGC
SK783	TIF1a	4311	ACAACAACAACAGGAAGTGGC
SK783	TIF1a	4312	ACCAGCAACCTTCCATCTCTC
XM_028867	KIAA0981	4313	ACTCCACCAGTTCTACTCATC
XM_028867	KIAA0981	4314	ACAAAGAGTAGCAGCCCTATC
XM_028867	KIAA0981	4315	ACGTTCCCTCTCCCACTCATC
XM_032749	KIAA1634	4316	ACCTGTTGTGGACATTGTTGC
XM_032749	KIAA1634	4317	ACCTGAACTAGTGACTATCCC
XM_032749	KIAA1634	4318	ACTTATCTTAAGAGGAGGTCC
XM_045292	KIAA0303	4319	ACAGTGATGAGATCAACTGGC
XM_045292	KIAA0303	4320	ACTCAGTTCTGGCCTACTTCC
XM_045292	KIAA0303	4321	ACATCAATGGAGAACCAGTGC
XM_047080	DKFZP564D0462	4322	ACCCTGCTGTTCCCTGAATCTC
XM_047080	DKFZP564D0462	4323	ACGCAGTGTTGGTTAGCTTGAC
XM_047080	DKFZP564D0462	4324	ACCTATGAGCATTCCTTCAAC
XM_048706	NXP-2	4325	ACTTATGATCCTGATGTGAAC
XM_048706	NXP-2	4326	ACGTTGAGCAAGGTGGTGTTC
XM_048706	NXP-2	4327	ACTGCTGGCTATGATTGTGCC
SK516	SgK496	4328	ACTACACCGGGATCTCTACAC
XM_050147	KIAA0472	4328	ACTACACCGGGATCTCTACAC
SK516	SgK496	4329	ACTCTTGGGCATTGTCCAGCC
XM_050147	KIAA0472	4329	ACTCTTGGGCATTGTCCAGCC
XM_054492	LOC113612	4330	ACAGATGAGGTGTGAGTGGAC
XM_054492	LOC113612	4331	ACTACAGTCAAGATGCTCAGC
XM_054492	LOC113612	4332	ACCATCTTTGGCTACTGTGCC
XM_055551	LOC220763	4333	ACTGAGCCCATTTGACGAGTAC
XM_055551	LOC220763	4334	ACCACATGATCAAGCTAGGTC
XM_058459	LOC120227	4335	ACTAGTTCCAGATCTGAAGCC
SK690	LRRK2	4336	ACTTAGCCTTGGTGCATCTTC
XM_058513	LOC120892	4336	ACTTAGCCTTGGTGCATCTTC
SK690	LRRK2	4337	ACATTGAGACAAGAACAAGCC
XM_058513	LOC120892	4337	ACATTGAGACAAGAACAAGCC
SK690	LRRK2	4338	ACAATCTTCCACATGAAGTGC
XM_058513	LOC120892	4338	ACAATCTTCCACATGAAGTGC
XM_059042	LOC126410	4339	ACTCTTGTCTCTCGCCAATGC

XM_059042	LOC126410	4340	ACTGGCCTATGTGCCCTTCTC
XM_059135	LOC127352	4341	ACATTAACCTCTGCTCTGCTTC
XM_059973	LOC138429	4342	ACTCAACTTTCAGGGCAAGAC
XM_059973	LOC138429	4343	ACAGATGGAAGCTGGATACCAC
XM_059973	LOC138429	4344	ACCTGATAGCCTTCCAACGTC
XM_060772	LOC127993	4345	ACCAGCAAGCTCAGCCATATC
XM_060772	LOC127993	4346	ACAAGCTCAGCCATATCTCCC
XM_061091	LOC118680	4347	ACACATGTGTTCCAGAAGGAC
XM_061091	LOC118680	4348	ACTCGTCTTCATGTTGGACAC
XM_061091	LOC118680	4349	ACAGGGATGGATTCTTGAGAC
XM_061208	LOC118923	4350	ACAACCGTGCTGGTGCTCATC
XM_061208	LOC118923	4351	ACTGCTCTTCTACGTGATGAC
XM_061208	LOC118923	4352	ACAGGACTGGTCATTGTGATC
XM_062692	LOC121554	4353	ACATCACAAGCACATCAAGTC
XM_062692	LOC121554	4354	ACCTGCTAAGGTGGAAGACAC
XM_063677	LOC123482	4355	ACTCCTCTTTGTGGTCTTCTC
XM_063677	LOC123482	4356	ACCCTCATCTACCTTCTGACC
XM_064062	LOC124274	4357	ACTGGAAGAGTCTGTTGATCC
XM_064126	LOC124410	4358	ACACTGAGTGTCTTCCAGGTC
XM_064126	LOC124410	4359	ACTGTGCTGGATTCTGAACAC
XM_064126	LOC124410	4360	ACGCAATGGGCAGTCAATTGC
XM_064900	LOC125980	4361	ACAGGAGGCTCAAAGGAGCAC
XM_064900	LOC125980	4362	ACAGTGACAACATGTTGTCCC
XM_064900	LOC125980	4363	ACTGCTCCATGGAGACGATGC
AB083607	AB083607	4364	ACCACTTAGTGATGAAGTCAC
XM_064908	LOC126022	4364	ACCACTTAGTGATGAAGTCAC
XM_064909	LOC126023	4365	ACAAGATACAAATGCGTGTGC
XM_064909	LOC126023	4366	ACAGTGACAGACATCAGTGGC
XM_065057	LOC126392	4367	ACGCGTTGTTCTGCTCTAACC
XM_065057	LOC126392	4368	ACTGACTGCACCTATGAGAGC
XM_065057	LOC126392	4369	ACCTCAGACCTCTACAGCTTC
XM_065068	LOC126407	4370	ACCTATGCCTTCTATGACAAC
XM_065068	LOC126407	4371	ACAGGAGTGTGAACATCATGC
XM_065069	LOC126408	4372	ACATCATGCACGCCAAATGGC
XM_065069	LOC126408	4373	ACTTCATTGACGTGCTCTTGC
XM_065124	LOC126502	4374	ACCTTTAAATGGTTCTCAACC
XM_065151	LOC126537	4375	ACTTCACTGATGTACTCCTGC
XM_065152	LOC126538	4376	ACTGTCCAGACCACATGGAGC
XM_065152	LOC126538	4377	ACCGGAGGTCTATAATGTATGC
XM_065152	LOC126538	4378	ACTTTGGCTGTGGGTGAAGCC
XM_065294	LOC129566	4379	ACCATGAACCTTTCATGAGGTC
XM_065294	LOC129566	4380	ACATGAACCTTTCATGAGGTCC
XM_065294	LOC129566	4381	ACTGGGCTCCAAGACACTGAC
XM_066397	LOC129223	4382	ACACCAATAGCAGGTGCAGTC
XM_066397	LOC129223	4383	ACTTCTATAAGCTGGATGCCC
XM_066397	LOC129223	4384	ACAGTACCTGGTACTCAGAGC

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XM_066648	LOC139354	4385	ACAATGATGGATTCTACCATC
XM_066648	LOC139354	4386	ACAAGATGGGAATAACAGCAC
XM_066648	LOC139354	4387	ACCTGACATGCATCAGCCTTC
XM_066655	LOC139378	4388	ACTGCCTACCCAGAGTATATC
XM_066655	LOC139378	4389	ACTTATTGAGACCACACCTGC
XM_066655	LOC139378	4390	ACCAATGATGCTACTACAGCC
XM_066809	LOC139649	4391	ACAATGATCAACAGTTCACTC
XM_068298	LOC133342	4392	ACAGTGAGTTGCTATATAGAC
XM_068298	LOC133342	4393	ACTTAGTGGAGCCATGTCTGC
XM_068298	LOC133342	4394	ACAGTCATTCCAACGGTCAGC
AF380189	TA3	4395	ACTACCATACCTCGTTGATGC
XM_069044	LOC134860	4395	ACTACCATACCTCGTTGATGC
XM_070769	LOC138128	4396	ACATCTGTGAGAAGCCACTAC
XM_070769	LOC138128	4397	ACTCATCGGATTCATGGGACC
XM_070769	LOC138128	4398	ACAGCAGATCTCAGTGGTGAC
XM_070869	LOC138342	4399	ACTGGCAAGATCGTGAAGAAC
XM_070869	LOC138342	4400	ACAGTGGATTCTAAGCCACAC
XM_071144	LOC138850	4401	ACCATTATGGCTGTGATAGCC
XM_071222	LOC138967	4402	ACATAAGCACCGTGAGCGACC
XM_071222	LOC138967	4403	ACCACTCTGAATGGCTATTTTC
XM_084421	LOC143098	4404	ACATTTCCAGGAAAGATTGGC
XM_084421	LOC143098	4405	ACCACCAGAGCAAGAAGAAGC
XM_084421	LOC143098	4406	ACTGTGGCATTCAATGAGCTC
XM_087239	LOC151556	4407	ACATTGGCCTGTTCGCTAATC
XM_087526	LOC152805	4408	ACCCTCCTAATGTCTCCTTCC
XM_088463	LOC158056	4409	ACCTCCTATTGCTCATGCTCC
XM_088965	LOC163535	4410	ACAAGCAGAAGAAGTGGGAAGC
XM_088965	LOC163535	4411	ACTGGATGGTGTCTCTTCATCC
XM_088965	LOC163535	4412	ACTTGCAGGAGGACAAGATGC
XM_089093	LOC163720	4413	ACTGGTGATCTCTGCTACAAC
XM_089955	LOC159948	4414	ACAGTGATGACTCTGTCCAGC
XM_089955	LOC159948	4415	ACAGATAGGTGGCCCTATTGC
XM_089955	LOC159948	4416	ACAGAATCTGCAGAAAGCCAC
NM_006018	HM74	4417	ACAGCCAGAATTATCTGGAGC
XM_090326	LOC160484	4417	ACAGCCAGAATTATCTGGAGC
XM_090589	LOC160924	4418	ACAGTGATTCAATTGAGACAGC
XM_090589	LOC160924	4419	ACTTGGGAATGTGAAGGCAAC
XM_090589	LOC160924	4420	ACAAATGTGTGTGGGAAGGTC
XM_090664	LOC161029	4421	ACTTCTCCAACCTGTCTTGC
XM_090664	LOC161029	4422	ACAGCTGCGCAACTTGATTGC
XM_090664	LOC161029	4423	ACTGGTGGGAAGTATAAGGCC
XM_091124	LOC161785	4424	ACTACGAGACAAGCAGAACAC
XM_091124	LOC161785	4425	ACAAGGCTGAGAAGCAGCTTC
XM_091124	LOC161785	4426	ACTCCAGCTCAGTGCTAATC
XM_091358	LOC162106	4427	ACGTAGTATGATCTGGGATTC
XM_092005	LOC163107	4428	ACCATTGCCTATCATGCTTCC

XM_092005	LOC163107	4429	ACTTCTTGACCAGTGATGGGC
XM_092005	LOC163107	4430	ACGTCTTGTGTGTCAGAATTTCC
XM_092299	LOC165002	4431	ACATAACTTGGTGGCCTCGAC
XM_092299	LOC165002	4432	ACGTTTGTCTACCGGAAGATC
XM_092299	LOC165002	4433	ACATTGCAAAGCAACGGTGTC
NM_148962	TG1019	4434	ACACCTACCTCAACAGTGTCC
XM_092406	LOC165140	4434	ACACCTACCTCAACAGTGTCC
XM_093332	LOC165621	4435	ACTGCCTGACTGTGATGTCTC
XM_093332	LOC165621	4436	ACCTTCACCAGGAACATCAGC
XM_093332	LOC165621	4437	ACATCAGGCGTTGGAGAGTAC
XM_093541	LOC165927	4438	ACTCAGCGAGCACATCGAGAC
XM_093541	LOC165927	4439	ACCTGTGGGAGAAACAGAGAC
SK340	RYK	4440	ACACCTAGAATAGTGCTATGC
XM_093692	RYK	4440	ACACCTAGAATAGTGCTATGC
NM_002958	RYK	4441	ACGGGTGCTTGAGTTGTTGTC
SK340	RYK	4441	ACGGGTGCTTGAGTTGTTGTC
XM_093692	RYK	4441	ACGGGTGCTTGAGTTGTTGTC
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XM_094015	LOC166680	4443	ACGTGTAGTGATTTATACCAC
XM_094015	LOC166680	4444	ACTGTTGTGTTTCATTGATGGC
XM_094471	LOC167417	4445	ACTTCGTCTACCTCTTCTTCC
XM_094471	LOC167417	4446	ACACCTCATTATCACCATGC
XM_094471	LOC167417	4447	ACCTTCATTATCACCATGCTC
XM_095787	LOC158067	4448	ACTGTTCTACAGGAACCTCAGC
XM_095787	LOC158067	4449	ACATACACAGTCTTCGAATAC
XM_095780	LOC169572	4450	ACACTAAGTGGCTACTGTCC
XM_095797	LOC169596	4450	ACACTAAGTGGCTACTGTCC
XM_095811	LOC169614	4451	ACAATCATGGAGCAGAATCCC
XM_095811	LOC169614	4452	ACAGGCTCCCTATTCTGTAGC
XM_095811	LOC169614	4453	ACAGTCGCAATGCACTTCCTC
XM_096824	LOC145624	4454	ACTTGCTGAGATGTGTTAGGC
XM_099810	LOC159203	4455	ACTCAGAAGAACTCATGGTC
XM_099810	LOC159203	4456	ACAGCACACCTGACTCACCAC
XM_099810	LOC159203	4457	ACTGAGCCCTCCTCTTATCCC
XM_103864	LOC165245	4458	ACCTTGCTCTTGACGGTGTAC
XM_103864	LOC165245	4459	ACCTGGTTATTGGCGGGTATC
XM_104192	LOC164193	4460	ACACGCGTGTTCCATTTCCAC
XM_104192	LOC164193	4461	ACAGTGCTGATCTGGGTCCAC
XM_106412	LOC166981	4462	ACTCATCCACCTCAGTATGGC
XM_106412	LOC166981	4463	ACATCATCTCTTCTCAAGGCC
XM_106412	LOC166981	4464	ACAGTTCAAGAAGGTGGCTCC
XM_108766	LOC169451	4465	ACCCATCTCACTGTTGACTTC
XM_108766	LOC169451	4466	ACATGCTCCTCAATTGTCCTC
XM_108766	LOC169451	4467	ACCCAACATACTTCCCTTGCC
XM_113849	LOC197259	4468	ACAGTCTTTGGAATCGTCCTC
XM_114099	LOC200047	4469	ACCAGGAAGTGGAAGGGTAC

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XM_114099	LOC200047	4470	ACAGCAATAGGAAATGGAGTC
SK169	HIPK1	4471	ACACTAATGGTAGCAACTCTC
XM_114729	KIAA0630	4471	ACACTAATGGTAGCAACTCTC
SK169	HIPK1	4472	ACAGCAATGATTCCAGAGGCC
XM_114729	KIAA0630	4472	ACAGCAATGATTCCAGAGGCC
SK169	HIPK1	4473	ACATGGCAACCAGTACAGCAC
XM_114729	KIAA0630	4473	ACATGGCAACCAGTACAGCAC
XM_114839	LOC200121	4474	ACGGTGTCTCTCTCCAAGCTC
XM_114839	LOC200121	4475	ACAAGTGTCTTGGGCTGTGTGC
XM_114839	LOC200121	4476	ACATCCTTGGCTACCTCAGAC
XM_115647	LOC199783	4477	ACGTGTCTGACTTTGAGGAGC
XM_115806	LOC205360	4478	ACCTGTTCCTGTTACTGTCCC
XM_115806	LOC205360	4479	ACCCAGATGACCAATGAGACC
XM_115806	LOC205360	4480	ACCATACACGGCTTGATCAGC
XM_116437	LOC206296	4481	ACCTCCTTGTCCCATAAGTAC
XM_116437	LOC206296	4482	ACTGAGCTCGTTATTGGGTAC
XM_116437	LOC206296	4483	ACCACAGAGCACTTCATCTCC
XM_119808	LOC205081	4484	ACCTCTGAGGACCACTCACAC
XM_119808	LOC205081	4485	ACAACGACTGTCCACCCACAC
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XM_166215	LOC220000	4487	ACTTCCACCTACCAGTCCACC
XM_166215	LOC220000	4488	ACCTTCCTGTATTATGCTCCC
XM_166215	LOC220000	4489	ACCATTGCCAACATCCAGAGC
XM_171463	LOC254524	4489	ACCATTGCCAACATCCAGAGC
XM_166354	LOC221395	4490	ACTCTATAGGTCCTACAAGAC
XM_166354	LOC221395	4491	ACTGGAACAACAGTCATCTAC
XM_166354	LOC221395	4492	ACCGGACCCAATTTCTGTTTC
XM_166408	KIAA0708	4493	ACCTGATCCGATGGAGTGTCC
XM_166408	KIAA0708	4494	ACTCTCAATGACCTGCTCAAC
XM_166408	KIAA0708	4495	ACTGAGATGAAGGAGGCAGCC
XM_166676	LOC219756	4496	ACTGGGCACACATCTCCAGTC
XM_166676	LOC219756	4497	ACTACGAAGGCCCTGAAGTTC
XM_166676	LOC219756	4498	ACAGCAGGAACATCTCTTCGC
XM_166742	LOC219896	4499	ACAGGGAATTGAGGATGATGC
XM_166794	LOC220328	4500	ACGCTCGGTGACTACCCTTTC
XM_166794	LOC220328	4501	ACAGTCGCATAGCAGAGTCAC
XM_166937	LOC220056	4502	ACAGCTGGTAGAGAAATTAGC
XM_166937	LOC220056	4503	ACCACAGCAATGGGAAAGAAC
XM_167315	LOC223048	4504	ACAGCAGAAAGAAGTGAAGCC
XM_167315	LOC223048	4505	ACATTAACCTTGGTGGTGGTCC
XM_167315	LOC223048	4506	ACACAAAGAGCTTGCTTACAC
XM_167317	LOC223053	4507	ACAGGCTAGCTACAAGAGATC
XM_167317	LOC223053	4508	ACTAATGCCTGCAACTGATCC
XM_167317	LOC223053	4509	ACCCAGACCAGAAGTTAGTTC
XM_167325	LOC223058	4510	ACCTCAGCATAGACAGATACC
XM_167325	LOC223058	4511	ACCTTCCTGGTGTACTTCATC

XM_167325	LOC223058	4512	ACAGCTGGTATTCTCAGAAGC
XM_169246	LOC220075	4513	ACAACCTGGCCCTAATGCTGC
XM_169439	LOC222487	4514	ACTTTGTGCTTCACCAAGTGC
XM_169439	LOC222487	4515	ACCATGATCTTCTCTGGCCTTC
XM_169439	LOC222487	4516	ACAGCCTGTTCTCTCTGAATC
XM_170778	LOC255195	4517	ACCATGTCTTCTCTGTACGGC
XM_170815	LOC256412	4518	ACCTTGACCTCTTCAGAAAGC
XM_170927	LOC253152	4519	ACAAACCACTTATGCTGCTGC
XM_170927	LOC253152	4520	ACTGCTCAGCTGTTGAAATCC
XM_171251	LOC255928	4521	ACAGAATACAAGGGCTGGATC
XM_171251	LOC255928	4522	ACTGCAGTTACCATAAGGAGC
XM_171251	LOC255928	4523	ACCTGTGATATTGGAACCTTC
XM_171276	LOC254817	4524	ACCTTCAATGACCTCAACTAC
XM_171276	LOC254817	4525	ACACTCCTCCACCTTTGATAC
XM_171337	LOC253989	4526	ACAAGAACCTTCTGGAAATCC
XM_171337	LOC253989	4527	ACTCACCTTGTGACTATGTC
XM_171337	LOC253989	4528	ACCTCAGCCATGAGAAGATTC
SK601	Obscn	4529	ACCACTTCATCAACACCAAGC
XM_171360	LOC255984	4529	ACCACTTCATCAACACCAAGC
XM_171360	LOC255984	4530	ACTCTGCATCTGATCACAACC
XM_171360	LOC255984	4531	ACTTTGCCCAAGAACTCTTCC
XM_171416	LOC256669	4532	ACCCAAGCAGATGCTCAAAGC
XM_171416	LOC256669	4533	ACCTAAGGAGGCTCGGAAATC
XM_171416	LOC256669	4534	ACATCTGCGCCATAAATTACC
XM_166215	LOC220000	4535	ACCGACATCGTCTTCACCATC
XM_171463	LOC254524	4535	ACCGACATCGTCTTCACCATC
XM_171536	LOC255309	4536	ACTTCTACCACTTCAGCTTCC
XM_171536	LOC255309	4537	ACTTACTGTCCAGTGTTCTGC
XM_171536	LOC255309	4538	ACTTCTACTGGAGCCTGCAGC
NM_001618	ADPRT	4539	ACCTGTTGGGAGAAGTTGCCC
XM_171663	LOC254927	4539	ACCTGTTGGGAGAAGTTGCCC
XM_171714	LOC253050	4540	ACGGATCAGAGAACACTAGCC
XM_171714	LOC253050	4541	ACTGGCTGCTCAATTGCTTCC
XM_171714	LOC253050	4542	ACATGTATGCCAGCATCTTCC
XM_171793	LOC257170	4543	ACTGCATAGGACTCAAGTGTC
XM_171793	LOC257170	4544	ACTAAAGTCTGGGCAGAAATC
XM_171793	LOC257170	4545	ACCTTAAGACACCATGGTTTC
XM_171967	LOC256991	4546	ACCTCATGACCTTGGATAGTC
XM_172003	LOC253809	4547	ACACAGACAGGGTTGATTGCC
XM_172034	LOC254337	4548	ACTTATCCACTTCTCTGATTC
XM_172116	LOC254665	4549	ACTCTCTGAAGGACTGGTAAC
XM_172160	LOC254796	4550	ACATTATGGCCTTCTTAGGGC
XM_172160	LOC254796	4551	ACCAGATGTATCTGCCAGGAC
XM_172160	LOC254796	4552	ACCATGCGGCTAGGAAAGGAC
XM_172181	LOC255782	4553	ACATGGACCTGACCTGCATTC
XM_172318	LOC253806	4554	ACTCTCTAGCAACTTGAAGGC

XM_172318	LOC253806	4555	ACGTCAGTTAGGACCTTGTCC
XM_172318	LOC253806	4556	ACCATTCCTTGTGTGCATTC
XM_172333	LOC255434	4557	ACTTTGCTTGCTTAGCAGTAC
XM_172333	LOC255434	4558	ACAGTTGCCAACACATAGGCC
XM_172351	LOC254325	4559	ACCATGGAGTGTCTAGATCC
XM_172356	LOC256424	4560	ACAGACCCTTCCAAGTTGGAC
XM_172356	LOC256424	4561	ACATCCTGCTGCATTGTGACC
AF411117	GPR103	4562	ACTGGTGTCTACGTGGTGAC
XM_172359	LOC253900	4562	ACTGGTGTCTACGTGGTGAC
XM_172359	LOC253900	4563	ACACTCAGCTATGATGATACC
XM_172359	LOC253900	4564	ACTGCAGAGTGGAGAGATAAC
XM_172523	LOC256135	4565	ACCTGCACAGTCAACACGGTC
XM_172523	LOC256135	4566	ACTGTGGCTGGACTTCACATC
XM_172523	LOC256135	4567	ACAGCTGTCTCAATCCAGTTC
XM_172524	LOC256138	4568	ACAGCTGAACTTGTACTGTTC
XM_172597	LOC256727	4569	ACCACCTCAAGTCAACTAGGC
XM_172597	LOC256727	4570	ACCTCCCTTATTATTGGCAGC
XM_172605	LOC255992	4571	ACTGAGGATCTGAGCATGACC
XM_172779	LOC256841	4572	ACAATTATACATGTGAGAGGC
XM_172781	LOC253491	4572	ACAATTATACATGTGAGAGGC
XM_172779	LOC256841	4573	ACTTATAGCCTGTAAGGCTAC
XM_172781	LOC253491	4573	ACTTATAGCCTGTAAGGCTAC
XM_172779	LOC256841	4574	ACTGTTCTGGGATTCTTGACC
XM_172781	LOC253491	4574	ACTGTTCTGGGATTCTTGACC
NG_001025	NG_001025	4575	ACTGTTTGCAGACAAGTTTCC
XM_064449	LOC125110	4575	ACTGTTTGCAGACAAGTTTCC
XM_064968	LOC126170	4575	ACTGTTTGCAGACAAGTTTCC
XM_065541	LOC130040	4575	ACTGTTTGCAGACAAGTTTCC
XM_066617	LOC139318	4575	ACTGTTTGCAGACAAGTTTCC
XM_067531	LOC131748	4575	ACTGTTTGCAGACAAGTTTCC
XM_116396	LOC202227	4575	ACTGTTTGCAGACAAGTTTCC
XM_172784	LOC253265	4575	ACTGTTTGCAGACAAGTTTCC
XM_172784	LOC253265	4576	ACAGCATTGCTGACTGCAGAC
XM_172789	LOC254989	4577	ACTCACTCCTCTTTCTGACCC
XM_173397	LOC253080	4578	ACCAACCAAGCACTGTCTGGC
XM_173397	LOC253080	4579	ACTGGCCCTCTTCTCATACC
XM_173397	LOC253080	4580	ACAGATAACCTCCTCTAGCTC
XM_174353	LOC257260	4581	ACGGCTCTGTCAAGGCCATTC
XM_174353	LOC257260	4582	ACTTGAGGGTTATATGAGCGC
XM_174554	LOC256999	4583	ACCAACATCTCTCAGTGAACC
XM_174554	LOC256999	4584	ACCAGAGACAAGTTATAGCTC
XM_174554	LOC256999	4585	ACAGAACCTGAACTCATTCC
NM_000103	CYP19	4586	ACTCAGACAGGTGTCTGGAAC
NM_031226	CYP19	4586	ACTCAGACAGGTGTCTGGAAC
NM_000498	CYP11B2	4587	ACCACGTGCTGAAGCACTTCC
NM_000499	CYP1A1	4588	ACACAGTGATTGGCAGGTCAC

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NM_000499	CYP1A1	4589	ACCAGAAGCTATGGGTCAACC
NM_000500	CYP21A2	4590	ACCGTGAGATTTCAGCAGCGAC
NG_000004	NG_000004	4591	ACTCAGATTATTCCCAGTTGC
NM_000765	CYP3A7	4591	ACTCAGATTATTCCCAGTTGC
NM_000777	CYP3A5	4591	ACTCAGATTATTCCCAGTTGC
NM_000766	CYP2A13	4592	ACCATCATGCAGAACTTTTCGC
U22028	HSU22028	4592	ACCATCATGCAGAACTTTTCGC
NG_000008	NG_000008	4593	ACCAGCTTCCGAGGGTACATC
NM_000767	CYP2B6	4593	ACCAGCTTCCGAGGGTACATC
NM_000777	CYP3A5	4594	ACACACCCCTTTGGAAGTGGAC
NM_000779	CYP4B1	4595	ACCTGCAGGAAGCCTGATCTC
NM_000781	CYP11A	4596	ACCGTGGCATGCTCTACAGAC
NM_000781	CYP11A	4597	ACATGGCCACGATGCTACAGC
NM_000896	CYP4F3	4598	ACAGCCATTGCCAGGAGAAGC
NM_001082	CYP4F2	4599	ACCATGTGCATGAAGGAGAGC
NM_006668	CYP46	4600	ACCTTCTTCATTGCTGGTCAC
NM_019885	P450RAI-2	4601	ACTCCAACCAGAACGAGATCC
NM_023944	CYP4F12	4602	ACACCTTCATGTTTGGAGGCC
NM_023944	CYP4F12	4603	ACATTGTTCTCCCAGATGGCC
NM_030984	TBXAS1	4604	ACCTTCAACCCTGAAAGGTAC
XM_065068	LOC126407	4605	ACACCTTCATGTTTGCAGGCC
NM_003242	TGFBR2	4606	ACCATGACTGCTAGTGCTCAC
NM_000167	GK	4607	ACGCTATTGGTGTGCAACC
NM_000167	GK	4608	ACGACAGGCCTTCCACTTAGC
NM_000167	GK	4609	ACGGAGTCGGCGTATGGAGTC
NM_000180	GUCY2D	4610	ACCAAGGGCCGGAAGACGAAC
NM_000180	GUCY2D	4611	ACCATGTCACTGGACATCCTC
NM_000289	PFKM	4612	ACGCGTGGGATCACCATCTC
NM_000289	PFKM	4613	ACGCAGTTTGATGAGCTCTGC
NM_000289	PFKM	4614	ACGCTGCCGTCTAAACCTCTC
NM_000294	PHKG2	4615	ACCCAGGTCCATCATGCGGTC
NM_000294	PHKG2	4616	ACGAATGCACTGTTGAGGGAC
NM_000294	PHKG2	4617	ACCTGTGCCTTCCGGCTCTAC
NM_000617	SLC11A2	4618	ACCCCTGCCTATAGTAATCCC
NM_000720	CACNA1D	4619	ACATGCAGCATCAACGGCAGC
NM_000720	CACNA1D	4620	ACAGAAACAGAAGGCGGGAAC
NM_000720	CACNA1D	4621	ACAGTCCTCTTGGCTCTGTTT
NM_000725	CACNB3	4622	ACGTAGAGAGCCAGGCTCAGC
NM_000725	CACNB3	4623	ACAGCAGGCGGAACATGTTCC
NM_000726	CACNB4	4624	ACAGAGGGCTGTGAAATTGGC
NM_000726	CACNB4	4625	ACCCAGTAGCACACCCATGAC
NM_000906	NPR1	4626	ACGGACGAGTATGCGCTGACC
NM_000906	NPR1	4627	ACCAGCAGCAACATCCTGGAC
NM_000933	PLCB4	4628	ACTGAATCAGTCGGTCTTGGC
NM_001522	GUCY2F	4629	ACGTTCTGTGGTGCTTGTGC
NM_001522	GUCY2F	4630	ACTGTCTCCAGCTGATGAAGC

NM_001665	ARHG	4631	ACACAGATCCACGCTGTGCGC
NM_000350	ABCA4	4632	ACACCACCACCTTGTCATCC
NM_000061	BTK	4633	ACGAGGCAGTAAGAAGGGTTC
NM_000061	BTK	4634	ACGCTGGTGCAGTTGTATGGC
NM_000061	BTK	4635	ACGTTTCAGCAGCAAATCTGAC
NM_000076	CDKN1C	4636	ACTTTAGAGCCCAAAGAGCCC
NM_000492	CFTR	4637	ACACTCTGTTCACAAAGCTC
NM_001348	DAPK3	4638	ACCATCATCACCTGCACGAC
NM_001348	DAPK3	4639	ACGCGCATCGCACACTTTGAC
NM_000788	DCK	4640	ACTAAGAGCTCAGCTTGCTC
NM_000788	DCK	4641	ACATGAAGAGCAAGGCATTCC
NM_000788	DCK	4642	ACCATGAAAGCTGGCTCCTGC
NM_001365	DLG4	4643	ACCTCAGGTCTGGGCTTCAGC
NM_001365	DLG4	4644	ACGAATGCGGGTCAGACGGTC
NM_001365	DLG4	4645	ACCAGCCACCTCTATGGGACC
NM_001433	ERN1	4646	ACGGAGACAGAGGCCAAGAGC
NM_001433	ERN1	4647	ACGATGGACTGGCGGGAGAAC
NM_000154	GALK1	4648	ACGGGAGTGATTCACTACTAC
NM_000154	GALK1	4649	ACCTCTAATGTCCGCCACTCC
NM_000222	KIT	4650	ACCCGTCTCCACCATCCATCC
NM_000222	KIT	4651	ACATGGGAGTTTCCCAGAAAC
NM_000431	MVK	4652	ACCATTGGTATCAAGCGGGCC
NM_000431	MVK	4653	ACGCTAAAGGAGGTTGCAGGC
NM_000431	MVK	4654	ACCCAGCACCATCTGAATGCC
NM_000459	TEK	4655	ACGCCTTAATGAACCAGCACC
NM_000459	TEK	4656	ACGGCAAGAATGAAGACCAGC
NM_000459	TEK	4657	ACACTTGGACACCATCCAAAC
NM_001895	CSNK2A1	4658	ACAGACCCTGTGTACGAACC
NM_001895	CSNK2A1	4659	ACGCGATGGGAACGCTTTGTC
NM_001895	CSNK2A1	4660	ACACTGCTGCGATATGACCAC
NM_001896	CSNK2A2	4661	ACAGCTCTGGATTACTGCCAC
NM_001896	CSNK2A2	4662	ACCTATGACCAGCTTGTTCGC
NM_001896	CSNK2A2	4663	ACGACTGGAAAGCGACGGGTC
NM_002020	FLT4	4664	ACGTACATCAAGGCACGCATC
NM_002020	FLT4	4665	ACGCACTGCCACAAGAAGTAC
NM_002020	FLT4	4666	ACGACGGGCTACCTGTCCATC
NM_002037	FYN	4667	ACGGAGATTGGTGGGAAGCCC
NM_002613	PDPK1	4668	ACTCGGTTCAATCGATGAGAC
NM_002613	PDPK1	4669	ACTCTCCTGAGCCAGTTTGGC
NM_002613	PDPK1	4670	ACGGTGAAATTCTTGGTCAC
NM_003010	MAP2K4	4671	ACGACCTTGGAGAAATTGGAC
NM_003010	MAP2K4	4672	ACTGCGGAGTAGTGATTGCCC
NG_001305	NG_001305	4673	ACGTCGTGAAAGGAGATCCTC
NM_003010	MAP2K4	4673	ACGTCGTGAAAGGAGATCCTC
NM_003158	STK6	4674	ACATTCTTCCCAGCGCGTTCC
NM_003158	STK6	4674	ACATTCTTCCCAGCGCGTTCC

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NM_003600	STK6	4674	ACATTCTTCCCAGCGCGTTCC
NM_003600	STK6	4674	ACATTCTTCCCAGCGCGTTCC
SK407	AurA	4674	ACATTCTTCCCAGCGCGTTCC
SK407	AurA	4674	ACATTCTTCCCAGCGCGTTCC
NM_003158	STK6	4675	ACTTGCAGGCAACCAGTGTAC
NM_003158	STK6	4675	ACTTGCAGGCAACCAGTGTAC
NM_003600	STK6	4675	ACTTGCAGGCAACCAGTGTAC
NM_003600	STK6	4675	ACTTGCAGGCAACCAGTGTAC
SK407	AurA	4675	ACTTGCAGGCAACCAGTGTAC
SK407	AurA	4675	ACTTGCAGGCAACCAGTGTAC
NM_003158	STK6	4676	ACATACAGTCCCACCTTCGGC
NM_003158	STK6	4676	ACATACAGTCCCACCTTCGGC
NM_003600	STK6	4676	ACATACAGTCCCACCTTCGGC
NM_003600	STK6	4676	ACATACAGTCCCACCTTCGGC
SK407	AurA	4676	ACATACAGTCCCACCTTCGGC
SK407	AurA	4676	ACATACAGTCCCACCTTCGGC
NM_003159	STK9	4677	ACATGCTTCGGACTCTCAAGC
NM_003159	STK9	4678	ACCAGCAGATCTCAGCAGAAC
NM_003159	STK9	4679	ACATGAGGGAACGCTGGACTC
NM_000217	KCNA1	4680	ACCGAGTACTTCTTCGACCGC
NM_002232	KCNA3	4680	ACCGAGTACTTCTTCGACCGC
NM_002234	KCNA5	4680	ACCGAGTACTTCTTCGACCGC
NM_002235	KCNA6	4680	ACCGAGTACTTCTTCGACCGC
NM_014379	KCNV1	4680	ACCGAGTACTTCTTCGACCGC
NM_002234	KCNA5	4681	ACGGCCAAGAGCAACGTGGAC
D16105	HUMLTKLP2	4682	ACCCACGGAGAGGTAGAGATC
NM_002344	LTK	4682	ACCCACGGAGAGGTAGAGATC
SK209	LTK	4682	ACCCACGGAGAGGTAGAGATC
X52213	HSLTKM	4682	ACCCACGGAGAGGTAGAGATC
X60702	HSLTK	4682	ACCCACGGAGAGGTAGAGATC
D16105	HUMLTKLP2	4683	ACCCTCTGCCATCAGGACAGC
NM_002344	LTK	4683	ACCCTCTGCCATCAGGACAGC
SK209	LTK	4683	ACCCTCTGCCATCAGGACAGC
X52213	HSLTKM	4683	ACCCTCTGCCATCAGGACAGC
X60702	HSLTK	4683	ACCCTCTGCCATCAGGACAGC
D16105	HUMLTKLP2	4684	ACCCTCAGAACCTTTGGAATC
NM_002344	LTK	4684	ACCCTCAGAACCTTTGGAATC
SK209	LTK	4684	ACCCTCAGAACCTTTGGAATC
X52213	HSLTKM	4684	ACCCTCAGAACCTTTGGAATC
X60702	HSLTK	4684	ACCCTCAGAACCTTTGGAATC
M79321	HUMLYNTK	4685	ACGCCAACCTCATGAAGACCC
NM_002350	LYN	4685	ACGCCAACCTCATGAAGACCC
M79321	HUMLYNTK	4686	ACCTAATGCCGACGTGATGAC
NM_002350	LYN	4686	ACCTAATGCCGACGTGATGAC
M79321	HUMLYNTK	4687	ACAGGCAGAAGAGAGACCAAC
NM_002350	LYN	4687	ACAGGCAGAAGAGAGACCAAC

NM_002447	MST1R	4688	ACCTCTGTCTGTGTGCCTTC
NM_002447	MST1R	4689	ACAGGCCACTTTGGAGTTGTC
NM_002447	MST1R	4690	ACGGACCTCATCAGCTTTGGC
NM_002530	NTRK3	4691	ACATTGTGTCTGCAGCAAGAC
NM_002530	NTRK3	4692	ACCTGCAGCTGTGACATCCGC
NM_002530	NTRK3	4693	ACCAAGCCCACCCACTACAAC
NM_002591	PCK1	4694	ACAGAGACACAGTGCCCATCC
NM_002591	PCK1	4695	ACGGCATTATCTTTGGAGGCC
NM_002591	PCK1	4696	ACCTTCGGCAAATACCTGGCC
NM_002625	PFKFB1	4697	ACCATGGAAGCCCTGCAAATC
NM_002625	PFKFB1	4698	ACTGAGATTGATGCGGGTGTC
NM_002625	PFKFB1	4699	ACGCCTGAGAATGTGGACATC
NM_002730	PRKACA	4700	ACACACAAGGAGACCGGGAAC
NM_002730	PRKACA	4701	ACGCTGTCAACTTTCCGTTCC
NM_002730	PRKACA	4702	ACGTGGTTTGCCACAAC TGAC
NM_002734	PRKAR1A	4703	ACAGCAGGCACTCGTACAGAC
NM_002734	PRKAR1A	4704	ACGACAATGGCCGCTTTAGCC
NM_002734	PRKAR1A	4705	ACGAATCCTCATGGGAAGCAC
NM_002736	PRKAR2B	4706	ACACCGATT CACAAGGCGTGC
NM_002736	PRKAR2B	4707	ACTGTACAATACACCCAGAGC
NM_002736	PRKAR2B	4708	ACTCATTGCTCAGGGAGATT C
NM_002737	PRKCA	4709	ACATCCACACTTACGGAAGCC
NM_002737	PRKCA	4710	ACATCCGCAGTGGAATGAGTC
NM_002737	PRKCA	4711	ACACTGGAGAACAGGGAGATC
NM_002742	PRKCM	4712	ACGACTTTCAGATTCTGTC
NM_002742	PRKCM	4713	ACAGTGCCGCACACATTTGTC
NM_002742	PRKCM	4714	ACTGTGGTCAATCCTTCCAGC
NM_002760	PRKY	4715	ACGGTGATGAGCATTC
NM_002760	PRKY	4716	ACGTCTGTCTCTGAAGGAAGTC
NM_005044	PRKX	4716	ACGTCTGTCTCTGAAGGAAGTC
NM_002929	RHOK	4717	ACGAAGTACCTGGCCAAGCTC
NM_002929	RHOK	4718	ACAGTACACAGCAGGTTTCATC
NM_002929	RHOK	4719	ACTTTGCCACTGGCAACTGCC
NM_003257	TJP1	4720	ACGGAGATAGTGTGGGTTTGC
NM_003257	TJP1	4721	ACGGCTTAGAGGAAGGTGATC
NM_003257	TJP1	4722	ACGAAGTGACCATATTGGCTC
NM_003258	TK1	4723	ACGTATGCCAAAGACACTCGC
NM_003258	TK1	4724	ACGCCGCCTATACCAAGAGGC
NM_003258	TK1	4725	ACCTCTCCTTTGTGTGGCTGC
NM_003318	TTK	4726	ACGCAATTGAAGCGCTTCCCC
SK383	TTK	4726	ACGCAATTGAAGCGCTTCCCC
NM_003318	TTK	4727	ACATGCTGGAAATTGCCCTGC
SK383	TTK	4727	ACATGCTGGAAATTGCCCTGC
NM_003318	TTK	4728	ACGACACCAAGCAGCAATACC
SK383	TTK	4728	ACGACACCAAGCAGCAATACC
NM_003328	TXK	4729	ACGAAGCAATCCAACACGGGC

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NM_003328	TXK	4730	ACTCCCAAGCAACTATGTGAC
NM_003328	TXK	4731	ACGTTCCCAATCAAGTGGTCC
NM_003331	TYK2	4732	ACGAAGACCAGCTTCAAGGAC
NM_003331	TYK2	4733	ACAGTGCTGGACCCTAGTCAC
NM_003331	TYK2	4734	ACTGTGTGTGGCCGGAACATC
NM_001827	CKS2	4735	ACGTACTTCGACGAACACTAC
NM_001827	CKS2	4736	ACCAGAGTCTAGGCTGGGTTC
NM_002747	MAPK4	4737	ACGCCCCGCAACATCTTCATC
NM_002747	MAPK4	4738	ACCTACACCAAAGCCATCGAC
NM_002747	MAPK4	4739	ACGATCCTGACCTTTAACCCC
NM_002578	PAK3	4740	ACGAGCGCCCAGAGATCTCTC
NM_002578	PAK3	4741	ACTGAGCCACCACCAGTTATC
NM_002578	PAK3	4742	ACATGGTGGAAGGTGAACCCC
NM_003384	VRK1	4743	ACGTAGGATTACCCATTGGCC
NM_003384	VRK1	4744	ACCCCACTGACAATGGACCTC
NM_003384	VRK1	4745	ACTTCACGAGCATCGATGCAC
NM_003496	TRRAP	4746	ACATTGTCCAGCAGAGACTGC
SK380	TRRAP	4746	ACATTGTCCAGCAGAGACTGC
NM_003496	TRRAP	4747	ACCACATCCTCACCACAGAGC
SK380	TRRAP	4747	ACCACATCCTCACCACAGAGC
NM_003551	NME5	4748	ACGTGATTGTTGAGCCCATTG
NM_003551	NME5	4749	ACCTCTGCTTGAAGGACTCAC
NM_003551	NME5	4750	ACCCCAAACCTTTGTCACCATC
NM_003557	PIP5K1A	4751	ACGACCTATGCACCTGTTGCC
NM_003557	PIP5K1A	4752	ACGGCTCAACCTACAAACGGC
NM_003557	PIP5K1A	4753	ACAGTTTCGGTCTGGCTCATC
NM_003558	PIP5K1B	4754	ACACACTTCAGAGAGACTGCC
NM_003558	PIP5K1B	4755	ACACGGTGCAATTCAATCGCC
NM_003558	PIP5K1B	4756	ACCAGCAAAGGGTTACCTTCC
NM_003607	PK428	4757	ACTGCTTTACGGAGAAACACC
SK299	MRCKa	4757	ACTGCTTTACGGAGAAACACC
NM_003607	PK428	4758	ACGGATCTTATTCTGAAGGCTC
SK299	MRCKa	4758	ACGGATCTTATTCTGAAGGCTC
NM_003607	PK428	4759	ACGAGTCAACACAGACTGTCC
SK299	MRCKa	4759	ACGAGTCAACACAGACTGTCC
AF035582	AF035582	4760	ACTTCACAGGGATGTGAAGCC
NM_003688	CASK	4760	ACTTCACAGGGATGTGAAGCC
SK064	CASK	4760	ACTTCACAGGGATGTGAAGCC
AF035582	AF035582	4761	ACGGAGGAAACTAAAGGGTGC
NM_003688	CASK	4761	ACGGAGGAAACTAAAGGGTGC
SK064	CASK	4761	ACGGAGGAAACTAAAGGGTGC
NM_003688	CASK	4762	ACTGGTCATAGCAGCACTAAC
AF035582	AF035582	4763	ACCTGCAGGTCTCATTCTTC
NM_003688	CASK	4763	ACCTGCAGGTCTCATTCTTC
SK064	CASK	4763	ACCTGCAGGTCTCATTCTTC
NM_003985	TNK1	4764	ACGTCTAAGAACTGGGTCTAC

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SK375	TNK1	4764	ACGTCTAAGAACTGGGTCTAC
NM_003985	TNK1	4765	ACGAGTGTCCAGTGGCTGTC
SK375	TNK1	4765	ACGAGTGTCCAGTGGCTGTC
NM_003985	TNK1	4766	ACCCTCAAGGTAGATCAGCTC
SK375	TNK1	4766	ACCCTCAAGGTAGATCAGCTC
NM_004333	BRAF	4767	ACTACCACAGGAAGAGGCGTC
NM_004333	BRAF	4768	ACAGTGGCATGGTGATGTGGC
NM_004333	BRAF	4769	ACGAGATTAATGGCAGAGTGC
AF212224	AF212224	4770	ACGCGCTGCAAATACAATCAC
NM_004071	CLK1	4770	ACGCGCTGCAAATACAATCAC
AF212224	AF212224	4771	ACGGATGTGAACCTGGACATC
NM_004071	CLK1	4771	ACGGATGTGAACCTGGACATC
AF212224	AF212224	4772	ACGTTGTGGAGTGCATCGATC
NM_004071	CLK1	4772	ACGTTGTGGAGTGCATCGATC
NM_004071	CLK1	4773	ACCATGAGCGTCTCTTTGACC
NM_004383	CSK	4774	ACGGTGGAGCACTACCGCATC
NM_004383	CSK	4775	ACACCAAAGGTCATGGAGGGC
NM_004383	CSK	4776	ACGTCTGACGTGTGGAGTTTC
NM_004384	CSNK1G3	4777	ACTCAAGAGCACCACAGCTAC
NM_004384	CSNK1G3	4778	ACCAGAGAAGCACATCAACAC
NM_004384	CSNK1G3	4779	ACTCATCTCTGTAGTGACCAC
NM_004431	EPHA2	4780	ACGTACCTGGCCAACATGAAC
NM_004431	EPHA2	4781	ACCCACGAGGTGATGAAAGCC
NM_004431	EPHA2	4782	ACAGCCATCAATGATGGCTTC
NM_004566	PFKFB3	4783	ACGAAGCTGACTCGCTACCTC
NM_004566	PFKFB3	4784	ACGCAGTACAGCTCCTACAAC
NM_004566	PFKFB3	4785	ACATGCCCTCTTCACACCGTC
NM_004157	PRKAR2A	4786	ACTCACTAGAGGTGTCAGAAC
NM_004157	PRKAR2A	4787	ACGGATGGAGAACGCATAATC
NM_004157	PRKAR2A	4788	ACCCAGGAGGTCGAGATTGCC
NM_004586	RPS6KA3	4789	ACCTGTGGAGTATATGGCTCC
NM_004586	RPS6KA3	4790	ACGATTCACCTGGCATTCCAC
NM_004586	RPS6KA3	4791	ACGACAAGGCTATGATGCTGC
NM_004612	TGFBR1	4792	ACCTGGGTCTGTGACTACAAC
NM_004612	TGFBR1	4793	ACGAAAGCATTGGCAAAGGTC
NM_004612	TGFBR1	4794	ACGGAAAGCCAGCCATTGCTC
NM_004614	TK2	4795	ACGTGGAGAAATGTCCGTGGC
NM_004614	TK2	4796	ACTCCTCTGGGCCTGATGTAC
NM_004614	TK2	4797	ACTACCTGGAAGCAATTACCC
NM_004747	DLG5	4798	ACAGATTGCCTGTTTGTGCGAC
NM_004747	DLG5	4799	ACGCGGAGAAGCGGCCATTTTC
NM_004747	DLG5	4800	ACGAGCARTTTGAGGCGGCGC
NM_004817	TJP2	4801	ACCAGTACACTGTGACCCTAC
NM_004963	GUCY2C	4802	ACTGGCAGCTATGAAATCAGC
NM_004963	GUCY2C	4803	ACACTGTTGGGAGGAAGATCC
NM_005027	PIK3R2	4804	ACGGTCTATCACCAGCAGTAC

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NM_005027	PIK3R2	4805	ACGATCCGAGACCAGTACCTC
NM_005027	PIK3R2	4806	ACGGAGCTGGTGCTGCACTAC
NM_005044	PRKX	4807	ACGGTGATGAGCATTCTGAC
NM_005044	PRKX	4808	ACAGAGATCGTCTACAGGGAC
NM_005044	PRKX	4809	ACGCTCACGGACTTTGGGTTC
XM_090977	LOC161559	4809	ACGCTCACGGACTTTGGGTTC
NM_005211	CSF1R	4810	ACGCTTGCTAATGCTACCACC
NM_005248	FGR	4811	ACAGGTGCCTACTCCCTGTCC
NM_005372	MOS	4812	ACGCAAGTGAACAAGTGCACC
NM_005372	MOS	4813	ACAGCATTTGTGCACTTGGACC
NM_005424	TIE	4814	ACGGTCACACACACTGTGAAC
NM_005424	TIE	4815	ACGGACGGGCTGAAGATGAAC
NM_005424	TIE	4816	ACTGTGCTGGTCGGAGAGAAC
L05186	HUMFAK	4817	ACGAAGGTGAACGGGCTTTGC
L13616	HUMFAKX	4817	ACGAAGGTGAACGGGCTTTGC
NM_005607	PTK2	4817	ACGAAGGTGAACGGGCTTTGC
SK138	FAK	4817	ACGAAGGTGAACGGGCTTTGC
L05186	HUMFAK	4818	ACAGCTCAGCTCAGCACAATC
L13616	HUMFAKX	4818	ACAGCTCAGCTCAGCACAATC
NM_005607	PTK2	4818	ACAGCTCAGCTCAGCACAATC
SK138	FAK	4818	ACAGCTCAGCTCAGCACAATC
L05186	HUMFAK	4819	ACAGCTGTCATCGAGATGTCC
L13616	HUMFAKX	4819	ACAGCTGTCATCGAGATGTCC
NM_005607	PTK2	4819	ACAGCTGTCATCGAGATGTCC
SK138	FAK	4819	ACAGCTGTCATCGAGATGTCC
NM_003954	MAP3K14	4820	ACTAGCCAAGAGTTTCAGCCCC
NM_003954	MAP3K14	4821	ACCTCCACAACTGATCAGCC
NM_003954	MAP3K14	4822	ACTACCTAGTGCATGCTCTGC
NM_004299	ABCB7	4823	ACAGGCTCTCCAGGTATGGCC
NM_004304	ALK	4824	ACGAGTCTGGCAGTTGACTTC
NM_004304	ALK	4825	ACCTGCAGTGAAGGAACATCC
NM_004304	ALK	4826	ACGAACACCATGATGCGGTCC
NM_004517	ILK	4827	ACTGGAACCCTGAACAAACAC
NM_004517	ILK	4828	ACTTTCGTCGTGGACCAGAGC
NM_004517	ILK	4829	ACGAAGCCTGAAGACACAAAC
NM_004938	DAPK1	4830	ACAGGAGGACTAAGTCCAGCC
NM_004938	DAPK1	4831	ACGACTTCTGGTCAAGGATCC
NM_004938	DAPK1	4832	ACAGCCATCATCCATGCCATC
NM_005160	ADRBK2	4833	ACTGAGGAAGACCGCCTTTGC
NM_005160	ADRBK2	4834	ACACTTCTGAGAGGTACAGC
NM_005160	ADRBK2	4835	ACTGTGGAACCTTCCAGACACC
NM_005793	NM23-H6	4836	ACTCCGAGCCTACATCCTTGC
NM_005793	NM23-H6	4837	ACCACCACCCATGGTTCCGAC
NM_005627	SGK	4838	ACACACCCTGAAGTTCAGTCC
NM_005627	SGK	4839	ACTGGTGGAGAGTTGTTCTAC
NM_005627	SGK	4840	ACCCCAAATGTGAGTGGGCCC

NM_005975	PTK6	4841	ACGAAGCTGCGGCACAAACAC
NM_005975	PTK6	4842	ACGGAGGACGTCTACCTCTCC
NM_005975	PTK6	4843	ACATGTGGAGTGTCTGCGTCC
NM_006343	MERTK	4844	ACTGTCACCAGAAACACAGCC
NM_006343	MERTK	4845	ACGACCATGAAGTTGGACAAC
NM_006343	MERTK	4846	ACTGAGCTCTCAAGGCATCCC
NM_006212	PFKFB2	4847	ACGAAACTAACACGCTACCTC
NM_006212	PFKFB2	4848	ACCAGAGTCCAGGACTACATC
NM_006212	PFKFB2	4849	ACGCCAACTAACAACCTCCCC
NM_006213	PHKG1	4850	ACCATCATACAGCTGAAGGAC
NM_006213	PHKG1	4851	ACCCAGAAAGATCATGCGAGC
XM_054871	LOC154966	4851	ACCCAGAAAGATCATGCGAGC
NM_006213	PHKG1	4852	ACAGAGGTGGACATGTGGAGC
NM_006213	PHKG1	4853	ACGGACCTGGTCTCCCGATTC
XM_054871	LOC154966	4853	ACGGACCTGGTCTCCCGATTC
XM_061691	LOC119794	4853	ACGGACCTGGTCTCCCGATTC
NM_006218	PIK3CA	4854	ACGCTGTGGATCTTAGGGATC
NM_006218	PIK3CA	4855	ACGAGTACCTTGTTCCAATCC
NM_006218	PIK3CA	4856	ACCCTGAACAGGCTATGGAAC
XM_066258	LOC128944	4856	ACCCTGAACAGGCTATGGAAC
NM_006251	PRKAA1	4857	ACTATGTCTCAGGAGGAGAGC
NM_006251	PRKAA1	4858	ACGAGTACCATTCTTGGTTGC
NM_006251	PRKAA1	4859	ACTCAGGGACTGCTACTCCAC
NM_006252	PRKAA2	4860	ACTGTCCTGTTGGATGCACAC
NM_006252	PRKAA2	4861	ACCCAAGCCAGTGAGTTCTAC
NM_006252	PRKAA2	4862	ACTCCGAAGTCAGAGCAAACC
NM_006255	PRKCH	4863	ACGCAGAAGACCAACAAACCC
NM_006255	PRKCH	4864	ACCATCCCACACAAGTTCAGC
NM_006255	PRKCH	4865	ACTAGAACCGCCTTTTCAGACC
NM_006257	PRKCQ	4866	ACGGGAAGAGTCATGCAGATC
NM_006257	PRKCQ	4867	ACTAGCCGAGAAACCATGTTC
NM_006257	PRKCQ	4868	ACGAGAGTTCTTTCTTGGCC
NM_006258	PRKG1	4869	ACCTTGGAGCTGTGCGAGATC
NM_006258	PRKG1	4870	ACGACTCACCAGGTGAAGACC
NM_006258	PRKG1	4871	ACCCTGAAGCTGTCTGATTTTC
NM_006259	PRKG2	4872	ACCAAGTGCATCCAGCTGAAC
NM_006259	PRKG2	4873	ACGGACTGCCTCTGTGAAAGC
NM_006259	PRKG2	4874	ACCATGGACATTCTGTGGGAC
NM_006282	STK4	4875	ACGTTCCCTGTGGAATCAGACC
NM_006282	STK4	4876	ACATGGCTGAAGGAAAGCCCC
NM_006282	STK4	4877	ACGAGTTGGACAGTGGAGGAC
NM_006293	TYRO3	4878	ACAGCTTTCCAGCAGCAACGC
NM_006293	TYRO3	4879	ACGGAGAGTTTGGTTCAGTGC
NM_006293	TYRO3	4880	ACGGAGTTTGACCATCCACAC
NM_006296	VRK2	4881	ACACTTCCCTGGGAACAGAAC
NM_006296	VRK2	4882	ACGGCTGCAACAAAGCAAGTC

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NM_006296	VRK2	4883	ACAGTCCACAGTGAGAGAAGC
NM_020547	AMHR2	4884	ACACTGGTTGCCATCAAGGCC
NM_006871	RIPK3	4885	ACGTTGAGTTGCCAACCGAAC
NM_006871	RIPK3	4886	ACCTGAATCTAGAGGAGCCTC
NM_006871	RIPK3	4887	ACATCCAGTAACAGGGCGACC
NM_007118	TRIO	4888	ACGATCCTGCAGGAGTCCTTC
NM_012145	DTYMK	4889	ACGTGACGTGGAGGATCACTC
NM_012145	DTYMK	4890	ACAGTTGAGCCAGGGCGTGAC
NM_012145	DTYMK	4891	ACGCTGTCCATGAGGAACTCC
NM_014370	STK23	4892	ACAGACTACTGCAAGGGCGGC
NM_014370	STK23	4893	ACGATCATCCACACGGACATC
NM_014370	STK23	4894	ACGAGGAAGAAGATGAGGCGC
NM_014496	RPS6KA6	4895	ACAGAAGACCGGTCTTGATGC
NM_014496	RPS6KA6	4896	ACCGGGAGGCTAGTGATATAC
NM_014496	RPS6KA6	4897	ACTGTTGGCTGGCTACACTCC
NM_016440	LOC51231	4898	ACAGTGAAATGGTCCAGCACC
NM_016440	LOC51231	4899	ACGCTGAAGTCCTTCCAGACC
NM_016440	LOC51231	4900	ACCAAGTGGAAGAAGCTGTAC
NM_016231	LOC51701	4901	ACCGTCTTCCAGAATCTGGTC
NM_016231	LOC51701	4902	ACGGCGCTAAGGCACATATAC
NM_016231	LOC51701	4903	ACGAATATCCGCTAAGGATGC
NM_007188	ABCB8	4904	ACGTCATCCTTCAAGCTTGTC
NM_007188	ABCB8	4905	ACGAAAGGCGGGCTATACGCC
NM_000352	ABCC8	4906	ACTGCCACTGTGGAGGAGAAC
NM_005692	ABCF2	4907	ACTCACCTGGATATCGAGACC
NM_012093	AK5	4908	ACCCGCCTTCTCCAAAGGAGC
NM_012093	AK5	4909	ACGCGCCTAGAAGCCTACTAC
NM_012093	AK5	4910	ACTCCTGACAGCACTGTTTGC
NM_013276	CARKL	4911	ACGTCTCATCTCAGTGTGGCC
NM_013276	CARKL	4912	ACCGTAAAGACACTGAGGAGC
NM_013276	CARKL	4913	ACTGTGCTGGCCACGTTCTGTC
NM_006182	DDR2	4914	ACCACATACTCAGTGCCCTGCC
NM_021120	DLG3	4915	ACTGGCAGTGATGGCATGTTC
NM_021133	RNASEL	4916	ACCGAAGATGTTGACCTGGTC
NM_021133	RNASEL	4917	ACTGACACAGACAGTGATGGC
NM_005246	FER	4918	ACGGCCAAGGAACGATACGAC
NM_005246	FER	4919	ACGAGGATACCGGATGTCAGC
NM_002759	PRKR	4920	ACATGCCGCAGCCAAATTAGC
NM_002759	PRKR	4921	ACCTTTGCGATACATGAGCCC
NM_002759	PRKR	4922	ACAGGAAGTGGACCTCTACGC
NM_001347	DGKQ	4923	ACGCGCAAGTTCTGTGCTGTC
NM_001347	DGKQ	4924	ACCCCTCATCAGGTCTTCGAC
NM_001347	DGKQ	4925	ACCTACTGTGGCATTTGGCATC
NM_000594	TNF	4926	ACGCCCTGGTATGAGCCCATC
NM_000594	TNF	4927	ACTCGGCCCGACTATCTCGAC
NM_000594	TNF	4928	ACCGGAGGCTGAACAATAGGC

NM_003646	DGKZ	4929	ACATTTCCGCTGTAAGCCGTC
NM_003646	DGKZ	4930	ACCCAGGGTGCAAAGATCATC
NM_003646	DGKZ	4931	ACCAACTACTTCAGCCTGGGC
L00727	HUMPROK	4932	ACGATCATGAACAAGTGGGAC
NM_004409	DMPK	4932	ACGATCATGAACAAGTGGGAC
SK111	DMPK1	4932	ACGATCATGAACAAGTGGGAC
L00727	HUMPROK	4933	ACATGTTCTATGGGCAGACGC
NM_004409	DMPK	4933	ACATGTTCTATGGGCAGACGC
SK111	DMPK1	4933	ACATGTTCTATGGGCAGACGC
NM_004409	DMPK	4934	ACCTTCGCCAGTCAACTACGC
SK111	DMPK1	4934	ACCTTCGCCAGTCAACTACGC
M18391	HUMTKR	4935	ACGATGGGTGGAGTGAACAGC
NM_005232	EPHA1	4935	ACGATGGGTGGAGTGAACAGC
XM_056982	EPHA1	4935	ACGATGGGTGGAGTGAACAGC
M18391	HUMTKR	4936	ACGACTGTGGCCATTAAGACC
NM_005232	EPHA1	4936	ACGACTGTGGCCATTAAGACC
XM_056982	EPHA1	4936	ACGACTGTGGCCATTAAGACC
M18391	HUMTKR	4937	ACACCTGTGCTGCAAGGTGTC
NM_005232	EPHA1	4937	ACACCTGTGCTGCAAGGTGTC
XM_056982	EPHA1	4937	ACACCTGTGCTGCAAGGTGTC
NM_003647	DGKE	4938	ACTGACACCAAGGTCCTGGAC
NM_003647	DGKE	4939	ACGCTTTGCGATTACAGGTGC
NM_003647	DGKE	4940	ACGCCCTACAACCTCTGTACTC
NM_001346	DGKG	4941	ACGCAAGCACCAGCTGAAGAC
NM_001346	DGKG	4942	ACCTCCTCCGTCAAGTGTGAC
NM_001346	DGKG	4943	ACTGACCTTGCCCGTTGTCTC
NM_002744	PRKCZ	4944	ACGTGAGAGACATGTGTCGTC
NM_002744	PRKCZ	4945	ACAGAGCTGGTGCATGATGAC
NM_002744	PRKCZ	4946	ACCGAGCACTTTCTGCGGAAC
NM_014413	HRI	4947	ACGGGAAGTAGCCTTGGAAGC
NM_014413	HRI	4948	ACGAACACAGACTGGACCAAC
NM_014413	HRI	4949	ACCTGGTCAGTTGCCGGAATC
NM_004783	TAO1	4950	ACTAGTGAGGTGGTGGCCATC
NM_016151	PSK	4950	ACTAGTGAGGTGGTGGCCATC
NM_004783	TAO1	4951	ACACATCCTGCTGTCAGAGCC
NM_016151	PSK	4951	ACACATCCTGCTGTCAGAGCC
NM_004783	TAO1	4952	ACCCGAGACCACTTTGCCACC
NM_016151	PSK	4952	ACCCGAGACCACTTTGCCACC
NM_005109	OSR1	4953	ACAGATGAGCTGTGGCTTGTC
NM_005109	OSR1	4954	ACAGACCAACAGCAGCAGAAC
NM_005109	OSR1	4955	ACTTGTGGAAGAACCCTCAGTC
NM_002627	PFKP	4956	ACTGATTTCTGCGGCACCGAC
NM_002627	PFKP	4957	ACGTACTTGGAAGAGATCGCC
NM_002627	PFKP	4958	ACCACTATCACCGACACCTGC
NM_005734	HIPK3	4959	ACAGGTCATAGCAGCTCAGGC
NM_005734	HIPK3	4960	ACTGCTTTCAGCACCGTAACC

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NM_005734	HIPK3	4961	ACGACCTATGTTACAGCATCC
NM_001345	DGKA	4962	ACATGGGATCCTGGACAGCTC
NM_001345	DGKA	4963	ACCCTGTCCCTAGAAGGCATC
NM_001345	DGKA	4964	ACGTGCTCTGAGATCACCTTC
NM_004996	ABCC1	4965	ACTCGGATCAAGCTGATGAAC
NM_019862	ABCC1	4965	ACTCGGATCAAGCTGATGAAC
NM_019898	ABCC1	4965	ACTCGGATCAAGCTGATGAAC
NM_019899	ABCC1	4965	ACTCGGATCAAGCTGATGAAC
NM_019900	ABCC1	4965	ACTCGGATCAAGCTGATGAAC
NM_019901	ABCC1	4965	ACTCGGATCAAGCTGATGAAC
NM_019902	ABCC1	4965	ACTCGGATCAAGCTGATGAAC
NM_004996	ABCC1	4966	ACGGCCATCGGACTCTTCATC
NM_019862	ABCC1	4966	ACGGCCATCGGACTCTTCATC
NM_019898	ABCC1	4966	ACGGCCATCGGACTCTTCATC
NM_019899	ABCC1	4966	ACGGCCATCGGACTCTTCATC
NM_019900	ABCC1	4966	ACGGCCATCGGACTCTTCATC
NM_019901	ABCC1	4966	ACGGCCATCGGACTCTTCATC
NM_019902	ABCC1	4966	ACGGCCATCGGACTCTTCATC
NM_005691	ABCC9	4967	ACTCTGAAACCTGCAGAGGCC
NM_020297	ABCC9	4967	ACTCTGAAACCTGCAGAGGCC
NM_020298	ABCC9	4967	ACTCTGAAACCTGCAGAGGCC
NM_005691	ABCC9	4968	ACTCTTACCACAACCTTCTC
NM_020297	ABCC9	4968	ACTCTTACCACAACCTTCTC
NM_020298	ABCC9	4968	ACTCTTACCACAACCTTCTC
NM_001786	CDC2	4969	ACCACTCTGGTACAGATCTCC
NM_033379	CDC2	4969	ACCACTCTGGTACAGATCTCC
NM_001786	CDC2	4970	ACCCAGGAAGCCTAGCATCCC
NM_033379	CDC2	4970	ACCCAGGAAGCCTAGCATCCC
NM_001786	CDC2	4971	ACATGGCTTGATTTGCTCTC
NM_033379	CDC2	4971	ACATGGCTTGATTTGCTCTC
NM_000020	ACVRL1	4972	ACCATCCTAGGCTTCATCGCC
NM_006285	TESK1	4973	ACGTGCAGCTGATGAACCGGC
NM_006285	TESK1	4974	ACTCTGACTCGAGTCAACCCC
NM_006285	TESK1	4975	ACCTTCATCAGCACCTGTTCC
NM_007170	TESK2	4976	ACCAGTTGCTAGACAGTAACC
XM_032399	TESK2	4976	ACCAGTTGCTAGACAGTAACC
NM_007170	TESK2	4977	ACCTGCTGTAACATGGATCCC
XM_032399	TESK2	4977	ACCTGCTGTAACATGGATCCC
NM_007170	TESK2	4978	ACGACGTACCATCTGGCTGTC
XM_032399	TESK2	4978	ACGACGTACCATCTGGCTGTC
NM_004670	PAPSS2	4979	ACTGATGGGCTGGACCAATAC
NM_003215	TEC	4980	ACCCTACTATGAGGGTCGAGC
NM_003215	TEC	4981	ACACAAAGAAGCGAAGGCCTC
NM_003215	TEC	4982	ACAGGGAAGAATGCACCCACC
NM_000221	KHK	4983	ACCTCCTGCACCGTTCTCTCC
NM_006488	KHK	4983	ACCTCCTGCACCGTTCTCTCC

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NM_000221	KHK	4984	ACGTGGATCCACATTGAGGGC
NM_006488	KHK	4984	ACGTGGATCCACATTGAGGGC
NM_000221	KHK	4985	ACGATGCTGCAGCGGATAGAC
NM_006488	KHK	4985	ACGATGCTGCAGCGGATAGAC
NM_001123	ADK	4986	ACGTGGCTCAGTGGATGATTC
NM_006721	ADK	4986	ACGTGGCTCAGTGGATGATTC
NM_001123	ADK	4987	ACAGGTGGCTCACCATGCTTC
NM_006721	ADK	4987	ACAGGTGGCTCACCATGCTTC
NM_001123	ADK	4988	ACCTGGTCTCTGACAAGCCTC
NM_006721	ADK	4988	ACCTGGTCTCTGACAAGCCTC
NM_001625	AK2	4989	ACTTCAGCATCCCAGACTCTC
NM_013411	AK2	4989	ACTTCAGCATCCCAGACTCTC
NM_002314	LIMK1	4990	ACACCTGTCTTGAGGAGCTGC
NM_002314	LIMK1	4991	ACGAGCATGGACAGCCAGTAC
NM_016735	LIMK1	4991	ACGAGCATGGACAGCCAGTAC
NM_002314	LIMK1	4992	ACCATCATCCACCGAGACCTC
NM_016735	LIMK1	4992	ACCATCATCCACCGAGACCTC
U63721	HSU63721	4992	ACCATCATCCACCGAGACCTC
NM_001292	CLK3	4993	ACGGTGGTGGAGTGCTTGGAC
NM_003992	CLK3	4993	ACGGTGGTGGAGTGCTTGGAC
NM_001292	CLK3	4994	ACTAACTCCAGCCTTACCCC
NM_003992	CLK3	4994	ACTAACTCCAGCCTTACCCC
NM_001292	CLK3	4995	ACGTCAGTGAAGAACACCAGC
NM_003992	CLK3	4995	ACGTCAGTGAAGAACACCAGC
NM_001291	CLK2	4996	ACGACCCTGACAACAAGAACC
NM_003993	CLK2	4996	ACGACCCTGACAACAAGAACC
NM_001291	CLK2	4997	ACCAACTACCTGCCCTACCCC
NM_003993	CLK2	4997	ACCAACTACCTGCCCTACCCC
NM_005569	LIMK2	4998	ACAGAGGTCAACCGGATGCAC
NM_016733	LIMK2	4998	ACAGAGGTCAACCGGATGCAC
NM_005569	LIMK2	4999	ACTTCGATGTGATGAGGAGAC
NM_016733	LIMK2	4999	ACTTCGATGTGATGAGGAGAC
NM_005569	LIMK2	5000	ACGACTGTGGTGGTGGCAGAC
NM_016733	LIMK2	5000	ACGACTGTGGTGGTGGCAGAC
NM_005688	ABCC5	5001	ACTGCCACCTTGGCATGGGAC
NM_001625	AK2	5002	ACGAGTGGCCGTTCTACCAC
NM_013411	AK2	5002	ACGAGTGGCCGTTCTACCAC
XM_086211	LOC148505	5002	ACGAGTGGCCGTTCTACCAC
NM_004996	ABCC1	5003	ACTGGCATGCTGGTGACGGAC
NM_019862	ABCC1	5003	ACTGGCATGCTGGTGACGGAC
NM_019898	ABCC1	5003	ACTGGCATGCTGGTGACGGAC
NM_019899	ABCC1	5003	ACTGGCATGCTGGTGACGGAC
NM_019900	ABCC1	5003	ACTGGCATGCTGGTGACGGAC
NM_019901	ABCC1	5003	ACTGGCATGCTGGTGACGGAC
NM_019902	ABCC1	5003	ACTGGCATGCTGGTGACGGAC
NM_002011	FGFR4	5004	ACGCACCCTACTGGACACACC

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NM_022963	FGFR4	5004	ACGCACCCTACTGGACACACC
NM_002011	FGFR4	5005	ACTAGCTCAGAGGTGGAGGTC
NM_022963	FGFR4	5005	ACTAGCTCAGAGGTGGAGGTC
NM_002011	FGFR4	5006	ACTGTGCTGGTGACTGAGGAC
NM_022963	FGFR4	5006	ACTGTGCTGGTGACTGAGGAC
NM_000141	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_022969	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_022972	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_022973	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_022974	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_022975	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_023028	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_023029	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_023030	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_023031	FGFR2	5007	ACTCGCCTGTATGGTGGTAAC
NM_000141	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_022969	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_022970	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_022972	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_022973	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_022974	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_022975	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_023028	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_023029	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_023030	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_023031	FGFR2	5008	ACATCTTCTTGGAGCCTGCAC
NM_000141	FGFR2	5009	ACTACTTGGACCTCAGCCAAC
NM_022969	FGFR2	5009	ACTACTTGGACCTCAGCCAAC
NM_022970	FGFR2	5009	ACTACTTGGACCTCAGCCAAC
NM_022972	FGFR2	5009	ACTACTTGGACCTCAGCCAAC
NM_023028	FGFR2	5009	ACTACTTGGACCTCAGCCAAC
NM_023029	FGFR2	5009	ACTACTTGGACCTCAGCCAAC
NM_023030	FGFR2	5009	ACTACTTGGACCTCAGCCAAC
NM_023031	FGFR2	5009	ACTACTTGGACCTCAGCCAAC
NM_000141	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_022969	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_022970	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_022971	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_022972	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_022973	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_022974	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_022976	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_023028	FGFR2	5010	ACGAGCCACCAACCAAAATACC
NM_000141	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_022969	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_022972	FGFR2	5011	ACCACGACCAAGAAGCCAGAC

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NM_022973	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_022974	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_022975	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_023028	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_023029	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_023030	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_023031	FGFR2	5011	ACCACGACCAAGAAGCCAGAC
NM_006852	TLK2	5012	ACCTAGCCAAGGGAAAGGCAC
XM_166672	LOC220231	5012	ACCTAGCCAAGGGAAAGGCAC
NM_006852	TLK2	5013	ACGGCGTTTATTTCGACGATGC
NM_006852	TLK2	5014	ACTTGAGACTGACTCCAAGGC
NM_004972	JAK2	5015	ACACGGTGGAATTCAGTGGTC
NM_004972	JAK2	5016	ACAGTGAGACACTGACAGAAC
NM_004972	JAK2	5017	ACGTACAAGGGAGTGTGCTAC
NM_002739	PRKCG	5018	ACGTCTGCAGCTTTGTGGTTC
NM_002739	PRKCG	5019	ACCTGAAGCTCATCCCAGACC
NM_002739	PRKCG	5020	ACGTCTGTGCGATTGGTGGTCC
NM_006904	PRKDC	5021	ACATGGGCCAGAAGATCGCAC
NM_006904	PRKDC	5022	ACGAAGAGTCTCTGGTGGAAAC
NM_006904	PRKDC	5023	ACCGGCATGTTAGACCAGAGC
NM_005906	MAK	5024	ACGTTGTTCCCTGAATCAGTC
NM_005906	MAK	5025	ACGAAACGACCGACAGCAAGC
NM_005906	MAK	5026	ACCCCTCCAAAGCAACAGAGTC
NM_003718	CDC2L5	5027	ACCCGTTGGGAGGAATTCAGC
NM_031267	CDC2L5	5027	ACCCGTTGGGAGGAATTCAGC
NM_003718	CDC2L5	5028	ACTTCAGCCTTCTTCTCAGAC
NM_031267	CDC2L5	5028	ACTTCAGCCTTCTTCTCAGAC
NM_004759	MAPKAPK2	5029	ACTGTTTGGACGGTGGAGAAC
NM_032960	MAPKAPK2	5029	ACTGTTTGGACGGTGGAGAAC
NM_004759	MAPKAPK2	5030	ACCATTGCCCCATCGGGATGTC
NM_032960	MAPKAPK2	5030	ACCATTGCCCCATCGGGATGTC
NM_004759	MAPKAPK2	5031	ACGTATGACAAGTCCTGTGAC
NM_032960	MAPKAPK2	5031	ACGTATGACAAGTCCTGTGAC
NM_004635	MAPKAPK3	5032	ACGTGCTGGAGTGCTTCCATC
NM_004635	MAPKAPK3	5033	ACGCGCTGTCTCCTCATCATC
NM_004635	MAPKAPK3	5034	ACAGACCACTGGGACGAAGTC
NM_006575	MAP4K5	5035	ACTGGTGGCTACAACCAACTC
NM_006575	MAP4K5	5036	ACACCTTTCAGCTCTACTCTC
NM_006575	MAP4K5	5037	ACCACAGTTGGAGAGAGATAC
NM_002755	MAP2K1	5038	ACGCTGGAAGAATTCTTGAAC
NM_002755	MAP2K1	5039	ACGCCCTCCAACATCCTAGTC
NM_002755	MAP2K1	5040	ACACTGCCCAGTGGAGTGTTT
NM_014922	DEFCAP	5041	ACATCAGAGAAAGGCAGGCCC
NM_033004	DEFCAP	5041	ACATCAGAGAAAGGCAGGCCC
NM_033005	DEFCAP	5041	ACATCAGAGAAAGGCAGGCCC
NM_033006	DEFCAP	5041	ACATCAGAGAAAGGCAGGCCC

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NM_033007	DEFCAP	5041	ACATCAGAGAAAGGCAGGCC
NM_014922	DEFCAP	5042	ACTTGGGAAGTCAACACTGGC
NM_033004	DEFCAP	5042	ACTTGGGAAGTCAACACTGGC
NM_033005	DEFCAP	5042	ACTTGGGAAGTCAACACTGGC
NM_033006	DEFCAP	5042	ACTTGGGAAGTCAACACTGGC
NM_033007	DEFCAP	5042	ACTTGGGAAGTCAACACTGGC
NM_014922	DEFCAP	5043	ACGATGGACTCTACCAAGCCC
NM_033004	DEFCAP	5043	ACGATGGACTCTACCAAGCCC
NM_033005	DEFCAP	5043	ACGATGGACTCTACCAAGCCC
NM_033006	DEFCAP	5043	ACGATGGACTCTACCAAGCCC
NM_033007	DEFCAP	5043	ACGATGGACTCTACCAAGCCC
NM_006201	PCTK1	5044	ACCTGGAGACCTACATTAAGC
NM_033018	PCTK1	5044	ACCTGGAGACCTACATTAAGC
NM_033019	PCTK1	5044	ACCTGGAGACCTACATTAAGC
NM_006201	PCTK1	5045	ACGGACCTCAAACACGCCAAC
NM_033018	PCTK1	5045	ACGGACCTCAAACACGCCAAC
NM_033019	PCTK1	5045	ACGGACCTCAAACACGCCAAC
NM_006201	PCTK1	5046	ACCGAGGAGTTCAAGACATAC
NM_033018	PCTK1	5046	ACCGAGGAGTTCAAGACATAC
NM_033019	PCTK1	5046	ACCGAGGAGTTCAAGACATAC
NM_033214	GKP2	5047	ACGGATGGGTGGAACAAGACC
NM_033214	GKP2	5048	ACGCTGTTGGTGTGAGCAATC
NM_033214	GKP2	5049	ACGATATATCTCGGGTGTGCC
NM_001715	BLK	5050	ACCACCTGGATGAAGACAAGC
NM_001715	BLK	5051	ACGGAGCCCATCTACATTGTC
NM_001715	BLK	5052	ACGGCTGATTGACATGTCGGC
NM_016308	UMP-CMPK	5053	ACAGGAAGAAGCCAGATTAC
NM_016308	UMP-CMPK	5054	ACTGGATCAGACAATGGCTGC
NM_016308	UMP-CMPK	5055	ACTTCAGACCTACCTTCAGTC
NM_018979	PRKWINK1	5056	ACGGCCGTGGGAATGTCTAAC
NM_018979	PRKWINK1	5057	ACAGGTCTGGACACTGAAACC
NM_018979	PRKWINK1	5058	ACGACCATGGCTAAAGCTATC
NM_018979	PRKWINK1	5059	ACCCTGAGGCAGATCAACATC
NM_018979	PRKWINK1	5060	ACCAGCTTCCAGTTTCCCAGC
NM_001204	BMPR2	5061	ACACTGTTGGAGCTGATTGGC
NM_033346	BMPR2	5061	ACACTGTTGGAGCTGATTGGC
NM_001204	BMPR2	5062	ACATAGCCTGGCAGTGAGGTC
NM_033346	BMPR2	5062	ACATAGCCTGGCAGTGAGGTC
NM_001204	BMPR2	5063	ACCGACAGCAAGCACAAGCTC
NM_001204	BMPR2	5064	ACCCCAATATGCCAATGGGAC
NM_033346	BMPR2	5065	ACTGAACGTAGGTGAGTCAAC
NM_002646	PIK3C2B	5066	ACCAATTGCCAGGCAAAGTGC
NM_002646	PIK3C2B	5067	ACGGACTCTCAGTTCAGCATC
NM_002646	PIK3C2B	5068	ACGTTACGGGCTCAGATGAC
NM_002732	PRKACG	5069	ACGATGAAGCAGGTGAGCAC
SK302	PKACg	5069	ACGATGAAGCAGGTGAGCAC

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NM_002732	PRKACG	5070	ACGGACAACCTCCTACCTGTAC
SK302	PKACg	5070	ACGGACAACCTCCTACCTGTAC
NM_002732	PRKACG	5071	ACGGTGGAAGCTCCCTTCATC
SK302	PKACg	5071	ACGGTGGAAGCTCCCTTCATC
NM_022128	RBSK	5072	ACAGGTGCCAACCAGTGTGTC
NM_022128	RBSK	5073	ACGGATGTGTGGTGCTGTCAC
NM_022128	RBSK	5074	ACAGTCAAGGCTGTGGATACC
NM_022048	CSNK1G1	5075	ACTCACGTGCTCCACAGCTTC
SK647	CK1g1	5075	ACTCACGTGCTCCACAGCTTC
NM_022048	CSNK1G1	5076	ACGACGGTGTTAATGATAGCC
SK647	CK1g1	5076	ACGACGGTGTTAATGATAGCC
NM_022048	CSNK1G1	5077	ACCAACTCAGCCATCTGGCAG
NM_000189	HK2	5078	ACAGTAACGGACAATGGGCTC
NM_000189	HK2	5079	ACAGGCTTCAAGGCATCTGGC
NM_000189	HK2	5080	ACGCTACATCCTCACTTTGCC
NM_002821	PTK7	5081	ACGACATGCCGCTATTTGAGC
NM_002821	PTK7	5082	ACGCAGTTCTTGAGGATTTCC
NM_002821	PTK7	5083	ACCCGCTTTGTGCATAAGGAC
NM_003137	SRPK1	5084	ACATGGAGAAAGAGTCGGGCC
SK358	SRPK1	5084	ACATGGAGAAAGAGTCGGGCC
NM_003137	SRPK1	5085	ACATGGAGACAGCAGCACATC
SK358	SRPK1	5085	ACATGGAGACAGCAGCACATC
NM_003137	SRPK1	5086	ACTTTGGCCTTGGTTGGGCTC
NM_000162	GCK	5087	ACGAGGCCAGTGTGAAGATGC
NM_033507	GCK	5087	ACGAGGCCAGTGTGAAGATGC
NM_033508	GCK	5087	ACGAGGCCAGTGTGAAGATGC
NM_000162	GCK	5088	ACGACATCGATAAGGGCATCC
NM_033507	GCK	5088	ACGACATCGATAAGGGCATCC
NM_033508	GCK	5088	ACGACATCGATAAGGGCATCC
NM_000162	GCK	5089	ACTGGTGAATGACACGGTGGC
NM_033507	GCK	5089	ACTGGTGAATGACACGGTGGC
NM_033508	GCK	5089	ACTGGTGAATGACACGGTGGC
NM_032409	PINK1	5090	ACGCCACCATGCCTACATTGC
NM_032409	PINK1	5091	ACCATCCTTGTGGAGCTGGAC
NM_032409	PINK1	5092	ACCCTGGAGTGTGAAACGCTC
NM_000188	HK1	5093	ACCACCAGTGATGTGTCAGCC
NM_033496	HK1	5093	ACCACCAGTGATGTGTCAGCC
NM_033497	HK1	5093	ACCACCAGTGATGTGTCAGCC
NM_033498	HK1	5093	ACCACCAGTGATGTGTCAGCC
NM_033500	HK1	5093	ACCACCAGTGATGTGTCAGCC
NM_000188	HK1	5094	ACAGGAGAGAGGAATTTGACC
NM_033496	HK1	5094	ACAGGAGAGAGGAATTTGACC
NM_033497	HK1	5094	ACAGGAGAGAGGAATTTGACC
NM_033498	HK1	5094	ACAGGAGAGAGGAATTTGACC
NM_033500	HK1	5094	ACAGGAGAGAGGAATTTGACC
NM_000188	HK1	5095	ACTGTGACTGTGGGAGTGGAC

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NM_033496	HK1	5095	ACTGTGACTGTGGGAGTGGAC
NM_033497	HK1	5095	ACTGTGACTGTGGGAGTGGAC
NM_033498	HK1	5095	ACTGTGACTGTGGGAGTGGAC
NM_033500	HK1	5095	ACTGTGACTGTGGGAGTGGAC
NM_002115	HK3	5096	ACGCCAGGAGTTTGTGATCCC
NM_002115	HK3	5097	ACGGGTTTCAAGGCATCAGAC
NM_002115	HK3	5098	ACGATGATCAGCGGCATGTAC
NM_031432	UCK1	5099	ACGGCCTTGAAAGGACAGTAC
NM_031432	UCK1	5100	ACCCTGATCGTGCAGCACATC
NM_031432	UCK1	5101	ACACGGTCACATTTGGAGTCC
NM_002577	PAK2	5102	ACGACCCTTTGTGAGCCAATC
NM_002577	PAK2	5103	ACAGTTCTACGACTCCAACAC
NM_002577	PAK2	5104	ACCGCCATACTGGATGGCACC
NM_002748	MAPK6	5105	ACTGGTACAGATCTCCACGTC
NM_002748	MAPK6	5106	ACGCACTGGATTTCTGGAAC
NM_002748	MAPK6	5107	ACGGAATGGCAAATCTGGCTC
NM_032387	PRKWINK4	5108	ACTGACAGAGTGGTTGAGTGC
NM_032387	PRKWINK4	5109	ACTGAAGAGCTCCAGAGCAGC
NM_032387	PRKWINK4	5110	ACGGAGATGATGGGAAGGAAC
NM_020439	CAMK1G	5111	ACCATTGTGACCCTGGAGGAC
NM_020439	CAMK1G	5112	ACGTGGAGGCAAGCCTTCAAC
NM_020439	CAMK1G	5113	ACAGGAAAGTCCTCCTACTGC
AB012305	AB012305	5114	ACGCTGCTGGATGTCATTAC
NM_001798	CDK2	5114	ACGCTGCTGGATGTCATTAC
NM_052827	CDK2	5114	ACGCTGCTGGATGTCATTAC
AB012305	AB012305	5115	ACTTCATGGATGCCTCTGCTC
NM_001798	CDK2	5115	ACTTCATGGATGCCTCTGCTC
NM_052827	CDK2	5115	ACTTCATGGATGCCTCTGCTC
NM_001798	CDK2	5116	ACCTTGCCCTTAAACACTCACC
NM_052827	CDK2	5116	ACCTTGCCCTTAAACACTCACC
AB012305	AB012305	5117	ACTCCGCCTGGACACTGAGAC
NM_001798	CDK2	5117	ACTCCGCCTGGACACTGAGAC
NM_052827	CDK2	5117	ACTCCGCCTGGACACTGAGAC
NM_000075	CDK4	5118	ACTGTTGTCCGGCTGATGGAC
NM_000075	CDK4	5118	ACTGTTGTCCGGCTGATGGAC
NM_032913	CDK4	5118	ACTGTTGTCCGGCTGATGGAC
NM_032913	CDK4	5118	ACTGTTGTCCGGCTGATGGAC
NM_052984	CDK4	5118	ACTGTTGTCCGGCTGATGGAC
NM_052984	CDK4	5118	ACTGTTGTCCGGCTGATGGAC
NM_000075	CDK4	5119	ACGGACATATCTGGACAAGGC
NM_000075	CDK4	5119	ACGGACATATCTGGACAAGGC
NM_032913	CDK4	5119	ACGGACATATCTGGACAAGGC
NM_032913	CDK4	5119	ACGGACATATCTGGACAAGGC
NM_000075	CDK4	5120	ACACGATCAAGGATCTGATGC
NM_000075	CDK4	5120	ACACGATCAAGGATCTGATGC
NM_032913	CDK4	5120	ACACGATCAAGGATCTGATGC

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NM_032913	CDK4	5120	ACACGATCAAGGATCTGATGC
NM_000075	CDK4	5121	ACTCTACAGCTACCAGATGGC
NM_032913	CDK4	5121	ACTCTACAGCTACCAGATGGC
NM_000075	CDK4	5122	ACGCCTCTCTTCTGTGGAAAC
NM_032913	CDK4	5122	ACGCCTCTCTTCTGTGGAAAC
NM_052984	CDK4	5122	ACGCCTCTCTTCTGTGGAAAC
NM_000075	CDK4	5123	ACATCTTTGACCTGATTGGGC
NM_032913	CDK4	5123	ACATCTTTGACCTGATTGGGC
NM_052984	CDK4	5123	ACATCTTTGACCTGATTGGGC
NM_005965	MYLK	5124	ACATTACCAGCAGAGAATGGC
NM_053025	MYLK	5124	ACATTACCAGCAGAGAATGGC
NM_053026	MYLK	5124	ACATTACCAGCAGAGAATGGC
NM_053027	MYLK	5124	ACATTACCAGCAGAGAATGGC
NM_053028	MYLK	5124	ACATTACCAGCAGAGAATGGC
NM_053029	MYLK	5124	ACATTACCAGCAGAGAATGGC
NM_053030	MYLK	5124	ACATTACCAGCAGAGAATGGC
NM_005965	MYLK	5125	ACGAAGCTGCTGCTCCAGTGC
NM_053025	MYLK	5125	ACGAAGCTGCTGCTCCAGTGC
NM_053026	MYLK	5125	ACGAAGCTGCTGCTCCAGTGC
NM_053027	MYLK	5125	ACGAAGCTGCTGCTCCAGTGC
NM_053028	MYLK	5125	ACGAAGCTGCTGCTCCAGTGC
NM_053029	MYLK	5125	ACGAAGCTGCTGCTCCAGTGC
NM_053030	MYLK	5125	ACGAAGCTGCTGCTCCAGTGC
NM_005965	MYLK	5126	ACGTCACCGTGGATGATGCTC
NM_053025	MYLK	5126	ACGTCACCGTGGATGATGCTC
NM_053026	MYLK	5126	ACGTCACCGTGGATGATGCTC
NM_053027	MYLK	5126	ACGTCACCGTGGATGATGCTC
NM_053028	MYLK	5126	ACGTCACCGTGGATGATGCTC
NM_053029	MYLK	5126	ACGTCACCGTGGATGATGCTC
NM_053030	MYLK	5126	ACGTCACCGTGGATGATGCTC
NM_003674	CDK10	5127	ACCCACCTGGAGAGCATCTTC
NM_052987	CDK10	5127	ACCCACCTGGAGAGCATCTTC
NM_052988	CDK10	5127	ACCCACCTGGAGAGCATCTTC
NM_003674	CDK10	5128	ACCTTCATTATCCACAGGGAC
NM_052987	CDK10	5128	ACCTTCATTATCCACAGGGAC
NM_052988	CDK10	5128	ACCTTCATTATCCACAGGGAC
NM_003674	CDK10	5129	ACGGTGGTCACTCTCTGGTAC
NM_052987	CDK10	5129	ACGGTGGTCACTCTCTGGTAC
NM_052988	CDK10	5129	ACGGTGGTCACTCTCTGGTAC
NM_016508	CDKL3	5130	ACGTGGGCAATTTGTACCTC
NM_016508	CDKL3	5131	ACGCCCCAAGGAGATCAAAGTC
NM_016508	CDKL3	5132	ACACCCATATCAATCCCAGCAC
NM_052841	STK22C	5133	ACATCTGCCTGGTGATGGAGC
NM_052841	STK22C	5134	ACGGTGTTGCCCAAGTCACAC
NM_052841	STK22C	5135	ACGTTAGTTGGCATCCATGGC
NM_002650	PIK4CA	5136	ACGTGGAGATCTTCTCCAGCC

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NM_058004	PIK4CA	5136	ACGTGGAGATCTTCTCCAGCC
NM_002650	PIK4CA	5137	ACATCCCAGCTTCTGGCACAC
NM_058004	PIK4CA	5137	ACATCCCAGCTTCTGGCACAC
NM_002650	PIK4CA	5138	ACGGGTCATATCATCCACATC
NM_058004	PIK4CA	5139	ACGAAGCTAAGCCTCGGTTAC
NM_004369	COL6A3	5140	ACCAAGCAGGACGTCGTCAAC
NM_057164	COL6A3	5140	ACCAAGCAGGACGTCGTCAAC
NM_057165	COL6A3	5140	ACCAAGCAGGACGTCGTCAAC
NM_057166	COL6A3	5140	ACCAAGCAGGACGTCGTCAAC
NM_057167	COL6A3	5140	ACCAAGCAGGACGTCGTCAAC
NM_031417	MARKL1	5141	ACGGAAGCTCGAGCCAAGTTC
SK515	MARK4	5141	ACGGAAGCTCGAGCCAAGTTC
NM_031417	MARKL1	5142	ACGTACAACGAAGTGACCGCC
SK515	MARK4	5142	ACGTACAACGAAGTGACCGCC
NM_031417	MARKL1	5143	ACCAAGTTCCAGCAAAGGCAC
SK515	MARK4	5143	ACCAAGTTCCAGCAAAGGCAC
NM_020666	CLK4	5144	ACGCAGCTCGTTTCAGAAATCC
SK484	CLK4	5144	ACGCAGCTCGTTTCAGAAATCC
NM_020666	CLK4	5145	ACCCCATACAGATCTGAAGCC
SK484	CLK4	5145	ACCCCATACAGATCTGAAGCC
NM_020666	CLK4	5146	ACTGAAACGTGATGAACGCAC
SK484	CLK4	5146	ACTGAAACGTGATGAACGCAC
M37712	HUMP58GTA	5147	ACCTATGTGGAGCACGACCTC
NM_001787	CDC2L1	5147	ACCTATGTGGAGCACGACCTC
NM_024011	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
NM_033486	CDC2L1	5147	ACCTATGTGGAGCACGACCTC
NM_033487	CDC2L1	5147	ACCTATGTGGAGCACGACCTC
NM_033488	CDC2L1	5147	ACCTATGTGGAGCACGACCTC
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NM_033527	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
NM_033528	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
NM_033529	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
NM_033531	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
NM_033532	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
NM_033536	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
NM_033537	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
NM_033621	CDC2L2	5147	ACCTATGTGGAGCACGACCTC
M37712	HUMP58GTA	5148	ACCAACCTCCGCAAGCGCTTC
NM_001787	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC
NM_024011	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033486	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC
NM_033487	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC

NM_033488	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC
NM_033489	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC
NM_033490	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC
NM_033491	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC
NM_033492	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC
NM_033493	CDC2L1	5148	ACCAACCTCCGCAAGCGCTTC
NM_033527	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033528	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033529	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033531	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033532	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033534	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033536	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033537	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
NM_033621	CDC2L2	5148	ACCAACCTCCGCAAGCGCTTC
M37712	HUMP58GTA	5149	ACCAAGTTCCTGACCTACTTC
NM_001787	CDC2L1	5149	ACCAAGTTCCTGACCTACTTC
NM_024011	CDC2L2	5149	ACCAAGTTCCTGACCTACTTC
NM_033486	CDC2L1	5149	ACCAAGTTCCTGACCTACTTC
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NM_033491	CDC2L1	5149	ACCAAGTTCCTGACCTACTTC
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NM_033493	CDC2L1	5149	ACCAAGTTCCTGACCTACTTC
NM_033527	CDC2L2	5149	ACCAAGTTCCTGACCTACTTC
NM_033528	CDC2L2	5149	ACCAAGTTCCTGACCTACTTC
NM_033529	CDC2L2	5149	ACCAAGTTCCTGACCTACTTC
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NM_033532	CDC2L2	5149	ACCAAGTTCCTGACCTACTTC
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NM_033621	CDC2L2	5149	ACCAAGTTCCTGACCTACTTC
NM_012424	RPS6KC1	5150	ACAGCTCAGGACACCATTAGC
NM_058253	RPS6KC1	5150	ACAGCTCAGGACACCATTAGC
NM_012424	RPS6KC1	5151	ACCACTATGCACAGGAGGATC
NM_058253	RPS6KC1	5151	ACCACTATGCACAGGAGGATC
NM_012424	RPS6KC1	5152	ACCTTCTCACTGGCAAGACTC
NM_058253	RPS6KC1	5152	ACCTTCTCACTGGCAAGACTC
NM_015978	LOC51086	5153	ACTGAAGACCATGTCCCACTC
NM_015978	LOC51086	5154	ACTCTAGTGGCTTGATGCC
NM_015978	LOC51086	5155	ACTGATCCCAGCCAGTTTGCC
NM_019884	GSK3A	5156	ACGGTGACCACAGTCGTAGCC
NM_019884	GSK3A	5157	ACGGTGATACATGTACCAGCTC

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NM_019884	GSK3A	5157	ACGGTGTACATGTACCAGCTC
NM_019884	GSK3A	5158	ACCAAATCCGAGAGATGAACC
NM_025195	C8FW	5159	ACATCAGGCCTTACATCCAGC
NM_025195	C8FW	5160	ACGCAGATTGTCTCCGCCGTC
NM_025195	C8FW	5161	ACAGCCAGGTGCCTCATTCGC
NM_052947	HAK	5162	ACTCTCTTGCCAGCCAGATGCC
NM_052947	HAK	5163	ACAGAAGGAGGTGACAAGAGC
NM_052947	HAK	5164	ACTGAGTGCTTTCAAGCGACC
NM_018401	HSA250839	5165	ACTATCCTGCTGGATGAACAC
NM_018401	HSA250839	5166	ACAGGAGCAGAAAGGGCTTCC
NM_018401	HSA250839	5167	ACGGGAGGTTGAACTGCGATC
NM_032037	SSTK	5168	ACGTACAAGGGTACCGTGGCC
NM_032037	SSTK	5169	ACGCTCACCGACTTCGGCTTC
NM_032037	SSTK	5170	ACGAAGTACGATGTGTGGAGC
NM_004563	PCK2	5171	ACCTGAGGCTGAGAATACTGC
NM_004563	PCK2	5172	ACGAAGTGCTTTGCCCTACGC
NM_004563	PCK2	5173	ACGGAAGGAGCCTTGGATCTC
NM_005400	PRKCE	5174	ACGCCTTGTCATTTGACAACC
NM_005400	PRKCE	5175	ACCTTCATCAAGGTGTTGGGC
NM_005400	PRKCE	5176	ACGAAGATCAAGCCACCCTTC
NM_015716	MINK	5177	ACGTACTCTCACCACCGCAAC
NM_015716	MINK	5178	ACTCACAGCCATCGAGATGGC
NM_015716	MINK	5179	ACGCGATTCAACTCCGAGATC
AF344883	AF344883	5180	ACAGCTGCCAATGTCTTGCTC
NM_016542	MST4	5180	ACAGCTGCCAATGTCTTGCTC
AF344883	AF344883	5181	ACTGGAGCTTTACCACCGTAC
NM_016542	MST4	5181	ACTGGAGCTTTACCACCGTAC
AF344883	AF344883	5182	ACGTATTGCTGTGGCTGAAGC
NM_016542	MST4	5182	ACGTATTGCTGTGGCTGAAGC
NM_004544	NDUFA10	5183	ACGCAGTGTGTGGACCACTAC
NM_018216	FLJ10782	5184	ACGAAGAGATCACTGCTCGAC
NM_018216	FLJ10782	5185	ACGAGCCTGCTGCACATGATC
NM_018216	FLJ10782	5186	ACGCTGGCCGTCATCAAGAAC
NM_024776	FLJ21140	5187	ACACCCTACCATGTCACTCAC
NM_024776	FLJ21140	5188	ACCCCTTCTGAGCGGATCCTC
AF321385	AF321385	5189	ACGGATGAAATTGGAAAGGGC
AF321386	AF321386	5189	ACGGATGAAATTGGAAAGGGC
AF321388	AF321388	5189	ACGGATGAAATTGGAAAGGGC
NM_006549	CAMKK2	5189	ACGGATGAAATTGGAAAGGGC
AF321385	AF321385	5190	ACGATCATCCACCGTGACATC
AF321386	AF321386	5190	ACGATCATCCACCGTGACATC
AF321388	AF321388	5190	ACGATCATCCACCGTGACATC
NM_006549	CAMKK2	5190	ACGATCATCCACCGTGACATC
AF321385	AF321385	5191	ACGATCTTCTCTGGGAAGGCC
AF321386	AF321386	5191	ACGATCTTCTCTGGGAAGGCC
AF321388	AF321388	5191	ACGATCTTCTCTGGGAAGGCC

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NM_006549	CAMKK2	5191	ACGATCTTCTCTGGGAAGGCC
NM_080283	ABCA9	5192	ACCCACAGGATCCTCTGACCC
NM_004336	BUB1	5193	ACACCATGGAACCTACCAGATC
NM_005476	GNE	5194	ACGAGATGGTTCGAGTGATGC
NM_005476	GNE	5195	ACCCCTCCGAGTTGCAATAGTC
NM_005476	GNE	5196	ACGCCATGGGTGCATTGAAGC
NM_005922	MAP3K4	5197	ACAGTCGACTATGGGAGCTTC
NM_006724	MAP3K4	5197	ACAGTCGACTATGGGAGCTTC
NM_005922	MAP3K4	5198	ACGGAGCTCTTCCATGAAGCC
NM_006724	MAP3K4	5198	ACGGAGCTCTTCCATGAAGCC
NM_005922	MAP3K4	5199	ACTGCAGCTGCAGGAAAGGAC
NM_006724	MAP3K4	5199	ACTGCAGCTGCAGGAAAGGAC
NM_033118	MYLK2	5200	ACGAACATCCTGGCAGAGAGC
SK675	skMLCK	5200	ACGAACATCCTGGCAGAGAGC
NM_033118	MYLK2	5201	ACGACAAGGAAATGGTGTTC
SK675	skMLCK	5201	ACGACAAGGAAATGGTGTTC
NM_033118	MYLK2	5202	ACATACCTCATGAAGAGGCGC
SK675	skMLCK	5202	ACATACCTCATGAAGAGGCGC
NM_002610	PDK1	5203	ACTCTTCTCAGGACACCATCC
NM_002610	PDK1	5204	ACTCACCAGGACAGCCAATAC
NM_002610	PDK1	5205	ACAGCTGCCTGGAAGCATTAC
NM_002031	FRK	5206	ACAGACGAGATGGCTCCAGTC
NM_002031	FRK	5207	ACATGACTTCCTGAGGGAGGC
NM_002031	FRK	5208	ACCAGGTAGACATGGCGGCAC
NM_003503	CDC7L1	5209	ACCAAGATTCCACTGAGTGGC
NM_003503	CDC7L1	5210	ACCACCTCCAGGACAATACTC
NM_002005	FES	5211	ACGGACAAGTGCGTGCTGAAC
NM_002576	PAK1	5212	ACGAGCGGCCAGAGATTTCTC
NM_002576	PAK1	5213	ACCTGACTTTGGATTCTGTGC
NM_002576	PAK1	5214	ACCCCTCTGAGAGCCTTGATC
NM_004443	EPHB3	5215	ACTATAATCCGGCTCGAGGGC
NM_004443	EPHB3	5216	ACGAAGATCCTGAGCAGTATC
AY056048	AY056048	5217	ACATACCATGAGAAGGGCGCC
NM_004444	EPHB4	5217	ACATACCATGAGAAGGGCGCC
AY056048	AY056048	5218	ACAGATTCCCATCCGATGGAC
NM_004444	EPHB4	5218	ACAGATTCCCATCCGATGGAC
AY056048	AY056048	5219	ACTCAGGACGTGATCAATGCC
NM_004444	EPHB4	5219	ACTCAGGACGTGATCAATGCC
NM_004064	CDKN1B	5220	ACGACTGATCCGTCGGACAGC
NM_004064	CDKN1B	5221	ACTAAGGAAGCGACCTGCAAC
NM_004064	CDKN1B	5222	ACATGTTTTAGACGGTTCCCC
NM_021158	C20orf97	5223	ACGAAGCTGGTGCTGGAGAAC
NM_015148	PASK	5224	ACGGACCAGCAAATCACTGCC
SK499	PASK	5224	ACGGACCAGCAAATCACTGCC
NM_015148	PASK	5225	ACGATTCTGAAGCTCCAGTCC
SK499	PASK	5225	ACGATTCTGAAGCTCCAGTCC

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NM_015148	PASK	5226	ACAGTACAGTACCATGAGCCC
SK499	PASK	5226	ACAGTACAGTACCATGAGCCC
NM_013233	STK39	5227	ACTTAGCAACAGGAGCAGCGC
NM_013233	STK39	5228	ACGCCAAGAACAGAGAGTACC
NM_013233	STK39	5229	ACATACAGTCCCTCTCTGTGC
NM_080823	C20orf148	5230	ACGTGACAGCTCTGGTCCTTC
NM_012247	SPS	5231	ACGGCCTGCGGAAACATGTTT
NM_080915	DGUOK	5232	ACCACGAAGCCTGGCTTATTC
NM_080916	DGUOK	5232	ACCACGAAGCCTGGCTTATTC
NM_080917	DGUOK	5232	ACCACGAAGCCTGGCTTATTC
NM_080916	DGUOK	5233	ACCATTGCTGTGGGAAAGTCC
NM_080918	DGUOK	5233	ACCATTGCTGTGGGAAAGTCC
NM_080916	DGUOK	5234	ACCATGGCAGAATATCCAGGC
NM_080918	DGUOK	5234	ACCATGGCAGAATATCCAGGC
NM_080916	DGUOK	5235	ACTATCCAGGCTGCTGGCACC
NM_080918	DGUOK	5235	ACTATCCAGGCTGCTGGCACC
NM_018492	TOPK	5236	ACGAACGATATAAAGCCAGCC
NM_018492	TOPK	5237	ACTCTGTGATGTAGGAGTCTC
NM_018492	TOPK	5238	ACGATCGTCCTTCTGCTGCAC
NM_033266	ERN2	5239	ACGCACCACTACAGGGAGCTC
SK498	IRE2	5239	ACGCACCACTACAGGGAGCTC
NM_004672	MAP3K6	5240	ACCACCTTCAGTGGGCTGCTC
NM_004672	MAP3K6	5241	ACCTCTGCAGTATATGGCCCC
NM_004672	MAP3K6	5242	ACTGTGGATTACAGGCACCATC
NM_006254	PRKCD	5243	ACGACTGCGGCATGAATGTGC
NM_006254	PRKCD	5244	ACGGACATCCTGGAGAAGCTC
NM_006281	STK3	5245	ACGGAATCCGGTCAAGTTGTC
NM_006281	STK3	5246	ACAGTTCCTCAAGATGGAGAC
NM_006281	STK3	5247	ACGACAGCCCATTCTGGATGC
NM_006875	PIM2	5248	ACGTAGTGGCAGCCATCCAGC
NM_017886	FLJ20574	5249	ACGTAGAGTCAAAGGATCTCC
SK457	ULK4	5249	ACGTAGAGTCAAAGGATCTCC
NM_017886	FLJ20574	5250	ACGGGCACAAGAGTGGTCAAC
SK457	ULK4	5250	ACGGGCACAAGAGTGGTCAAC
NM_017886	FLJ20574	5251	ACTCCAGCATTTGCGGATAGC
SK457	ULK4	5251	ACTCCAGCATTTGCGGATAGC
NM_017988	FLJ10074	5252	ACGGACTGCCAAAGGTTCTAC
SK475	SCYL2	5252	ACGGACTGCCAAAGGTTCTAC
NM_017988	FLJ10074	5253	ACGCTCCTTCCATTTCAGATCC
SK475	SCYL2	5253	ACGCTCCTTCCATTTCAGATCC
AK027493	AK027493	5254	ACCAACAGCACTCTTCAGTCC
NM_018650	MARK1	5254	ACCAACAGCACTCTTCAGTCC
AK027493	AK027493	5255	ACGACGGCTCTGAAGCTTACC
NM_018650	MARK1	5255	ACGACGGCTCTGAAGCTTACC
NM_018650	MARK1	5256	ACCCGACACCTCAAGAAGTAC
AK027493	AK027493	5257	ACGACCACTAGTTCAATGGAC

NM_018650	MARK1	5257	ACGACCACTAGTTCAATGGAC
NM_003681	PDXK	5258	ACCCACACAGGCTATGCCAC
NM_003681	PDXK	5259	ACAGTGGTGCCGCTTGACAGAC
NM_003681	PDXK	5260	ACCGCATCCGGATGGACATTC
NM_004073	CNK	5261	ACGAAGACCATCTGTGGCACC
SK316	PLK3	5261	ACGAAGACCATCTGTGGCACC
NM_004073	CNK	5262	ACAGACTGTGCACTACAATCC
SK316	PLK3	5262	ACAGACTGTGCACTACAATCC
NM_004073	CNK	5263	ACGACGGATCAGGCTCTCCTC
SK316	PLK3	5263	ACGACGGATCAGGCTCTCCTC
NM_014326	DAPK2	5264	ACTGTCATCACGCTGCACGAC
NM_014326	DAPK2	5265	ACATTGTGAACTACGAGCCCC
NM_014326	DAPK2	5266	ACCTTCAGGAAGCAGTATGTC
NM_005884	PAK4	5267	ACCATGTGCGTGACACGCTCC
NM_005884	PAK4	5268	ACATGGGATGCCAGAGGAGCC
NM_005884	PAK4	5269	ACTGTGGTGGAGATGTACAAC
NM_005884	PAK4	5270	ACGCTGTCAGACTTTGGGTTT
NM_005884	PAK4	5271	ACCATGTATGAGTGTGTGCAC
NM_001396	DYRK1A	5272	ACGCGAAGACACCAACAGGGC
NM_101395	DYRK1A	5272	ACGCGAAGACACCAACAGGGC
NM_130436	DYRK1A	5272	ACGCGAAGACACCAACAGGGC
NM_130437	DYRK1A	5272	ACGCGAAGACACCAACAGGGC
NM_130438	DYRK1A	5272	ACGCGAAGACACCAACAGGGC
NM_001396	DYRK1A	5273	ACGTTTGCGCAACAGATGTGC
NM_101395	DYRK1A	5273	ACGTTTGCGCAACAGATGTGC
NM_130436	DYRK1A	5273	ACGTTTGCGCAACAGATGTGC
NM_130437	DYRK1A	5273	ACGTTTGCGCAACAGATGTGC
NM_130438	DYRK1A	5273	ACGTTTGCGCAACAGATGTGC
NM_001396	DYRK1A	5274	ACCCACCAGGAACCCGTAAAC
NM_101395	DYRK1A	5274	ACCCACCAGGAACCCGTAAAC
NM_130436	DYRK1A	5274	ACCCACCAGGAACCCGTAAAC
NM_130437	DYRK1A	5274	ACCCACCAGGAACCCGTAAAC
NM_130438	DYRK1A	5274	ACCCACCAGGAACCCGTAAAC
NM_005108	XYLB	5275	ACGATGAAGGCTTCGGGCTTC
NM_005108	XYLB	5276	ACCCACAAGGTTGCAGCATTC
NM_005108	XYLB	5277	ACATCCCAGACTAGCTGCTAC
NM_014572	LATS2	5278	ACTGAGTGGGTGGTCAAACCTC
NM_003390	WEE1	5279	ACGCAGAGTTGAAGGATCTCC
NM_013254	TBK1	5280	ACGAGGAGACAACAACAAGAC
NM_013254	TBK1	5281	ACCTTATCTACGAAGGGCGAC
NM_013254	TBK1	5282	ACGGCTGGCACAACATTTCCC
NM_005012	ROR1	5283	ACGAAGATGGATTCTGTGACG
NM_005012	ROR1	5284	ACTCAGATCACAGCTGCCTTC
NM_005012	ROR1	5285	ACATGCCACCACACAGACAAC
NM_004560	ROR2	5286	ACCGGGATGAAGACCATTACC
NM_004560	ROR2	5287	ACTTCCTGGTCATGCGCTCGC

NM_004560	ROR2	5288	ACGATCTCAGACTTGGGCCTC
NM_003319	TTN	5289	ACGAGGTAGAGAAGGCATTAC
NM_133378	TTN	5289	ACGAGGTAGAGAAGGCATTAC
NM_133379	TTN	5289	ACGAGGTAGAGAAGGCATTAC
NM_133432	TTN	5289	ACGAGGTAGAGAAGGCATTAC
NM_133437	TTN	5289	ACGAGGTAGAGAAGGCATTAC
NM_003319	TTN	5290	ACGGCTCCTACTGTGAAGCCC
NM_133378	TTN	5290	ACGGCTCCTACTGTGAAGCCC
NM_133379	TTN	5290	ACGGCTCCTACTGTGAAGCCC
NM_133432	TTN	5290	ACGGCTCCTACTGTGAAGCCC
NM_133437	TTN	5290	ACGGCTCCTACTGTGAAGCCC
AB004885	TLK1	5291	ACGTCCAGTAAGAGGCATACC
NM_012290	TLK1	5291	ACGTCCAGTAAGAGGCATACC
SK373	TLK1	5291	ACGTCCAGTAAGAGGCATACC
XM_002626	TLK1	5291	ACGTCCAGTAAGAGGCATACC
AB004885	TLK1	5292	ACTTCTCAGGCACCCCTCTACC
NM_012290	TLK1	5292	ACTTCTCAGGCACCCCTCTACC
SK373	TLK1	5292	ACTTCTCAGGCACCCCTCTACC
XM_002626	TLK1	5292	ACTTCTCAGGCACCCCTCTACC
AB004885	TLK1	5293	ACAGCCACAGAAGTCCAGTTC
NM_012290	TLK1	5293	ACAGCCACAGAAGTCCAGTTC
SK373	TLK1	5293	ACAGCCACAGAAGTCCAGTTC
XM_002626	TLK1	5293	ACAGCCACAGAAGTCCAGTTC
NM_004567	PFKFB4	5294	ACCTGCCCAACTCTCATTGTC
NM_004567	PFKFB4	5295	ACATCAGGAAGCAGTGTGCC
NM_004567	PFKFB4	5296	ACTTATCCACTGGAGTTCGCC
NM_005026	PIK3CD	5297	ACTGCCAACCTCAGCACCATC
NM_005026	PIK3CD	5298	ACCGCTGCCTCTACATGTGGC
NM_005026	PIK3CD	5299	ACCTGGCTGAAGTCCAAGAAC
NM_014397	NEK6	5300	ACGAAGCAGAAGCGGCTCATC
NM_014397	NEK6	5301	ACGTACTTTGTGCAGCTGTGC
NM_014397	NEK6	5302	ACGCCTGCCAACGTGTTTCATC
NM_014397	NEK6	5303	ACCGGCTACAACCTTCAAGTCC
NM_014397	NEK6	5304	ACGTTACGAGAAGTGGTCAGC
NM_016282	AKL3L	5305	ACACAACGCCTTACTGCTCGC
NM_016282	AKL3L	5306	ACCATTGAATTCAACCCCTCCC
NM_016282	AKL3L	5307	ACCATTCTCCGGAACAGAAAC
NM_016281	JK	5308	ACTGGCTTCTCCTGCCAACTC
NM_016281	JK	5309	ACTGAGGACCATAGCACACCC
NM_016281	JK	5310	ACGCTACGCATGGATCTGATC
AB051428	AB051428	5311	ACATTCTTCCAGGAGCTGAGC
NM_020680	NTKL	5311	ACATTCTTCCAGGAGCTGAGC
SK454	SCYL1	5311	ACATTCTTCCAGGAGCTGAGC
XM_166235	NTKL	5311	ACATTCTTCCAGGAGCTGAGC
AB051428	AB051428	5312	ACTGTGGAGCTGATGAAGCAC
NM_020680	NTKL	5312	ACTGTGGAGCTGATGAAGCAC

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SK454	SCYL1	5312	ACTGTGGAGCTGATGAAGCAC
XM_166235	NTKL	5312	ACTGTGGAGCTGATGAAGCAC
AB051428	AB051428	5313	ACGATCCTGCCTGTGCTCTGC
NM_020680	NTKL	5313	ACGATCCTGCCTGTGCTCTGC
SK454	SCYL1	5313	ACGATCCTGCCTGTGCTCTGC
XM_166235	NTKL	5313	ACGATCCTGCCTGTGCTCTGC
NM_021135	RPS6KA2	5314	ACGCTCTACCTGATCCTGGAC
NM_021135	RPS6KA2	5315	ACGAGATTGAGATCCTCCTGC
NM_021135	RPS6KA2	5316	ACCTGGGACTCGATATCTGAC
NM_033550	C20orf64	5317	ACGGGAGTAGACCTCTATGTC
NM_033550	C20orf64	5318	ACGAGCTACTCCACCTCCTCC
NM_017433	MYO3A	5319	ACGCGGTACTACCTTCTCTGC
NM_001320	CSNK2B	5320	ACGATCCATGCGATGGCCTAC
NM_002944	ROS1	5321	ACTTCATCGTGGGATGTGACC
NM_002944	ROS1	5322	ACCATCTCTGTCACTTCGAGC
NM_004958	FRAP1	5323	ACGGAGCTCCAGCACTATGTC
NM_003576	STK24	5324	ACGGCATTGACAATCGGACTC
SK246	MST3	5324	ACGGCATTGACAATCGGACTC
NM_003576	STK24	5325	ACGGAGCCGAGCTTTAGACCC
SK246	MST3	5325	ACGGAGCCGAGCTTTAGACCC
NM_003576	STK24	5326	ACACTTCCTACTTGACCGAGC
SK246	MST3	5326	ACACTTCCTACTTGACCGAGC
NM_004103	PTK2B	5327	ACCAGTTCCGGAAGATGATCC
NM_004103	PTK2B	5328	ACCATTACTGTGGACCTGGTC
NM_004103	PTK2B	5329	ACGACCTGCAAGAAAGACTGC
NM_014920	ICK	5330	ACGCCTGAGAACCTCCTCTGC
NM_016513	ICK	5330	ACGCCTGAGAACCTCCTCTGC
NM_014920	ICK	5331	ACGACTGACTGGCCTGAAGGC
NM_016513	ICK	5331	ACGACTGACTGGCCTGAAGGC
NM_014920	ICK	5332	ACGCAGCACTATTTGAAGCAC
NM_016513	ICK	5332	ACGCAGCACTATTTGAAGCAC
NM_000858	GUK1	5333	ACCACTGAAACCGAGGAGAGC
AF081572	AF081572	5334	ACCACCAAGAAGCTGTCAGCC
AF081924	AF081924	5334	ACCACCAAGAAGCTGTCAGCC
AF083419	AF083419	5334	ACCACCAAGAAGCTGTCAGCC
AF112471	AF112471	5334	ACCACCAAGAAGCTGTCAGCC
AF112472	AF112472	5334	ACCACCAAGAAGCTGTCAGCC
AJ252236	HSA252236	5334	ACCACCAAGAAGCTGTCAGCC
AJ252237	HSA252237	5334	ACCACCAAGAAGCTGTCAGCC
AJ252238	HSA252238	5334	ACCACCAAGAAGCTGTCAGCC
BC019070	BC019070	5334	ACCACCAAGAAGCTGTCAGCC
NM_001220	CAMK2B	5334	ACCACCAAGAAGCTGTCAGCC
SK058	CaMK2b	5334	ACCACCAAGAAGCTGTCAGCC
AF081572	AF081572	5335	ACGCTCAAGGGAGCCATCCTC
AF081924	AF081924	5335	ACGCTCAAGGGAGCCATCCTC
AF083419	AF083419	5335	ACGCTCAAGGGAGCCATCCTC

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AF112471	AF112471	5335	ACGCTCAAGGGAGCCATCCTC
AF112472	AF112472	5335	ACGCTCAAGGGAGCCATCCTC
AJ252236	HSA252236	5335	ACGCTCAAGGGAGCCATCCTC
AJ252237	HSA252237	5335	ACGCTCAAGGGAGCCATCCTC
AJ252238	HSA252238	5335	ACGCTCAAGGGAGCCATCCTC
BC019070	BC019070	5335	ACGCTCAAGGGAGCCATCCTC
NM_001220	CAMK2B	5335	ACGCTCAAGGGAGCCATCCTC
SK058	CaMK2b	5335	ACGCTCAAGGGAGCCATCCTC
AF081572	AF081572	5336	ACGAACAGCAAGCCGATCCAC
AF081924	AF081924	5336	ACGAACAGCAAGCCGATCCAC
AF083419	AF083419	5336	ACGAACAGCAAGCCGATCCAC
AF112471	AF112471	5336	ACGAACAGCAAGCCGATCCAC
AF112472	AF112472	5336	ACGAACAGCAAGCCGATCCAC
AJ252236	HSA252236	5336	ACGAACAGCAAGCCGATCCAC
AJ252237	HSA252237	5336	ACGAACAGCAAGCCGATCCAC
AJ252238	HSA252238	5336	ACGAACAGCAAGCCGATCCAC
BC019070	BC019070	5336	ACGAACAGCAAGCCGATCCAC
NM_001220	CAMK2B	5336	ACGAACAGCAAGCCGATCCAC
SK058	CaMK2b	5336	ACGAACAGCAAGCCGATCCAC
NM_002738	PRKCB1	5337	ACGAACCACAAATTCACCGCC
NM_002738	PRKCB1	5338	ACGTGAGAGCAAACAGAAGAC
NM_002738	PRKCB1	5339	ACAGACGACCAACACTGTCTC
NM_016276	SGK2	5340	ACGGGAACCTACGGGAAGGTCC
SK523	SGK2	5340	ACGGGAACCTACGGGAAGGTCC
NM_016276	SGK2	5341	ACGCTCTACTTCGTGCTCGAC
SK523	SGK2	5341	ACGCTCTACTTCGTGCTCGAC
NM_016276	SGK2	5342	ACAGCCTTCTCCACAAGGACC
SK523	SGK2	5342	ACAGCCTTCTCCACAAGGACC
NM_016276	SGK2	5343	ACCTGGGATGACCTGTACCAC
SK523	SGK2	5343	ACCTGGGATGACCTGTACCAC
NM_016276	SGK2	5344	ACTGTGACAGGACCTGTGAC
SK523	SGK2	5344	ACTGTGACAGGACCTGTGAC
NM_001184	ATR	5345	ACCCTTTCTCTGAACACGGAC
NM_001211	BUB1B	5346	ACGGCAAGGGCGGATCATGTC
NM_002953	RPS6KA1	5347	ACGCTCTATCTCATTCCTGGAC
NM_002953	RPS6KA1	5348	ACGGAGACAATTGGTGTGGGC
NM_002953	RPS6KA1	5349	ACCACAGTTTCAGAGACAGCC
AF326592	AF326592	5350	ACGTTCCAACCTGGGACATGAC
NM_022740	HIPK2	5350	ACGTTCCAACCTGGGACATGAC
AF326592	AF326592	5351	ACCACAAGCAGCGTGCAGATC
NM_022740	HIPK2	5351	ACCACAAGCAGCGTGCAGATC
AF326592	AF326592	5352	ACTGCTTCCAGCACAAAGAACC
NM_022740	HIPK2	5352	ACTGCTTCCAGCACAAAGAACC
NM_016123	IRAK4	5353	ACACAGATGCCTTTCTGTGAC
NM_016123	IRAK4	5354	ACGCTATATGCCACCTGACTC
NM_016123	IRAK4	5355	ACCAACAGCTTATATGGCACC

NM_002834	PTPN11	5356	ACGTAACCCCTGGAGACTTCAC
NM_080601	PTPN11	5356	ACGTAACCCCTGGAGACTTCAC
NM_012474	UMPK	5357	ACCAGCTAGCGGCAAGTCTTC
NM_012474	UMPK	5358	ACGGGCCAGTTCAACTTTGAC
NM_005356	LCK	5359	ACGACAACCTGGTTATCGCTC
XM_034528	LCK	5359	ACGACAACCTGGTTATCGCTC
NM_005356	LCK	5360	ACACTCCTGGACATGGCAGCC
XM_034528	LCK	5360	ACACTCCTGGACATGGCAGCC
NM_005356	LCK	5361	ACCTGTCCAGAGGAGCTGTAC
XM_034528	LCK	5361	ACCTGTCCAGAGGAGCTGTAC
NM_138995	MYO3B	5362	ACACCAGGCATGAGAGGATGC
NM_001893	CSNK1D	5363	ACACCAAACACCCCTCAGCTCC
NM_139062	CSNK1D	5363	ACACCAAACACCCCTCAGCTCC
NM_001893	CSNK1D	5364	ACGAAGGGCAACCTGGTGTAC
NM_139062	CSNK1D	5364	ACGAAGGGCAACCTGGTGTAC
NM_001893	CSNK1D	5365	ACTCTGTTCCATCGCCAGGGC
NM_139062	CSNK1D	5365	ACTCTGTTCCATCGCCAGGGC
NM_001221	CAMK2D	5366	ACTGGCATAGTTCACAGGGAC
NM_001221	CAMK2D	5367	ACGACCAACACAGACTCTATC
NM_001221	CAMK2D	5368	ACAGGGTGCCATCTTGACAAC
NM_025052	FLJ23074	5369	ACTGCAGCAGACTTTGTGCGC
NM_025052	FLJ23074	5370	ACGAGGAGGAAGATAAATGCC
NM_030952	DKFZP434J037	5371	ACGATTGCTGACTTCGGCCTC
SK472	Nuak2	5371	ACGATTGCTGACTTCGGCCTC
NM_030952	DKFZP434J037	5372	ACTGACATGGCCCAGTCTCTC
SK472	Nuak2	5372	ACTGACATGGCCCAGTCTCTC
NM_032844	FLJ14813	5373	ACATCAGTGGGCTGTGGATTC
NM_033126	PSKH2	5374	ACAGCTCTTATTGGGACAGGC
NM_033126	PSKH2	5375	ACGGAAGCCTTATACCAAGTGC
NM_033126	PSKH2	5376	ACATCCAGGCATATGTGGAGC
NM_002647	PIK3C3	5377	ACAGCTCATCGACAAGGACAC
NM_002647	PIK3C3	5378	ACCTTACCAAGAAGGATAGTC
NM_002647	PIK3C3	5379	ACAGTGCCCTTATGCCTGCAC
NM_003629	PIK3R3	5380	ACATGGATCCTCCAGCTCTTC
NM_003629	PIK3R3	5381	ACGCTGATGTACCCAGTGTCC
NM_003629	PIK3R3	5382	ACCTGACCTGATCCAGCTGC
NM_003648	DGKD	5383	ACCCAGGGTGTGAAGTTCTC
NM_003648	DGKD	5384	ACGGCCTATGAGAAGACGACC
NM_003648	DGKD	5385	ACATGTCCGGGCTGGAATGTC
NM_003804	RIPK1	5386	ACTGAGCTGAGGGAAGTGGAC
NM_003804	RIPK1	5387	ACACTCCAAGACGAAGCCAAC
NM_003804	RIPK1	5388	ACCTGGGCTTCACACAGTCTC
NM_004438	EPHA4	5389	ACCTTGGGTGGATAGCAAGCC
NM_004438	EPHA4	5390	ACGTCTCCATCACTGACCTCC
NM_006219	PIK3CB	5391	ACGACTCTGTGATGTCAGACC
NM_006219	PIK3CB	5392	ACTGATTGCCATAGAGGCTGC

NM_006219	PIK3CB	5393	ACTATGCTGTAGGCTGCCTGC
NM_006256	PRKCL2	5394	ACCTCCATGGTACAGCTCAGC
NM_006256	PRKCL2	5395	ACCTGGACAGGTCACGTGAAC
NM_006256	PRKCL2	5396	ACTGCTTGTTGGTGAGTCTCC
NM_007064	TRAD	5397	ACGCGAGAATGGAGGCAAGTC
NM_007064	TRAD	5398	ACAGCAGTGGAGTTAATGTGC
NM_007064	TRAD	5399	ACTGTGGACAATGATCCCTGC
NM_013355	pknbeta	5400	ACCAGTTGCTGACAGCCGTGC
NM_013355	pknbeta	5401	ACTGCCTGTCACCAACTGTCC
NM_013355	pknbeta	5402	ACTTTCCTGCCCAAGAAGACC
NM_014002	IKKE	5403	ACGGTCTTCAACACTACCAGC
NM_014002	IKKE	5404	ACGGAGATCATGTACCGGATC
NM_014002	IKKE	5405	ACAGACTCCTGCAGGTGTTCC
NM_014683	ULK2	5406	ACCAGCACCAATTCCAGTTCC
NM_014683	ULK2	5407	ACCAATCATTTGGCTCTCCTAC
NM_014683	ULK2	5408	ACCACACAGACACCTTACGCC
NM_014720	SLK	5409	ACGGCCCAGAATAAAGAGACC
XM_032564	SLK	5409	ACGGCCCAGAATAAAGAGACC
NM_014720	SLK	5410	ACGGACAGACCCTATGACTAC
XM_032564	SLK	5410	ACGGACAGACCCTATGACTAC
NM_014720	SLK	5411	ACGAGCACACAAATCGCTTGC
XM_032564	SLK	5411	ACGAGCACACAAATCGCTTGC
NM_014840	KIAA0537	5412	ACAGACCCAGCAGAGAGAATC
NM_016616	LOC51314	5413	ACTGTTATCTGTGGGTCCATC
NM_016616	LOC51314	5414	ACTGGAGACGATTGATGGGCC
AF091486	AF091486	5415	ACCATCGTCCGACTACATGAC
AF145710	AF145710	5415	ACCATCGTCCGACTACATGAC
NM_015981	CAMK2A	5415	ACCATCGTCCGACTACATGAC
SK057	CaMK2a	5415	ACCATCGTCCGACTACATGAC
XM_042551	CAMK2A	5415	ACCATCGTCCGACTACATGAC
NM_016292	TRAP1	5416	ACAGACACAGAGTTCTCTTC
NM_016292	TRAP1	5417	ACGAAGCTGAATCAGCTGCGC
NM_018423	DKFZp761P1010	5418	ACAGTGATCTCACTGCTAAGC
NM_018423	DKFZp761P1010	5419	ACGTACCAGAGTTGGTGGTAC
NM_020397	LOC57118	5420	ACGGATGCCAGCACTCTGATC
NM_020397	LOC57118	5421	ACGCTCTTTGAGCAGATCCTC
NM_020397	LOC57118	5422	ACGATACACGTGTGAGCAGGC
NM_020423	LOC57147	5423	ACGAGACCCAGCATCTATCCC
NM_020423	LOC57147	5424	ACCTCCTTGCTTGCTCTCACC
NM_020423	LOC57147	5425	ACCTGAGGACAGAAATGGTCC
NM_020526	EPHA8	5426	ACCCAGAACTGGCTGCGC
NM_020526	EPHA8	5427	ACGAAGAGGCACTGTGGCTAC
NM_002044	GALK2	5428	ACTCCCTTGATCCGGACTTC
NM_002044	GALK2	5429	ACGGCAGCAACTTCCCATTTC
NM_002044	GALK2	5430	ACAGCATGTGTACAGCGAGGC
NM_002401	MAP3K3	5431	ACGAACAAAGACACAGGTCAC

NM_002401	MAP3K3	5432	ACTTCCTTGTCTGGAAGCTGC
NM_002401	MAP3K3	5433	ACCATGATTGTTTACCGGGAC
NM_005028	PIP5K2A	5434	ACGGAATACTGCCCGATGGTC
NM_005028	PIP5K2A	5435	ACAGAAAGCTGCCCATGCTGC
NM_003913	PRP4	5436	ACTGGAAGGAAAGGTCCAGTC
NM_003913	PRP4	5437	ACGAGCCAACCAAGAAGTGGC
XM_095699	LOC169457	5437	ACGAGCCAACCAAGAAGTGGC
NM_005406	ROCK1	5438	ACGAGTCACACAGAGATGAGC
NM_005406	ROCK1	5439	ACGAGAAGCTCGAGAGAAGGC
NM_002749	MAPK7	5440	ACTGCTTTTCGATGTGGTGACC
NM_139033	MAPK7	5440	ACTGCTTTTCGATGTGGTGACC
NM_139034	MAPK7	5440	ACTGCTTTTCGATGTGGTGACC
SK408	Erk5	5440	ACTGCTTTTCGATGTGGTGACC
NM_002749	MAPK7	5441	ACAGATGGTGCCATCTCAGAC
NM_139032	MAPK7	5441	ACAGATGGTGCCATCTCAGAC
NM_139033	MAPK7	5441	ACAGATGGTGCCATCTCAGAC
NM_139034	MAPK7	5441	ACAGATGGTGCCATCTCAGAC
SK408	Erk5	5441	ACAGATGGTGCCATCTCAGAC
NM_002749	MAPK7	5442	ACGCCTGTTGGAACGCTGGAC
NM_139032	MAPK7	5442	ACGCCTGTTGGAACGCTGGAC
NM_139033	MAPK7	5442	ACGCCTGTTGGAACGCTGGAC
NM_139034	MAPK7	5442	ACGCCTGTTGGAACGCTGGAC
SK408	Erk5	5442	ACGCCTGTTGGAACGCTGGAC
NM_002749	MAPK7	5443	ACCCAGTCTTTTCGACATGGGC
NM_139032	MAPK7	5443	ACCCAGTCTTTTCGACATGGGC
NM_139033	MAPK7	5443	ACCCAGTCTTTTCGACATGGGC
NM_139034	MAPK7	5443	ACCCAGTCTTTTCGACATGGGC
SK408	Erk5	5443	ACCCAGTCTTTTCGACATGGGC
AF001174	AF001174	5444	ACCGTGGCTGTGAACGAGGAC
AF031135	AF031135	5444	ACCGTGGCTGTGAACGAGGAC
NM_002751	MAPK11	5444	ACCGTGGCTGTGAACGAGGAC
NM_138993	MAPK11	5444	ACCGTGGCTGTGAACGAGGAC
SK342	p38b	5444	ACCGTGGCTGTGAACGAGGAC
U53442	HSU53442	5444	ACCGTGGCTGTGAACGAGGAC
Y14440	HSY14440	5444	ACCGTGGCTGTGAACGAGGAC
AF001174	AF001174	5445	ACCACGCCCCGGACATATATCC
AF031135	AF031135	5445	ACCACGCCCCGGACATATATCC
NM_002751	MAPK11	5445	ACCACGCCCCGGACATATATCC
NM_138993	MAPK11	5445	ACCACGCCCCGGACATATATCC
SK342	p38b	5445	ACCACGCCCCGGACATATATCC
U53442	HSU53442	5445	ACCACGCCCCGGACATATATCC
Y14440	HSY14440	5445	ACCACGCCCCGGACATATATCC
AF001174	AF001174	5446	ACGCACCTGAAGCACGAGAAC
AF031135	AF031135	5446	ACGCACCTGAAGCACGAGAAC
NM_002751	MAPK11	5446	ACGCACCTGAAGCACGAGAAC
NM_138993	MAPK11	5446	ACGCACCTGAAGCACGAGAAC

SK342	p38b	5446	ACGCACCTGAAGCACGAGAAC
U53442	HSU53442	5446	ACGCACCTGAAGCACGAGAAC
Y14440	HSY14440	5446	ACGCACCTGAAGCACGAGAAC
NM_005433	YES1	5447	ACGTGTGAGCCATTATGGAGC
NM_005433	YES1	5448	ACGATGCTTGGGAAATCCCTC
NM_018638	EKI1	5449	ACCACCATGGAGGATGTAGTC
NM_018638	EKI1	5450	ACGCATGTCTGCAACCCAGCC
NM_018638	EKI1	5451	ACCTACAGAGTCAGTGGCTGC
NM_007271	STK38	5452	ACGGTGATGGAAGAAGAAGGC
SK249	NDR1	5452	ACGGTGATGGAAGAAGAAGGC
NM_007271	STK38	5453	ACGAGCAGGTTGGCCACATTC
SK249	NDR1	5453	ACGAGCAGGTTGGCCACATTC
NM_007271	STK38	5454	ACGAACAAAGACTGGGTCTTC
SK249	NDR1	5454	ACGAACAAAGACTGGGTCTTC
NM_002649	PIK3CG	5455	ACGATTGCCAACAACCTGCATC
NM_002649	PIK3CG	5456	ACACTGGAGAGCTTGGAGGAC
NM_002649	PIK3CG	5457	ACCATGGTGATGATCTGCGCC
NM_005781	ACK1	5458	ACGCGCTTTATTACCGTGAC
SK009	ACK	5458	ACGCGCTTTATTACCGTGAC
NM_005781	ACK1	5459	ACTGATGTCATCACCGTCATC
SK009	ACK	5459	ACTGATGTCATCACCGTCATC
NM_005781	ACK1	5460	ACCTTCTCCACCAACAACAGC
SK009	ACK	5460	ACCTTCTCCACCAACAACAGC
NM_139158	ALS2CR7	5461	ACCACGTTCTTCACAGGGACC
SK462	PFTAIRE2	5461	ACCACGTTCTTCACAGGGACC
NM_001744	CAMK4	5462	ACCTCGTCACAGGAGGAGAAC
SK061	CaMK4	5462	ACCTCGTCACAGGAGGAGAAC
NM_017662	TRPM6	5463	ACGCCGTGATTGCGTGTATCC
NM_000298	PKLR	5464	ACCATTGCGCGACTCAACTTC
NM_000298	PKLR	5465	ACGATGATGATTGGGCGCTGC
NM_000298	PKLR	5466	ACGATGCAGCATGCGATTGCC
NM_005030	PLK	5467	ACGATGCTTCAGACAGATCCC
SK315	PLK1	5467	ACGATGCTTCAGACAGATCCC
NM_005030	PLK	5468	ACTAAAGGCTTGGAGAACCCC
SK315	PLK1	5468	ACTAAAGGCTTGGAGAACCCC
NM_005030	PLK	5469	ACCTTCTTCCAGGATCACACC
SK315	PLK1	5469	ACCTTCTTCCAGGATCACACC
NM_018571	ALS2CR2	5470	ACTTCCCAGTCAGGTGTAGAC
SK434	STLK6	5470	ACTTCCCAGTCAGGTGTAGAC
NM_006622	SNK	5471	ACGAAAGGTGTTGACAGAGCC
SK353	PLK2	5471	ACGAAAGGTGTTGACAGAGCC
NM_006622	SNK	5472	ACGTCTCAACAACAAGGAC
SK353	PLK2	5472	ACGTCTCAACAACAAGGAC
NM_006622	SNK	5473	ACGTGTTGCAGACACAGTGGC
SK353	PLK2	5473	ACGTGTTGCAGACACAGTGGC
NM_002626	PFKL	5474	ACGAGGAAGTGACCTCAGAGC

NM_002626	PFKL	5475	ACGTGCCATGACTACTACACC
NM_002626	PFKL	5476	ACGACACTGATTTTCGAGCACC
AF387637	AF387637	5477	ACGTTACCTCTCGTACCAGCC
AF465413	AF465413	5477	ACGTTACCTCTCGTACCAGCC
M80359	HUMP78A	5477	ACGTTACCTCTCGTACCAGCC
NM_002376	MARK3	5477	ACGTTACCTCTCGTACCAGCC
SK096	MARK3	5477	ACGTTACCTCTCGTACCAGCC
U64205	HSU64205	5477	ACGTTACCTCTCGTACCAGCC
AF387637	AF387637	5478	ACGGCGGATATTCCTGAACGC
AF465413	AF465413	5478	ACGGCGGATATTCCTGAACGC
M80359	HUMP78A	5478	ACGGCGGATATTCCTGAACGC
NM_002376	MARK3	5478	ACGGCGGATATTCCTGAACGC
SK096	MARK3	5478	ACGGCGGATATTCCTGAACGC
U64205	HSU64205	5478	ACGGCGGATATTCCTGAACGC
M80359	HUMP78A	5479	ACGGAGTCGCAATGTATCTGC
NM_002376	MARK3	5479	ACGGAGTCGCAATGTATCTGC
SK096	MARK3	5479	ACGGAGTCGCAATGTATCTGC
U64205	HSU64205	5479	ACGGAGTCGCAATGTATCTGC
NM_004836	EIF2AK3	5480	ACGTGGAATTTTCAGTGTGGC
SK281	PEK	5480	ACGTGGAATTTTCAGTGTGGC
NM_004836	EIF2AK3	5481	ACCTCCTGTCTTGGTAGGATC
SK281	PEK	5481	ACCTCCTGTCTTGGTAGGATC
NM_004836	EIF2AK3	5482	ACAGGACTGATGCACAGGGAC
SK281	PEK	5482	ACAGGACTGATGCACAGGGAC
NM_005233	EPHA3	5483	ACGACCCTGAAAGTTGGCTAC
NM_005233	EPHA3	5484	ACCCTTCTTCTGGACCAAAGC
SK123	EphA3	5484	ACCCTTCTTCTGGACCAAAGC
NM_006180	NTRK2	5485	ACATGCAGTGCCTCTCGGATC
SK378	TRKB	5485	ACATGCAGTGCCTCTCGGATC
NM_006180	NTRK2	5486	ACTCTCCAACCTCAGACCACC
SK378	TRKB	5486	ACTCTCCAACCTCAGACCACC
NM_006180	NTRK2	5487	ACTTGACGATGGTGCAAACCC
SK378	TRKB	5487	ACTTGACGATGGTGCAAACCC
NM_001894	CSNK1E	5488	ACTTCAGCCTCAAGACGGTGC
SK084	CK1e	5488	ACTTCAGCCTCAAGACGGTGC
NM_001894	CSNK1E	5489	ACGGGCAACCTGGTCTACATC
SK084	CK1e	5489	ACGGGCAACCTGGTCTACATC
NM_001894	CSNK1E	5490	ACGAAGATGTCAACGCCCATC
SK084	CK1e	5490	ACGAAGATGTCAACGCCCATC
NM_006374	STK25	5491	ACGAGCACCAAGCTATGGATC
SK395	YSK1	5491	ACGAGCACCAAGCTATGGATC
NM_006374	STK25	5492	ACGAGGAACACATTTCGTGGGC
SK395	YSK1	5492	ACGAGGAACACATTTCGTGGGC
NM_006374	STK25	5493	ACAGAGAAGCACAAAGCAGAGC
SK395	YSK1	5493	ACAGAGAAGCACAAAGCAGAGC
NM_014264	STK18	5494	ACGCTCGACACTTCATGCACC

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SK341	PLK4	5494	ACGCTCGACACTTCATGCACC
NM_014264	STK18	5495	ACAGGCCACATTCTCGATACC
SK341	PLK4	5495	ACAGGCCACATTCTCGATACC
NM_014264	STK18	5496	ACCAAGAGCTGGTACCGCGTC
SK341	PLK4	5496	ACCAAGAGCTGGTACCGCGTC
BC011399	BC011399	5497	ACGGCACACCACTACACCATC
NM_003177	SYK	5497	ACGGCACACCACTACACCATC
SK363	SYK	5497	ACGGCACACCACTACACCATC
Z29630	HSSYKPTK	5497	ACGGCACACCACTACACCATC
BC011399	BC011399	5498	ACGGTGCTGCACTATCGCATC
NM_003177	SYK	5498	ACGGTGCTGCACTATCGCATC
SK363	SYK	5498	ACGGTGCTGCACTATCGCATC
Z29630	HSSYKPTK	5498	ACGGTGCTGCACTATCGCATC
BC011399	BC011399	5499	ACACTACTACAAGGCCAGAC
NM_003177	SYK	5499	ACACTACTACAAGGCCAGAC
SK363	SYK	5499	ACACTACTACAAGGCCAGAC
Z29630	HSSYKPTK	5499	ACACTACTACAAGGCCAGAC
NM_000455	STK11	5500	ACGGTGAAGGAGGTGCTGGAC
SK208	LKB1	5500	ACGGTGAAGGAGGTGCTGGAC
NM_000455	STK11	5501	ACCATCACCACGGGTCTGTAC
SK208	LKB1	5501	ACCATCACCACGGGTCTGTAC
NM_000455	STK11	5502	ACGGGATGCTTGAGTACGAAC
SK208	LKB1	5502	ACGGGATGCTTGAGTACGAAC
AF037333	AF037333	5503	ACACCTGAACACCATCCGCAC
NM_004441	EPHB1	5503	ACACCTGAACACCATCCGCAC
SK127	EphB1	5503	ACACCTGAACACCATCCGCAC
XM_172299	LOC256947	5503	ACACCTGAACACCATCCGCAC
AF037333	AF037333	5504	ACCCTGGTGTGCAAGGTGTCC
NM_004441	EPHB1	5504	ACCCTGGTGTGCAAGGTGTCC
SK127	EphB1	5504	ACCCTGGTGTGCAAGGTGTCC
AF037333	AF037333	5505	ACGACTGTGGCAACCATCACC
NM_004441	EPHB1	5505	ACGACTGTGGCAACCATCACC
SK127	EphB1	5505	ACGACTGTGGCAACCATCACC
NM_002378	MATK	5506	ACCAAGAGCTGGTACCGCGTC
NM_139354	MATK	5506	ACCAAGAGCTGGTACCGCGTC
NM_139355	MATK	5506	ACCAAGAGCTGGTACCGCGTC
SK418	CTK	5506	ACCAAGAGCTGGTACCGCGTC
NM_002378	MATK	5507	ACGGTGGCCGTGAAGAATATC
NM_139354	MATK	5507	ACGGTGGCCGTGAAGAATATC
NM_139355	MATK	5507	ACGGTGGCCGTGAAGAATATC
SK418	CTK	5507	ACGGTGGCCGTGAAGAATATC
NM_002378	MATK	5508	ACCATCCTGGTCTCAGAGGAC
NM_139354	MATK	5508	ACCATCCTGGTCTCAGAGGAC
NM_139355	MATK	5508	ACCATCCTGGTCTCAGAGGAC
SK418	CTK	5508	ACCATCCTGGTCTCAGAGGAC
NM_006738	AKAP13	5509	ACTGCTGGAGAACCAGACTCC

NM_007200	AKAP13	5509	ACTGCTGGAGAACCAGACTCC
NM_006738	AKAP13	5510	ACCACAGTGACTTCTAGTGGC
NM_007200	AKAP13	5510	ACCACAGTGACTTCTAGTGGC
NM_006738	AKAP13	5511	ACTGGAGAAAGAACTGGTGCC
NM_007200	AKAP13	5511	ACTGGAGAAAGAACTGGTGCC
NM_003656	CAMK1	5512	ACCATTGTAGCCCTGGATGAC
SK056	CaMK1a	5512	ACCATTGTAGCCCTGGATGAC
NM_003656	CAMK1	5513	ACATACCTGCATGACCTGGGC
SK056	CaMK1a	5513	ACATACCTGCATGACCTGGGC
NM_003656	CAMK1	5514	ACGGCCGAGTACGAGTTTGAC
SK056	CaMK1a	5514	ACGGCCGAGTACGAGTTTGAC
NM_004194	ADAM22	5515	ACGATGGGACACCTTGTGGTC
NM_016351	ADAM22	5515	ACGATGGGACACCTTGTGGTC
NM_021721	ADAM22	5515	ACGATGGGACACCTTGTGGTC
NM_021722	ADAM22	5515	ACGATGGGACACCTTGTGGTC
NM_021723	ADAM22	5515	ACGATGGGACACCTTGTGGTC
NM_020168	PAK6	5516	ACAGAAGGCAAGTTTGTGGGC
SK429	PAK6	5516	ACAGAAGGCAAGTTTGTGGGC
NM_020168	PAK6	5517	ACGCGCAGGCTATTCCGAAGC
SK429	PAK6	5517	ACGCGCAGGCTATTCCGAAGC
NM_020168	PAK6	5518	ACGTCAGGCTGAATGAGGAGC
SK429	PAK6	5518	ACGTCAGGCTGAATGAGGAGC
NM_020168	PAK6	5519	ACACTCTCACAAGGTCTCCCC
SK429	PAK6	5519	ACACTCTCACAAGGTCTCCCC
NM_032237	FLJ23356	5520	ACTGACTTGGACGCCTTACCC
NM_018291	FLJ10986	5521	ACGTTGTGTTCCCCGAGACTAC
NM_014006	SMG1	5522	ACTATCTGTCTGCAGGCATGC
NM_015092	SMG1	5522	ACTATCTGTCTGCAGGCATGC
SK665	SMG1	5522	ACTATCTGTCTGCAGGCATGC
NM_014006	SMG1	5523	ACGGCCATGGTAACAACCAAC
NM_015092	SMG1	5523	ACGGCCATGGTAACAACCAAC
SK665	SMG1	5523	ACGGCCATGGTAACAACCAAC
NM_014006	SMG1	5524	ACATCGGTGCTCACCTTAGCC
NM_015092	SMG1	5524	ACATCGGTGCTCACCTTAGCC
SK665	SMG1	5524	ACATCGGTGCTCACCTTAGCC
NM_015092	SMG1	5525	ACTCTTCTTCGGAGGATCACC
NM_031211	LAT1-3TM	5525	ACTCTTCTTCGGAGGATCACC
SK665	SMG1	5525	ACTCTTCTTCGGAGGATCACC
NM_014006	SMG1	5526	ACTGCATTAACCTTCACCTCCC
NM_015092	SMG1	5526	ACTGCATTAACCTTCACCTCCC
SK665	SMG1	5526	ACTGCATTAACCTTCACCTCCC
NM_014006	SMG1	5527	ACTTGCTGTCTGGTCATCATC
NM_015092	SMG1	5527	ACTTGCTGTCTGGTCATCATC
SK665	SMG1	5527	ACTTGCTGTCTGGTCATCATC
NG_001070	NG_001070	5528	ACGTTGGTGAGATGGCAAAGC
NM_013410	AK3	5528	ACGTTGGTGAGATGGCAAAGC

NG_001070	NG_001070	5529	ACAGACGTGGCAAAGCCAGTC
NM_013410	AK3	5529	ACAGACGTGGCAAAGCCAGTC
NG_001070	NG_001070	5530	ACTCTGGCCCTACGTTTACAC
NM_013410	AK3	5530	ACTCTGGCCCTACGTTTACAC
NM_030662	MAP2K2	5531	ACGATGCTCACAAACCACACC
SK218	MAP2K2	5531	ACGATGCTCACAAACCACACC
NM_001570	IRAK2	5532	ACTCAGGTGTCCATTCCAGC
SK180	IRAK2	5532	ACTCAGGTGTCCATTCCAGC
NM_001570	IRAK2	5533	ACGAAGCTCAGAGAGACAGCC
SK180	IRAK2	5533	ACGAAGCTCAGAGAGACAGCC
NM_001570	IRAK2	5534	ACCGTCAAGAGCTCTAATGTC
SK180	IRAK2	5534	ACCGTCAAGAGCTCTAATGTC
NM_001570	IRAK2	5535	ACTTCCAGCCTTGATGCCTCC
SK180	IRAK2	5535	ACTTCCAGCCTTGATGCCTCC
NM_005546	ITK	5536	ACTACCCGTTTCAGGTGGTGC
SK184	ITK	5536	ACTACCCGTTTCAGGTGGTGC
NM_005546	ITK	5537	ACAGAAGCCTCTTCCTCCTAC
SK184	ITK	5537	ACAGAAGCCTCTTCCTCCTAC
NM_005546	ITK	5538	ACCTCAGAGGTGGTGGGAAGAC
SK184	ITK	5538	ACCTCAGAGGTGGTGGGAAGAC
NM_002756	MAP2K3	5539	ACCATGACAATTCCAGAGGAC
NM_145109	MAP2K3	5539	ACCATGACAATTCCAGAGGAC
NM_145110	MAP2K3	5539	ACCATGACAATTCCAGAGGAC
SK238	MAP2K3	5539	ACCATGACAATTCCAGAGGAC
NM_002756	MAP2K3	5540	ACGCCCTCCAATGTCTTATC
NM_145109	MAP2K3	5540	ACGCCCTCCAATGTCTTATC
NM_145110	MAP2K3	5540	ACGCCCTCCAATGTCTTATC
SK238	MAP2K3	5540	ACGCCCTCCAATGTCTTATC
NM_002756	MAP2K3	5541	ACCCAGAAGGGCTACAATGTC
NM_145109	MAP2K3	5541	ACCCAGAAGGGCTACAATGTC
NM_145110	MAP2K3	5541	ACCCAGAAGGGCTACAATGTC
SK238	MAP2K3	5541	ACCCAGAAGGGCTACAATGTC
XM_064224	LOC124609	5541	ACCCAGAAGGGCTACAATGTC
NM_002756	MAP2K3	5542	ACGAAGACGGACATTGCTGCC
NM_145109	MAP2K3	5542	ACGAAGACGGACATTGCTGCC
NM_145110	MAP2K3	5542	ACGAAGACGGACATTGCTGCC
SK238	MAP2K3	5542	ACGAAGACGGACATTGCTGCC
XM_064224	LOC124609	5542	ACGAAGACGGACATTGCTGCC
NM_002756	MAP2K3	5543	ACGACGGACATTGCTGCCTTC
NM_145109	MAP2K3	5543	ACGACGGACATTGCTGCCTTC
NM_145110	MAP2K3	5543	ACGACGGACATTGCTGCCTTC
SK238	MAP2K3	5543	ACGACGGACATTGCTGCCTTC
XM_064224	LOC124609	5543	ACGACGGACATTGCTGCCTTC
NM_016457	PKD2	5544	ACGATGCTGCTCTCCAAGGTC
SK480	PKD2	5544	ACGATGCTGCTCTCCAAGGTC
NM_016457	PKD2	5545	ACCTCCTCAAGGGCCTCTTCC

SK480	PKD2	5545	ACCTCCTCAAGGGCCTCTTCC
NM_016457	PKD2	5546	ACCCACACTGCTTTGAGATC
SK480	PKD2	5546	ACCCACACTGCTTTGAGATC
NM_016457	PKD2	5547	ACGTTCCCTCATCACCAGATC
SK480	PKD2	5547	ACGTTCCCTCATCACCAGATC
NM_016457	PKD2	5548	ACTGACCAGATCCAGAACGCC
SK480	PKD2	5548	ACTGACCAGATCCAGAACGCC
NM_016457	PKD2	5549	ACGATGGGAGAGCGATACATC
SK480	PKD2	5549	ACGATGGGAGAGCGATACATC
NM_005813	PRKCN	5550	ACGTCCTAAGACGGGACTCTC
SK489	PKD3	5550	ACGTCCTAAGACGGGACTCTC
NM_005813	PRKCN	5551	ACCGATGTGCCTTCAAGATTC
SK489	PKD3	5551	ACCGATGTGCCTTCAAGATTC
NM_005813	PRKCN	5552	ACATGTGCTGCTTGATCAGC
SK489	PKD3	5552	ACATGTGCTGCTTGATCAGC
NM_002740	PRKCI	5553	ACTGGCCACACTTTCCAAGCC
SK308	PKCi	5553	ACTGGCCACACTTTCCAAGCC
XM_052135	LOC88137	5553	ACTGGCCACACTTTCCAAGCC
NM_002740	PRKCI	5554	ACTTGAATGTGGGCGGCATTC
SK308	PKCi	5554	ACTTGAATGTGGGCGGCATTC
XM_052135	LOC88137	5554	ACTTGAATGTGGGCGGCATTC
NM_002740	PRKCI	5555	ACATTTCGCATACCACGTTCTC
SK308	PKCi	5555	ACATTTCGCATACCACGTTCTC
XM_052135	LOC88137	5555	ACATTTCGCATACCACGTTCTC
NM_001892	CSNK1A1	5556	ACCTATTGTGCTGGGCTACGC
SK082	CK1a	5556	ACCTATTGTGCTGGGCTACGC
XM_046996	CSNK1A1	5556	ACGCAAGCGTACCATCTACAC
NM_017859	URKL1	5557	ACCAAGTTTGTCAAGCCCTCC
NM_017859	URKL1	5558	ACGCAAGTACCCGGTGTGTCC
NM_017859	URKL1	5559	ACGCAAGTACCCGGTGTGTCC
NM_002757	MAP2K5	5560	ACGTGATGAGGAAATGAAGGC
NM_145160	MAP2K5	5560	ACGTGATGAGGAAATGAAGGC
NM_145161	MAP2K5	5560	ACGTGATGAGGAAATGAAGGC
SK219	MAP2K5	5560	ACGTGATGAGGAAATGAAGGC
NM_002757	MAP2K5	5561	ACCAAATGCTTATATGGCGCC
NM_145160	MAP2K5	5561	ACCAAATGCTTATATGGCGCC
NM_145161	MAP2K5	5561	ACCAAATGCTTATATGGCGCC
NM_145162	MAP2K5	5561	ACCAAATGCTTATATGGCGCC
SK219	MAP2K5	5561	ACCAAATGCTTATATGGCGCC
NM_002757	MAP2K5	5562	ACACCAGGGATCTTTAATGCC
NM_145160	MAP2K5	5562	ACACCAGGGATCTTTAATGCC
NM_145161	MAP2K5	5562	ACACCAGGGATCTTTAATGCC
NM_145162	MAP2K5	5562	ACACCAGGGATCTTTAATGCC
SK219	MAP2K5	5562	ACACCAGGGATCTTTAATGCC
NM_002757	MAP2K5	5563	ACCCAAGGAGAACAACCCACC
NM_145160	MAP2K5	5563	ACCCAAGGAGAACAACCCACC

NM_145162	MAP2K5	5563	ACCCAAGGAGAACAACCCACC
SK219	MAP2K5	5563	ACCCAAGGAGAACAACCCACC
NM_005043	MAP2K7	5564	ACCAAGGAGGAGAACAAGCGC
NM_145185	MAP2K7	5564	ACCAAGGAGGAGAACAAGCGC
SK230	MAP2K7	5564	ACCAAGGAGGAGAACAAGCGC
NM_005043	MAP2K7	5565	ACCACGGACGTCTTCATCGCC
NM_145185	MAP2K7	5565	ACCACGGACGTCTTCATCGCC
SK230	MAP2K7	5565	ACCACGGACGTCTTCATCGCC
NM_005043	MAP2K7	5566	ACGCTACTTGAACACAGCTTC
NM_145185	MAP2K7	5566	ACGCTACTTGAACACAGCTTC
SK230	MAP2K7	5566	ACGCTACTTGAACACAGCTTC
NM_002446	MAP3K10	5567	ACGTCCATCAACATCCTGATC
SK233	MLK2	5567	ACGTCCATCAACATCCTGATC
NM_002446	MAP3K10	5568	ACGTCATCGAACAGTCAGCCC
SK233	MLK2	5568	ACGTCATCGAACAGTCAGCCC
NM_002446	MAP3K10	5569	ACACAGTGGTCATCAAGTGCC
SK233	MLK2	5569	ACACAGTGGTCATCAAGTGCC
NM_002419	MAP3K11	5570	ACGGCAGCGGGTTATGCCAAC
SK356	MLK3	5570	ACGGCAGCGGGTTATGCCAAC
NM_002419	MAP3K11	5571	ACCTGGGCTGTGCAGATTGCC
SK356	MLK3	5571	ACCTGGGCTGTGCAGATTGCC
NM_002419	MAP3K11	5572	ACCAAGCTCACACTGCCCATC
SK356	MLK3	5572	ACCAAGCTCACACTGCCCATC
NM_004721	MAP3K13	5573	ACGGGTGTTTGTACTIONCAGGCC
SK398	LZK	5573	ACGGGTGTTTGTACTIONCAGGCC
NM_004721	MAP3K13	5574	ACCAGACGTGGCAGAGTAAAC
SK398	LZK	5574	ACCAGACGTGGCAGAGTAAAC
NM_004721	MAP3K13	5575	ACTCTGGGATGCAGACCAAAC
SK398	LZK	5575	ACTCTGGGATGCAGACCAAAC
NM_006609	MAP3K2	5576	ACTCACGAATGCCTAGGGCTC
SK222	MAP3K2	5576	ACTCACGAATGCCTAGGGCTC
NM_006609	MAP3K2	5577	ACCGGCTTCAGACCATCTGTC
SK222	MAP3K2	5577	ACCGGCTTCAGACCATCTGTC
NM_006609	MAP3K2	5578	ACAGCTGCCACCTCATGTCTC
SK222	MAP3K2	5578	ACAGCTGCCACCTCATGTCTC
NM_003188	MAP3K7	5579	ACGTGATAACCGCTCGGAAAC
NM_145331	MAP3K7	5579	ACGTGATAACCGCTCGGAAAC
NM_145332	MAP3K7	5579	ACGTGATAACCGCTCGGAAAC
NM_145333	MAP3K7	5579	ACGTGATAACCGCTCGGAAAC
SK364	TAK1	5579	ACGTGATAACCGCTCGGAAAC
NM_003188	MAP3K7	5580	ACTATGGAGCAAGTTCCTGCC
NM_145331	MAP3K7	5580	ACTATGGAGCAAGTTCCTGCC
NM_145332	MAP3K7	5580	ACTATGGAGCAAGTTCCTGCC
NM_145333	MAP3K7	5580	ACTATGGAGCAAGTTCCTGCC
SK364	TAK1	5580	ACTATGGAGCAAGTTCCTGCC
NM_003188	MAP3K7	5581	ACCTAGTTGCAGAACTGGACC

NM_145331	MAP3K7	5581	ACCTAGTTGCAGAACTGGACC
NM_145332	MAP3K7	5581	ACCTAGTTGCAGAACTGGACC
NM_145333	MAP3K7	5581	ACCTAGTTGCAGAACTGGACC
SK364	TAK1	5581	ACCTAGTTGCAGAACTGGACC
NM_053006	STK22B	5582	ACATCTGCCTACTCTGAGCGC
SK474	TSSK2	5582	ACATCTGCCTACTCTGAGCGC
NM_053006	STK22B	5583	ACGCTGTCTGACTTTGGCTTC
SK474	TSSK2	5583	ACGCTGTCTGACTTTGGCTTC
NM_053006	STK22B	5584	ACACTGGACACCAAGACAGGC
SK474	TSSK2	5584	ACACTGGACACCAAGACAGGC
NM_000690	ALDH2	5585	ACGAAGATCCTCGGCTACATC
NM_014586	HUNK	5586	ACATATTTCAGCAGGCACTGGC
SK502	HUNK	5586	ACATATTTCAGCAGGCACTGGC
NM_014586	HUNK	5587	ACTTGTGTGGCTTCTTCTTCC
SK502	HUNK	5587	ACTTGTGTGGCTTCTTCTTCC
NM_014586	HUNK	5588	ACGCATGTGCGCTCTCCATAC
SK502	HUNK	5588	ACGCATGTGCGCTCTCCATAC
NM_014791	MELK	5589	ACTTTCCCAGGATCGCCTGTC
SK298	MELK	5589	ACTTTCCCAGGATCGCCTGTC
NM_014791	MELK	5590	ACCTCCAGCCTTATGCAGAAC
SK298	MELK	5590	ACCTCCAGCCTTATGCAGAAC
NM_014791	MELK	5591	ACTGACAGGTGTCATTAGCCC
SK298	MELK	5591	ACTGACAGGTGTCATTAGCCC
NM_001319	CSNK1G2	5592	ACATTGGAGCCGATCAAGTCC
SK086	CK1g2	5592	ACATTGGAGCCGATCAAGTCC
NM_001319	CSNK1G2	5593	ACGACGGTGCTGATGATCGCC
SK086	CK1g2	5593	ACGACGGTGCTGATGATCGCC
NM_001319	CSNK1G2	5594	ACACCAGGCGTTGAACTCCAC
SK086	CK1g2	5594	ACACCAGGCGTTGAACTCCAC
L11315	HUMRTK	5595	ACGAGGAGCTGACGGTTCACC
L20817	HUMCAK	5595	ACGAGGAGCTGACGGTTCACC
L57508	HUMCAKA	5595	ACGAGGAGCTGACGGTTCACC
NM_001954	DDR1	5595	ACGAGGAGCTGACGGTTCACC
NM_013993	DDR1	5595	ACGAGGAGCTGACGGTTCACC
NM_013994	DDR1	5595	ACGAGGAGCTGACGGTTCACC
SK400	DDR1	5595	ACGAGGAGCTGACGGTTCACC
U48705	HSU48705	5595	ACGAGGAGCTGACGGTTCACC
XM_165738	DDR1	5595	ACGAGGAGCTGACGGTTCACC
Z29093	HSRETYK1	5595	ACGAGGAGCTGACGGTTCACC
L11315	HUMRTK	5596	ACGATCTTACGGCCAGATGCC
L20817	HUMCAK	5596	ACGATCTTACGGCCAGATGCC
L57508	HUMCAKA	5596	ACGATCTTACGGCCAGATGCC
NM_001954	DDR1	5596	ACGATCTTACGGCCAGATGCC
NM_013993	DDR1	5596	ACGATCTTACGGCCAGATGCC
NM_013994	DDR1	5596	ACGATCTTACGGCCAGATGCC
SK400	DDR1	5596	ACGATCTTACGGCCAGATGCC

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U48705	HSU48705	5596	ACGATCTTACGGCCAGATGCC
XM_165738	DDR1	5596	ACGATCTTACGGCCAGATGCC
Z29093	HSRETYK1	5596	ACGATCTTACGGCCAGATGCC
L11315	HUMRTK	5597	ACCAAGAGGACACAATGGCAC
L20817	HUMCAK	5597	ACCAAGAGGACACAATGGCAC
L57508	HUMCAKA	5597	ACCAAGAGGACACAATGGCAC
NM_001954	DDR1	5597	ACCAAGAGGACACAATGGCAC
NM_013993	DDR1	5597	ACCAAGAGGACACAATGGCAC
NM_013994	DDR1	5597	ACCAAGAGGACACAATGGCAC
SK400	DDR1	5597	ACCAAGAGGACACAATGGCAC
U48705	HSU48705	5597	ACCAAGAGGACACAATGGCAC
XM_165738	DDR1	5597	ACCAAGAGGACACAATGGCAC
Z29093	HSRETYK1	5597	ACCAAGAGGACACAATGGCAC
NM_000389	CDKN1A	5598	ACGACCATGTGGACCTGTCAC
NM_078467	CDKN1A	5598	ACGACCATGTGGACCTGTCAC
NM_000389	CDKN1A	5599	ACAGGCCCGCTCTACATCTTC
NM_078467	CDKN1A	5599	ACAGGCCCGCTCTACATCTTC
NM_000389	CDKN1A	5600	ACCACCTCCTCATGTACATAC
NM_078467	CDKN1A	5600	ACCACCTCCTCATGTACATAC
NM_004714	DYRK1B	5601	ACGCTCTCTGTGGACCTCATC
NM_006483	DYRK1B	5601	ACGCTCTCTGTGGACCTCATC
NM_006484	DYRK1B	5601	ACGCTCTCTGTGGACCTCATC
SK114	DYRK1B	5601	ACGCTCTCTGTGGACCTCATC
NM_004714	DYRK1B	5602	ACGGAGAAGAAGGTCCTGAAC
NM_006483	DYRK1B	5602	ACGGAGAAGAAGGTCCTGAAC
NM_006484	DYRK1B	5602	ACGGAGAAGAAGGTCCTGAAC
SK114	DYRK1B	5602	ACGGAGAAGAAGGTCCTGAAC
NM_004714	DYRK1B	5603	ACTGAGGTCGACCAGATGAAC
NM_006483	DYRK1B	5603	ACTGAGGTCGACCAGATGAAC
NM_006484	DYRK1B	5603	ACTGAGGTCGACCAGATGAAC
SK114	DYRK1B	5603	ACTGAGGTCGACCAGATGAAC
NM_003583	DYRK2	5604	ACACTCACAGCCTTCGAACAC
NM_006482	DYRK2	5604	ACACTCACAGCCTTCGAACAC
SK115	DYRK2	5604	ACACTCACAGCCTTCGAACAC
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SK115	DYRK2	5605	ACCTGCTGGATGCATCCAAAC
NM_003583	DYRK2	5606	ACGTTACCTCCACCTTCTAGC
NM_006482	DYRK2	5606	ACGTTACCTCCACCTTCTAGC
SK115	DYRK2	5606	ACGTTACCTCCACCTTCTAGC
NM_003583	DYRK2	5607	ACTTTCACCTTCCGCAACCAC
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SK115	DYRK2	5607	ACTTTCACCTTCCGCAACCAC
NM_004442	EPHB2	5608	ACTGGCTACTACAGAGCAGAC
NM_017449	EPHB2	5608	ACTGGCTACTACAGAGCAGAC
SK128	EphB2	5608	ACTGGCTACTACAGAGCAGAC

NM_004442	EPHB2	5609	ACGTTGCCACTCATCATCGGC
NM_017449	EPHB2	5609	ACGTTGCCACTCATCATCGGC
SK128	EphB2	5609	ACGTTGCCACTCATCATCGGC
NM_004442	EPHB2	5610	ACGTACCTGGCAGACATGAAC
NM_017449	EPHB2	5610	ACGTACCTGGCAGACATGAAC
SK128	EphB2	5610	ACGTACCTGGCAGACATGAAC
NM_000604	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
NM_015850	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
NM_023105	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
NM_023106	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
NM_023107	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
NM_023108	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
NM_023109	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
NM_023111	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
SK143	FGFR1	5611	ACTGAGTACGGCAGCATCAAC
NM_000604	FGFR1	5612	ACGACTGCTGGAGTTAATACC
NM_015850	FGFR1	5612	ACGACTGCTGGAGTTAATACC
NM_023105	FGFR1	5612	ACGACTGCTGGAGTTAATACC
NM_023106	FGFR1	5612	ACGACTGCTGGAGTTAATACC
NM_023109	FGFR1	5612	ACGACTGCTGGAGTTAATACC
NM_023111	FGFR1	5612	ACGACTGCTGGAGTTAATACC
SK143	FGFR1	5612	ACGACTGCTGGAGTTAATACC
NM_000604	FGFR1	5613	ACCTGCACCAACGAGCTGTAC
NM_015850	FGFR1	5613	ACCTGCACCAACGAGCTGTAC
NM_023105	FGFR1	5613	ACCTGCACCAACGAGCTGTAC
NM_023106	FGFR1	5613	ACCTGCACCAACGAGCTGTAC
NM_023109	FGFR1	5613	ACCTGCACCAACGAGCTGTAC
SK143	FGFR1	5613	ACCTGCACCAACGAGCTGTAC
NM_002758	MAP2K6	5614	ACTGGAAGTGGGACGAGGTGC
NM_031988	MAP2K6	5614	ACTGGAAGTGGGACGAGGTGC
SK220	MAP2K6	5614	ACTGGAAGTGGGACGAGGTGC
NM_002758	MAP2K6	5615	ACTTGATGCAGGTTGCAAACC
NM_031988	MAP2K6	5615	ACTTGATGCAGGTTGCAAACC
SK220	MAP2K6	5615	ACTTGATGCAGGTTGCAAACC
NM_002758	MAP2K6	5616	ACCGGCCTACATACCCAGAGC
NM_031988	MAP2K6	5616	ACCGGCCTACATACCCAGAGC
SK220	MAP2K6	5616	ACCGGCCTACATACCCAGAGC
NM_003559	PIP5K2B	5617	ACAGTGAAGCTATTCCGGGCC
NM_138687	PIP5K2B	5617	ACAGTGAAGCTATTCCGGGCC
NM_003559	PIP5K2B	5618	ACCTACTCTGCTCCTATGGC
NM_003559	PIP5K2B	5619	ACAGAAGAAAGCTGCACATGC
NM_000323	RET	5620	ACCTCTCCATCTCGGAGAAC
NM_020629	RET	5620	ACCTCTCCATCTCGGAGAAC
NM_020630	RET	5620	ACCTCTCCATCTCGGAGAAC
NM_020975	RET	5620	ACCTCTCCATCTCGGAGAAC
SK326	RET	5620	ACCTCTCCATCTCGGAGAAC

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NM_031414	STK31	5621	ACACAGAGAAGGACGCTCTTC
NM_032944	STK31	5621	ACACAGAGAAGGACGCTCTTC
SK652	SgK396	5621	ACACAGAGAAGGACGCTCTTC
NM_031414	STK31	5622	ACGACTGAGTCAAGTGTCTGC
NM_032944	STK31	5622	ACGACTGAGTCAAGTGTCTGC
SK652	SgK396	5622	ACGACTGAGTCAAGTGTCTGC
NM_031414	STK31	5623	ACATCTGTGAGTCAGCGAGCC
NM_032944	STK31	5623	ACATCTGTGAGTCAGCGAGCC
SK652	SgK396	5623	ACATCTGTGAGTCAGCGAGCC
AL121939	HSDJ223E3	5624	ACCTCCTGACCTCAAGTGATC
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NG_001332	NG_001332	5624	ACCTCCTGACCTCAAGTGATC
NG_001333	NG_001333	5624	ACCTCCTGACCTCAAGTGATC
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NM_000098	CPT2	5624	ACCTCCTGACCTCAAGTGATC
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NM_003678	C22orf19	5624	ACCTCCTGACCTCAAGTGATC
NM_003831	SUDD	5624	ACCTCCTGACCTCAAGTGATC
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NM_005128	C21orf5	5624	ACCTCCTGACCTCAAGTGATC
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NM_013306	SNX15	5624	ACCTCCTGACCTCAAGTGATC
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NM_014395	DAPP1	5624	ACCTCCTGACCTCAAGTGATC
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NM_014860	STAF65(gamma)	5624	ACCTCCTGACCTCAAGTGATC
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NM_014948	UBCE7IP5	5624	ACCTCCTGACCTCAAGTGATC
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NM_015989	CSAD	5624	ACCTCCTGACCTCAAGTGATC
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NM_016225	RHD	5624	ACCTCCTGACCTCAAGTGATC
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NM_024656	FLJ22329	5624	ACCTCCTGACCTCAAGTGATC
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NM_024840	FLJ13590	5624	ACCTCCTGACCTCAAGTGATC
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NM_024976	FLJ11996	5624	ACCTCCTGACCTCAAGTGATC
NM_025012	FLJ13769	5624	ACCTCCTGACCTCAAGTGATC
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NM_031409	CCR6	5624	ACCTCCTGACCTCAAGTGATC
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NM_032151	DCOHM	5624	ACCTCCTGACCTCAAGTGATC
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NM_032831	CBCIP2	5624	ACCTCCTGACCTCAAGTGATC
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NM_145044	MGC21738	5624	ACCTCCTGACCTCAAGTGATC
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NM_145759	TRAF5	5624	ACCTCCTGACCTCAAGTGATC
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U63721	HSU63721	5624	ACCTCCTGACCTCAAGTGATC
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XM_113904	LOC201164	5624	ACCTCCTGACCTCAAGTGATC
XM_166943	LOC220370	5624	ACCTCCTGACCTCAAGTGATC
Z84476	HS25J6	5624	ACCTCCTGACCTCAAGTGATC
Z98744	HS193B12	5624	ACCTCCTGACCTCAAGTGATC
NM_001699	AXL	5625	ACTCACCTCCCTGCAGCTTTC
NM_021913	AXL	5625	ACTCACCTCCCTGCAGCTTTC
SK044	AXL	5625	ACTCACCTCCCTGCAGCTTTC
NM_001699	AXL	5626	ACCTGCATGCTGAATGAGAAC
NM_021913	AXL	5626	ACCTGCATGCTGAATGAGAAC
SK044	AXL	5626	ACCTGCATGCTGAATGAGAAC
NM_001699	AXL	5627	ACGAGCGATGTGTGGTCCTTC
NM_021913	AXL	5627	ACGAGCGATGTGTGGTCCTTC
SK044	AXL	5627	ACGAGCGATGTGTGGTCCTTC
NM_000051	ATM	5628	ACGTCAGGTTTGCCAGACAGC
NM_138292	ATM	5628	ACGTCAGGTTTGCCAGACAGC
SK038	ATM	5628	ACGTCAGGTTTGCCAGACAGC
NM_005204	MAP3K8	5632	ACGTCTCTGCTGCTTAGTGCC
SK093	COT	5632	ACGTCTCTGCTGCTTAGTGCC
NM_005204	MAP3K8	5633	ACCATCGCAGAGCTGTATGGC
SK093	COT	5633	ACCATCGCAGAGCTGTATGGC
NM_005204	MAP3K8	5634	ACCGCTCTCTCTACATCGACC
SK093	COT	5634	ACCGCTCTCTCTACATCGACC
NM_002741	PRKCL1	5635	ACCATGATCCAGACCTACAGC
SK317	PKN1	5635	ACCATGATCCAGACCTACAGC

NM_002741	PRKCL1	5636	ACTGCCTGGGACCAGAGCTTC
SK317	PKN1	5636	ACTGCCTGGGACCAGAGCTTC
NM_002741	PRKCL1	5637	ACGATCGCAGACTTTGGCCTC
SK317	PKN1	5637	ACGATCGCAGACTTTGGCCTC
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NM_000291	PGK1	5639	ACGATTACCTTGCCCTGTTGAC
NM_000291	PGK1	5640	ACCACGGAGGATAAAGTCAGC
NM_001826	CKS1B	5641	ACCCCATCTGATGTCTGAATC
NM_001826	CKS1B	5642	ACCCAGAACCTCACATCTTGC
NM_001826	CKS1B	5643	ACCCAAAGAAATGAAGCTGGC
NM_017593	BIKE	5644	ACGCTGTTGCAAGGTTGCATC
SK704	BIKE	5644	ACGCTGTTGCAAGGTTGCATC
NM_017593	BIKE	5645	ACCTCTGTCATACAGAGCCCC
SK704	BIKE	5645	ACCTCTGTCATACAGAGCCCC
NM_017593	BIKE	5646	ACCCTTTATGGAGGGAAACCC
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NM_017593	BIKE	5647	ACTTCTCGTTACTCCCGTAAC
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NM_007194	CHEK2	5649	ACACGCCTGAAAGAAGCTACC
NM_145862	CHEK2	5649	ACACGCCTGAAAGAAGCTACC
NM_007194	CHEK2	5650	ACTGAATCCACAGCTCTACCC
NM_145862	CHEK2	5650	ACTGAATCCACAGCTCTACCC
NM_032294	CAMKK1	5651	ACGCTGCAGAGTGAGATTGGC
NM_032294	CAMKK1	5652	ACGTTACTGAAGCAGTATGGC
NM_032294	CAMKK1	5653	ACGGCCTTGGATGTATGGGCC
NM_032028	STK22D	5654	ACATCTGCTTACTCTGAGCGC
SK705	TSSK1	5654	ACATCTGCTTACTCTGAGCGC
NM_032028	STK22D	5655	ACGCAAGACCTTCTGTGGGTC
SK705	TSSK1	5655	ACGCAAGACCTTCTGTGGGTC
NM_032028	STK22D	5656	ACTGCAAATGTCCAGGCAGTC
SK705	TSSK1	5656	ACTGCAAATGTCCAGGCAGTC
XM_066264	LOC128968	5656	ACTGCAAATGTCCAGGCAGTC
NM_017719	SNRK	5657	ACGACCTAATCACACGGATGC
NM_017719	SNRK	5658	ACTGGCCACAGGAGCAAAGGC
NM_017719	SNRK	5659	ACATAACGTGCTGCAGCTACC
NM_003161	RPS6KB1	5660	ACACTAGTGTGAACAGAGGGC
SK265	p70S6K	5660	ACACTAGTGTGAACAGAGGGC
NM_003161	RPS6KB1	5661	ACCTCAATTTGCCTCCCTACC
SK265	p70S6K	5661	ACCTCAATTTGCCTCCCTACC
NM_003161	RPS6KB1	5662	ACAGAAATGCTGCTTCTCGTC
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SK256	NEK4	5663	ACACTGAACCTCCGAAATGCC
NM_003157	NEK4	5664	ACCACATCCTTCATCGAGATC
SK256	NEK4	5664	ACCACATCCTTCATCGAGATC

NM_003157	NEK4	5665	ACGGAGCAGTGAGATGTCATC
SK256	NEK4	5665	ACGGAGCAGTGAGATGTCATC
NM_004317	ASNA1	5666	ACGAAGATGATGCAGGAGGCC
NM_004317	ASNA1	5667	ACCAGTTCAAGGACCCTGAGC
NM_007199	IRAK3	5668	ACTTACTTTGGTCCTGGGCAC
SK181	IRAK3	5668	ACTTACTTTGGTCCTGGGCAC
NM_007199	IRAK3	5669	ACGGAAACAGCCAATGTCACC
SK181	IRAK3	5669	ACGGAAACAGCCAATGTCACC
NM_007199	IRAK3	5670	ACAGTCCTTCAGGTGTCCTTC
SK181	IRAK3	5670	ACAGTCCTTCAGGTGTCCTTC
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SK236	MKNK2	5671	ACACATCCTCTGTGAGCACCC
NM_017572	MKNK2	5672	ACCATGCTGTTTGAGAGCATC
SK236	MKNK2	5672	ACCATGCTGTTTGAGAGCATC
NM_017572	MKNK2	5673	ACGACCTCATCTCCAAGCTGC
SK236	MKNK2	5673	ACGACCTCATCTCCAAGCTGC
NM_004954	MARK2	5674	ACAGAGGTAGCTGTGAAGATC
NM_017490	MARK2	5674	ACAGAGGTAGCTGTGAAGATC
SK120	MARK2	5674	ACAGAGGTAGCTGTGAAGATC
NM_004954	MARK2	5675	ACGCAAAGACCGAGTGGAGAC
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SK120	MARK2	5675	ACGCAAAGACCGAGTGGAGAC
NM_004954	MARK2	5676	ACGAATTTCTGGGAGGCCAAGC
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SK120	MARK2	5676	ACGAATTTCTGGGAGGCCAAGC
NM_004900	APOBEC3B	5677	ACCACACACGTGAGACTGCGC
NM_145699	APOBEC3A	5677	ACCACACACGTGAGACTGCGC
NM_006587	PRSC	5678	ACTGGGAGTGAACCTTTGGTC
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NM_006587	PRSC	5680	ACGACCATCATCCTGCATCCC
NM_014058	DESC1	5681	ACTGAGCCAGAGACTTGAATC
NM_014058	DESC1	5682	ACGTAGAAGAGGGTGAATGGC
NM_014058	DESC1	5683	ACCTTGCAATGAACCTCAAGC
NM_001935	DPP4	5684	ACAGGCAGGAGCTGTGAATCC
NM_001935	DPP4	5685	ACGATGGAACTGCTTAGTGGC
NM_001935	DPP4	5686	ACCCTCAATGGTCCTGGGATC
NM_001936	DPP6	5687	ACGGTGTGATTTACAATGGCC
NM_130797	DPP6	5687	ACGGTGTGATTTACAATGGCC
NM_001936	DPP6	5688	ACCACGGTGGGCAACTTCAAC
NM_130797	DPP6	5688	ACCACGGTGGGCAACTTCAAC
NM_001936	DPP6	5689	ACCAGAGCATACGAGATGACC
NM_130797	DPP6	5689	ACCAGAGCATACGAGATGACC
NM_002772	PRSS7	5690	ACCCAACTTTGGTGCCAACTC
NM_002772	PRSS7	5691	ACGTGGACAGCAATCCTAGGC
NM_004262	HAT	5692	ACTCCTCGTGACTGGATTGCC
NM_004262	HAT	5693	ACTATGCTGGCCACACAGTTC

NM_004262	HAT	5694	ACTGCTGTGTGCTGGAGTACC
NM_002151	HPN	5695	ACCAGCGAGGAGAACAGCAAC
NM_002151	HPN	5696	ACGATGTTCTGTGCTGGCTAC
NM_002773	PRSS8	5697	ACGGTCAGCACCCCTGAAGGAC
NM_002773	PRSS8	5698	ACCTGCCTGTACAACATCGAC
NM_002773	PRSS8	5699	ACAGCAAGGTGACAGAACTCC
NM_021978	ST14	5700	ACTTCTTCTACCTGCTGGAGC
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NM_021978	ST14	5702	ACGAACAAGTTCTGCAAGCCC
NM_005656	TMPRSS2	5703	ACTCGGTGTGTTTCGCTCTAC
NM_005656	TMPRSS2	5704	ACTAGTGGATGACAGCGGATC
NM_005656	TMPRSS2	5705	ACGGGAAGACCTCAGAAAGTGC
AB038157	AB038157	5706	ACGTACAGATGTGCTCATCC
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NM_032404	TMPRSS3	5706	ACGTACAGATGTGCTCATCC
NM_032405	TMPRSS3	5706	ACGTACAGATGTGCTCATCC
AB038157	AB038157	5707	ACGACCATGTGCTCCGATGAC
AB038158	AB038158	5707	ACGACCATGTGCTCCGATGAC
AB038159	AB038159	5707	ACGACCATGTGCTCCGATGAC
AB038160	AB038160	5707	ACGACCATGTGCTCCGATGAC
NM_024022	TMPRSS3	5707	ACGACCATGTGCTCCGATGAC
NM_032401	TMPRSS3	5707	ACGACCATGTGCTCCGATGAC
NM_032404	TMPRSS3	5707	ACGACCATGTGCTCCGATGAC
NM_032405	TMPRSS3	5707	ACGACCATGTGCTCCGATGAC
AB038157	AB038157	5708	ACGGTGACTGCATTACACCAC
AB038158	AB038158	5708	ACGGTGACTGCATTACACCAC
AB038159	AB038159	5708	ACGGTGACTGCATTACACCAC
AB038160	AB038160	5708	ACGGTGACTGCATTACACCAC
NM_024022	TMPRSS3	5708	ACGGTGACTGCATTACACCAC
NM_032401	TMPRSS3	5708	ACGGTGACTGCATTACACCAC
NM_032404	TMPRSS3	5708	ACGGTGACTGCATTACACCAC
NM_032405	TMPRSS3	5708	ACGGTGACTGCATTACACCAC
AF179224	AF179224	5709	ACTACTACTTCTCTGCGGGC
NM_019894	TMPRSS4	5709	ACTACTACTTCTCTGCGGGC
AF179224	AF179224	5710	ACCTGGTTCTCTGCCTGTTTC
NM_019894	TMPRSS4	5710	ACCTGGTTCTCTGCCTGTTTC
AF179224	AF179224	5711	ACTGGAGGGAAGATGTCTGAC
NM_019894	TMPRSS4	5711	ACTGGAGGGAAGATGTCTGAC
NM_030770	TMPRSS5	5712	ACCTTTGAGCTGCTCAGAGGC
NM_030770	TMPRSS5	5713	ACGGGAGTAAACCTCACTGAC
NM_030770	TMPRSS5	5714	ACTCATGACTACGACGTCGCC
NM_003961	RHBDL	5715	ACCAAGTGGGTGCTGCAGACC

Y17108	HSY17108	5715	ACCAAGTGGGTGCTGCAGACC
NM_004460	FAP	5716	ACCAAAGACCAGGAGATCCAC
NM_004460	FAP	5717	ACAGGCTGGAGCTAAGAATCC
NM_004460	FAP	5718	ACTTCAAGTGTATGGTGGTCC
NM_001907	CTRL	5719	ACCGAGGCTCTGACTGAAGGC
NM_001907	CTRL	5720	ACACTGCAATGTGCGCGCACC
NM_001907	CTRL	5721	ACGTTTCAGCACCTGGATCAAC
NM_001906	CTRB1	5722	ACCATCCAGGTCTCTGAAGATC
NM_001906	CTRB1	5723	ACGTACAACGCCAACAAGACC
NM_001906	CTRB1	5724	ACTGCCGAATGCAAGAAGTCC
AJ319876	HSA319876	5725	ACGATGCTCAAGGAGCTCATC
AJ319876	HSA319876	5726	ACTTCCACGCTGGGTTGTTAC
AJ319876	HSA319876	5727	ACGTGGATGTGCAGTTGATCC
NM_000506	F2	5728	ACGTCACTGTAGCGATGACTC
NM_000506	F2	5729	ACCTTCTGCCGCAACCCAGAC
NM_000506	F2	5730	ACCCGCTGGTATCAAATGGGC
NM_001528	HGFAC	5731	ACATGCTTTGATGAGACCCGC
NM_001528	HGFAC	5732	ACTCCCTCACCAGAGTCCAAC
NM_001528	HGFAC	5733	ACCATGCTCTGTGCCGGCTAC
NM_000301	PLG	5734	ACACTATCGCGGGAATGTGGC
NM_000301	PLG	5735	ACCAATTGGCTCCACAGCAC
NM_000301	PLG	5736	ACGCGAGTGTTGTAGCACCTC
NM_000892	KLKB1	5737	ACAGTACAGTCCCGGAGGAAC
NM_000892	KLKB1	5738	ACCTAGGATTGCGTATGGGAC
NM_000892	KLKB1	5739	ACACCAATATGCCTACCTTCC
NM_032046	MSP	5740	ACATCTACTCTGGGTCTCTCC
NM_032046	MSP	5741	ACCTCCACCATCCAGGAAAGC
NM_032046	MSP	5742	ACCAAACCTGGTGTGTACACC
NM_033440	ELA2A	5743	ACTGGCAAGTGGTACCACACC
NM_033440	ELA2A	5744	ACCCAAATCTCCAAAGGGAAC
NM_033440	ELA2A	5745	ACCTACTACCACAAGCCCTCC
NM_015849	LOC51032	5746	ACTGGCCAGTGGTACCACACC
NM_015849	LOC51032	5747	ACCCAGGTCTCCAAAGGGAAC
NM_015849	LOC51032	5748	ACCTACTACTACAAGCCCTCC
NM_006144	GZMA	5749	ACTAACCAGGGAAGAGCCAAC
NM_006144	GZMA	5750	ACAGAGTTCCCTATCCATGC
NM_006144	GZMA	5751	ACTATGGTTTGTGCTGGAAGC
NM_000504	F10	5752	ACGCCATATGATGCAGCCGAC
NM_000504	F10	5753	ACCCGGTTCACAAAGGAGACC
NM_000504	F10	5754	ACGCTGTCCAGCAGCTTCATC
NM_000128	F11	5755	ACGTACTGCCAGGTAGTCTGC
NM_019559	F11	5755	ACGTACTGCCAGGTAGTCTGC
NM_000128	F11	5756	ACGAGTGAATAGGACAGCAGC
NM_019559	F11	5756	ACGAGTGAATAGGACAGCAGC
NM_000128	F11	5757	ACCACAATGAGGTCTGGCATC
NM_019559	F11	5757	ACCACAATGAGGTCTGGCATC

NM_000039	APOA1	5758	ACGGACCTGGCCACTGTGTAC
NM_000039	APOA1	5759	ACGCTCCTTGACAACCTGGGAC
NM_000039	APOA1	5760	ACGCTCAACACCCAGTGAGGC
NM_007272	CTRC	5761	ACCAACCTGGAGGTGGAAGAC
NM_007272	CTRC	5762	ACGAAGCCGGTAGTCTACACC
NM_007272	CTRC	5763	ACACTTCCTTCTCCTCGGGCC
NM_003293	TPS1	5764	ACATACCACCTTGGCGCCTAC
NM_003293	TPS1	5764	ACATACCACCTTGGCGCCTAC
NM_003293	TPS1	5764	ACATACCACCTTGGCGCCTAC
NM_003294	TPSB1	5764	ACATACCACCTTGGCGCCTAC
NM_003294	TPSB1	5764	ACATACCACCTTGGCGCCTAC
NM_003294	TPSB1	5764	ACATACCACCTTGGCGCCTAC
NM_024164	TPSB2	5764	ACATACCACCTTGGCGCCTAC
NM_024164	TPSB2	5764	ACATACCACCTTGGCGCCTAC
NM_024164	TPSB2	5764	ACATACCACCTTGGCGCCTAC
AK000442	AK000442	5765	ACAGGTCCACAGGATTGTCTC
NM_017821	FLJ20435	5765	ACAGGTCCACAGGATTGTCTC
AK000442	AK000442	5766	ACATGGTCCACAAAGGCCTCC
NM_017821	FLJ20435	5766	ACATGGTCCACAAAGGCCTCC
NM_000791	DHFR	5767	ACGCCATGAATCACCAGGCC
NM_000476	AK1	5768	ACGATCGTGCAGAAGTATGGC
NM_000476	AK1	5769	ACGGAGAAGAGTTTGAGCGAC
NM_013302	EEF2K	5770	ACGATGGCATCTCAGCCCTTC
NM_013302	EEF2K	5771	ACCTCCAACCTCTGGCTTTGTC
XM_171967	LOC256991	5771	ACCTCCAACCTCTGGCTTTGTC
NM_013302	EEF2K	5772	ACCATGAGCGACGTGACCTTC
NM_002654	PKM2	5773	ACCACTGGCATCATCTGTACC
NM_002654	PKM2	5774	ACGATGATGATTGGACGGTGC
NM_002654	PKM2	5775	ACCTTTGCCATGAATGTTGGC
NM_001963	EGF	5776	ACTGCAGCCATGACTGTGTTC
NM_001963	EGF	5777	ACAGCTGTGCAGCTTCAGGAC
NM_001963	EGF	5778	ACCCACGAGGAATTGCTGTTC
NM_001963	EGF	5779	ACGGTCATCGTGGTGGCTGTC
NM_004465	FGF10	5780	ACTCACCTTCAAGGAGATGTC
NM_004465	FGF10	5781	ACGAAGGAGAACTGCCCCGTAC
NM_004465	FGF10	5782	ACGGAGCTCCAAGGAGAGGAC
NM_000619	IFNG	5783	ACTTGGAAAGAGGAGAGTGAC
NM_000619	IFNG	5784	ACTGCAGAGCCAAATTGTCTC
NM_000619	IFNG	5785	ACGTGATGGCTGAACTGTCCG
NM_000619	IFNG	5786	ACAGGAGTCAGATGCTGTTTC
NM_006238	PPARD	5787	ACGATTCAGAAGAAGAACCGC
NM_006238	PPARD	5788	ACCGACCAGGTTACCCTTCTC
NM_006238	PPARD	5789	ACCGGCAGTGGCTTTGTACC
NM_006238	PPARD	5790	ACCGCCCTGGAACCTTGATGAC
NM_006238	PPARD	5791	ACGAAGACCGAAACCGAGACC
NM_000962	PTGS1	5792	ACGAAGCAGTTGCCAGATGCC

NM_080591	PTGS1	5792	ACGAAGCAGTTGCCAGATGCC
NM_000962	PTGS1	5793	ACACTTCTGGCAAGATGGGTC
NM_080591	PTGS1	5793	ACACTTCTGGCAAGATGGGTC
NM_002472	MYH8	5794	ACTGTCCGTGCCTTCATGAAC
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NM_002513	NME3	5796	ACACGTGCCAGGAGCACTGTC
NM_002009	FGF7	5797	ACATGTGAACTGTTCCAGCCC
NM_000930	PLAT	5798	ACCATCAGTCATGGCTGCGCC
NM_000931	PLAT	5798	ACCATCAGTCATGGCTGCGCC
NM_000930	PLAT	5799	ACGTACAGCTCAGAGTTCTGC
NM_000931	PLAT	5799	ACGTACAGCTCAGAGTTCTGC
NM_033011	PLAT	5799	ACGTACAGCTCAGAGTTCTGC
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NM_000931	PLAT	5800	ACTTCCATGATCCTGATAGGC
NM_033011	PLAT	5800	ACTTCCATGATCCTGATAGGC
NM_000930	PLAT	5801	ACGGTTACCAACTACCTAGAC
NM_000931	PLAT	5801	ACGGTTACCAACTACCTAGAC
NM_033011	PLAT	5801	ACGGTTACCAACTACCTAGAC
NM_002658	PLAU	5802	ACCGTACCATGCCCACAGATC
NM_002658	PLAU	5803	ACTTCACCACCATCGAGAACC
NM_002658	PLAU	5804	ACATGCTATGTGCTGCTGACC
NM_002658	PLAU	5805	ACGGACAAGCCAGGCGTCTAC
NM_002506	NGFB	5806	ACACTTCAGCATTCCTTGAC
NM_002506	NGFB	5807	ACGCTGCAGACACTCAGGATC
NM_002506	NGFB	5808	ACGCGGTCATCATCCCATCCC
NM_002506	NGFB	5809	ACGACCACCGCCACAGACATC
NM_001371	DNAH8	5810	ACCTGTGTTGATTTCTCTGCC
NM_001371	DNAH8	5811	ACTGGACATGACTTTGGGACC
NM_001394	DUSP4	5812	ACCGTGCGCTGTAACACCATC
NM_001395	DUSP9	5813	ACGCTGCGAGAGGAAGGCTAC
NM_001395	DUSP9	5814	ACACTGGGCATCCGCTACATC
NM_001395	DUSP9	5815	ACCGATGCCTATGACCTGGTC
NM_001946	DUSP6	5816	ACGGTGGCTTCAGTAAGTTCC
NM_001946	DUSP6	5817	ACCAGACTCGGATGGTAGTCC
NM_001946	DUSP6	5818	ACGTACATCTTGAACGTCACC
NM_002138	HNRPD	5819	ACGTAGCCATGTCTGAAGGAAC
NM_031369	HNRPD	5819	ACGTAGCCATGTCTGAAGGAAC
NM_031370	HNRPD	5819	ACGTAGCCATGTCTGAAGGAAC
NM_002472	MYH8	5820	ACAGACTGAAGGTGGAGCAAC
NM_002472	MYH8	5821	ACTCAGTCCATCCTGATCACC
M37712	HUMP58GTA	5822	ACTGGAGAGGCACCCAAATGC
XM_087511	LOC152715	5822	ACTGGAGAGGCACCCAAATGC
M37712	HUMP58GTA	5823	ACAGCAATGGGCAGGAGGGAC
XM_087511	LOC152715	5823	ACAGCAATGGGCAGGAGGGAC
NM_000723	CACNB1	5824	ACTACAGCAAGAGGAAAGGGC
NM_000723	CACNB1	5825	ACATGTTGGCTACAATCCGTC

NM_000723	CACNB1	5826	ACACACATCATCATTGAGCGC
NM_000724	CACNB2	5827	ACACAATCCCAGTAAGCACGC
NM_000724	CACNB2	5828	ACGCTAAACACCTCAACGTCC
NM_000724	CACNB2	5829	ACGGTGATCAGAGGACTGATC
NM_001371	DNAH8	5830	ACGAAGCTGGTGATTGAGGTC
M37712	HUMP58GTA	5831	ACACCCGAATTCGGGACCATC
AK027011	AK027011	5832	ACCCAGAAAGTGGATCTCTTC
BC009350	BC009350	5832	ACCCAGAAAGTGGATCTCTTC
SK490	GCN2	5832	ACCCAGAAAGTGGATCTCTTC
AK027011	AK027011	5833	ACCTGCTCAAGAGTGAGCTGC
BC009350	BC009350	5833	ACCTGCTCAAGAGTGAGCTGC
SK490	GCN2	5833	ACCTGCTCAAGAGTGAGCTGC
AK027011	AK027011	5834	ACACTCGACTTCAGACCTCCC
BC009350	BC009350	5834	ACACTCGACTTCAGACCTCCC
SK490	GCN2	5834	ACACTCGACTTCAGACCTCCC
BC011526	BC011526	5835	ACGCACGCCAATATTGTGACC
SK273	PCTAIRE3	5835	ACGCACGCCAATATTGTGACC
XM_053746	PCTK3	5835	ACGCACGCCAATATTGTGACC
BC011526	BC011526	5836	ACGGAGGAGCTGCACCTCATC
SK273	PCTAIRE3	5836	ACGGAGGAGCTGCACCTCATC
XM_053746	PCTK3	5836	ACGGAGGAGCTGCACCTCATC
BC011526	BC011526	5837	ACGAACAGGCGGCAGAGCATC
SK273	PCTAIRE3	5837	ACGAACAGGCGGCAGAGCATC
XM_053746	PCTK3	5837	ACGAACAGGCGGCAGAGCATC
L33801	HUMGLSYKIN	5838	ACGAATCGAGAGCTCCAGATC
NM_002093	GSK3B	5838	ACGAATCGAGAGCTCCAGATC
SK163	GSK3B	5838	ACGAATCGAGAGCTCCAGATC
L33801	HUMGLSYKIN	5839	ACACATCCAAATGGGCGAGAC
SK163	GSK3B	5839	ACACATCCAAATGGGCGAGAC
L33801	HUMGLSYKIN	5840	ACCTGTCAAGTAATCCACCTC
NM_002093	GSK3B	5840	ACCTGTCAAGTAATCCACCTC
SK163	GSK3B	5840	ACCTGTCAAGTAATCCACCTC
L33801	HUMGLSYKIN	5841	ACGTAATCCACCTCTGGCTAC
NM_002093	GSK3B	5841	ACGTAATCCACCTCTGGCTAC
SK163	GSK3B	5841	ACGTAATCCACCTCTGGCTAC
BC005169	BC005169	5842	ACGAGCTCCATCCATGACGCC
BC007835	BC007835	5842	ACGAGCTCCATCCATGACGCC
SK492	SgK495	5842	ACGAGCTCCATCCATGACGCC
XM_029031	MGC4796	5842	ACGAGCTCCATCCATGACGCC
AL136697	HSM801665	5843	ACGAATCTCTTCCGCAAGATC
NM_024046	MGC8407	5843	ACGAATCTCTTCCGCAAGATC
AL136697	HSM801665	5844	ACGAAGGCTGTCCGAGTGACC
NM_024046	MGC8407	5844	ACGAAGGCTGTCCGAGTGACC
AL136697	HSM801665	5845	ACGAGGCTGCTGGTTATGCCC
AL136764	HSM801732	5846	ACCAGTTGCCAAGGCACAGAC
SK513	QIK	5846	ACCAGTTGCCAAGGCACAGAC

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XM_041314	KIAA0781	5846	ACCAGTTGCCAAGGCACAGAC
AL136764	HSM801732	5847	ACCAGGTCTCCAGTGAGCTTC
SK513	QIK	5847	ACCAGGTCTCCAGTGAGCTTC
XM_041314	KIAA0781	5847	ACCAGGTCTCCAGTGAGCTTC
AL136764	HSM801732	5848	ACTACAGCCCTTTCCTCAGCC
SK513	QIK	5848	ACTACAGCCCTTTCCTCAGCC
XM_041314	KIAA0781	5848	ACTACAGCCCTTTCCTCAGCC
AY049015	AY049015	5849	ACCTAGCGGAAAGGAAGCCTC
SK436	TAO1	5849	ACCTAGCGGAAAGGAAGCCTC
XM_030845	KIAA1361	5849	ACCTAGCGGAAAGGAAGCCTC
AY049015	AY049015	5850	ACGATGCGCTGTGAGTTGATC
SK436	TAO1	5850	ACGATGCGCTGTGAGTTGATC
XM_030845	KIAA1361	5850	ACGATGCGCTGTGAGTTGATC
AY049015	AY049015	5851	ACGCAGTTTCAGGATACCTGC
SK436	TAO1	5851	ACGCAGTTTCAGGATACCTGC
XM_030845	KIAA1361	5851	ACGCAGTTTCAGGATACCTGC
AJ311797	HSA311797	5852	ACGGGAAGCGACATCTGGAGC
AJ311798	HSA311798	5852	ACGGGAAGCGACATCTGGAGC
SK691	MLK4	5852	ACGGGAAGCGACATCTGGAGC
AJ311797	HSA311797	5853	ACGAATGCTGGCAACAAGACC
AJ311798	HSA311798	5853	ACGAATGCTGGCAACAAGACC
SK691	MLK4	5853	ACGAATGCTGGCAACAAGACC
AJ311797	HSA311797	5854	ACGGTAAAGAAGAGGAAGGGC
AJ311798	HSA311798	5854	ACGGTAAAGAAGAGGAAGGGC
SK691	MLK4	5854	ACGGTAAAGAAGAGGAAGGGC
AK057247	AK057247	5855	ACAGTAACAGACACCATCAGC
SK645	NEK10	5855	ACAGTAACAGACACCATCAGC
XM_087381	LOC152110	5855	ACAGTAACAGACACCATCAGC
AK057247	AK057247	5856	ACCGGGAACGAAGACGCACAC
SK645	NEK10	5856	ACCGGGAACGAAGACGCACAC
XM_087381	LOC152110	5856	ACCGGGAACGAAGACGCACAC
AK057247	AK057247	5857	ACATGACCCTACAGGTTTACC
SK645	NEK10	5857	ACATGACCCTACAGGTTTACC
XM_087381	LOC152110	5857	ACATGACCCTACAGGTTTACC
AL136697	HSM801665	5858	ACGAACGAGATAGGCATCCTC
NM_024046	MGC8407	5858	ACGAACGAGATAGGCATCCTC
AF387637	AF387637	5859	ACGGAGTCAGACCAGCACTGC
AF465413	AF465413	5859	ACGGAGTCAGACCAGCACTGC
M80359	HUMP78A	5859	ACGGAGTCAGACCAGCACTGC
SK096	MARK3	5859	ACGGAGTCAGACCAGCACTGC
AF399753	AF399753	5860	ACCAGCTTACAGATTGCAGGC
BC014479	BC014479	5860	ACCAGCTTACAGATTGCAGGC
SK528	Slob	5860	ACCAGCTTACAGATTGCAGGC
AF399753	AF399753	5861	ACCAGGTTTCCATGTTCTTCC
BC014479	BC014479	5861	ACCAGGTTTCCATGTTCTTCC
SK528	Slob	5861	ACCAGGTTTCCATGTTCTTCC

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AF399753	AF399753	5862	ACTGGCATGCCTACCATCTCC
BC014479	BC014479	5862	ACTGGCATGCCTACCATCTCC
SK528	Slob	5862	ACTGGCATGCCTACCATCTCC
AJ247087	HSA247087	5863	ACCCACAGTGGTGGAGAAAC
SK536	caMLCK	5863	ACCCACAGTGGTGGAGAAAC
XM_040819	LOC91807	5863	ACCCACAGTGGTGGAGAAAC
AJ247087	HSA247087	5864	ACGCTGAAGGTGAAC TTCGGC
SK536	caMLCK	5864	ACGCTGAAGGTGAAC TTCGGC
XM_040819	LOC91807	5864	ACGCTGAAGGTGAAC TTCGGC
AJ247087	HSA247087	5865	ACCTTCGGCACTCCTGAGTTC
SK536	caMLCK	5865	ACCTTCGGCACTCCTGAGTTC
XM_040819	LOC91807	5865	ACCTTCGGCACTCCTGAGTTC
AJ272212	HSA272212	5866	ACGAGTGACGTGTACAAGCAC
SK322	PSKH1	5866	ACGAGTGACGTGTACAAGCAC
XM_043047	PSKH1	5866	ACGAGTGACGTGTACAAGCAC
AJ272212	HSA272212	5867	ACGTACAGGGCCAAGTTTGAC
SK322	PSKH1	5867	ACGTACAGGGCCAAGTTTGAC
XM_043047	PSKH1	5867	ACGTACAGGGCCAAGTTTGAC
AJ272212	HSA272212	5868	ACCCTCCTTAAACGTGCCTCC
SK322	PSKH1	5868	ACCCTCCTTAAACGTGCCTCC
XM_043047	PSKH1	5868	ACCCTCCTTAAACGTGCCTCC
AJ303380	HSA303380	5869	ACCCTCCAGGAAAGATTTGCC
SK463	STK33	5869	ACCCTCCAGGAAAGATTTGCC
XM_031831	STK33	5869	ACCCTCCAGGAAAGATTTGCC
AJ303380	HSA303380	5870	ACGCAAAGTAGGAGTGAAGCC
SK463	STK33	5870	ACGCAAAGTAGGAGTGAAGCC
XM_031831	STK33	5870	ACGCAAAGTAGGAGTGAAGCC
AJ303380	HSA303380	5871	ACGGAACAGCAACCAAGTACC
SK463	STK33	5871	ACGGAACAGCAACCAAGTACC
XM_031831	STK33	5871	ACGGAACAGCAACCAAGTACC
AF172264	AF172264	5872	ACGGTGACTGATTACTCCTCC
AF172265	AF172265	5872	ACGGTGACTGATTACTCCTCC
AF172266	AF172266	5872	ACGGTGACTGATTACTCCTCC
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AF172268	AF172268	5872	ACGGTGACTGATTACTCCTCC
AF172269	AF172269	5872	ACGGTGACTGATTACTCCTCC
AF172270	AF172270	5872	ACGGTGACTGATTACTCCTCC
AF172271	AF172271	5872	ACGGTGACTGATTACTCCTCC
XM_039796	KIAA0551	5872	ACGGTGACTGATTACTCCTCC
AF200815	AF200815	5873	ACCTTCCTGAAGACCAGGTTC
AX040393	AX040393	5873	ACCTTCCTGAAGACCAGGTTC
SK199	Fused	5873	ACCTTCCTGAAGACCAGGTTC
XM_050803	STK36	5873	ACCTTCCTGAAGACCAGGTTC
AF200815	AF200815	5874	ACCCATCGTCTCGTTTCTCTC
AX040393	AX040393	5874	ACCCATCGTCTCGTTTCTCTC
SK199	Fused	5874	ACCCATCGTCTCGTTTCTCTC

XM_050803	STK36	5874	ACCCATCGTCTCGTTTCTCTC
AF200815	AF200815	5875	ACTGTTGCATCAGCTCTGGGC
AX040393	AX040393	5875	ACTGTTGCATCAGCTCTGGGC
SK199	Fused	5875	ACTGTTGCATCAGCTCTGGGC
XM_050803	STK36	5875	ACTGTTGCATCAGCTCTGGGC
AF308302	AF308302	5876	ACCTATTTGGAGAGCAGCCTC
SK433	STLK5	5876	ACCTATTTGGAGAGCAGCCTC
XM_044379	LOC92335	5876	ACCTATTTGGAGAGCAGCCTC
AF308302	AF308302	5877	ACTATCGTGCCATATCGAGCC
SK433	STLK5	5877	ACTATCGTGCCATATCGAGCC
XM_044379	LOC92335	5877	ACTATCGTGCCATATCGAGCC
AF308302	AF308302	5878	ACTGAGCTGGCGATTGCTTAC
SK433	STLK5	5878	ACTGAGCTGGCGATTGCTTAC
XM_044379	LOC92335	5878	ACTGAGCTGGCGATTGCTTAC
AF172264	AF172264	5879	ACCCCATCAGAGCAAGCAACC
AF172265	AF172265	5879	ACCCCATCAGAGCAAGCAACC
AF172266	AF172266	5879	ACCCCATCAGAGCAAGCAACC
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AF172271	AF172271	5879	ACCCCATCAGAGCAAGCAACC
XM_039796	KIAA0551	5879	ACCCCATCAGAGCAAGCAACC
AF031416	AF031416	5880	ACGGTGCCATCCTCACCTTGC
BC006231	BC006231	5880	ACGGTGCCATCCTCACCTTGC
SK176	IKKb	5880	ACGGTGCCATCCTCACCTTGC
XM_032491	IKBKB	5880	ACGGTGCCATCCTCACCTTGC
AF031416	AF031416	5881	ACCTGATGCTGATGTGGCACC
SK176	IKKb	5881	ACCTGATGCTGATGTGGCACC
XM_032491	IKBKB	5881	ACCTGATGCTGATGTGGCACC
AF031416	AF031416	5882	ACACCAGCATCCAGATTGACC
SK176	IKKb	5882	ACACCAGCATCCAGATTGACC
XM_032491	IKBKB	5882	ACACCAGCATCCAGATTGACC
AF172264	AF172264	5883	ACCAGGAATACATCAGGCGAC
AF172266	AF172266	5883	ACCAGGAATACATCAGGCGAC
AF172267	AF172267	5883	ACCAGGAATACATCAGGCGAC
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AF172264	AF172264	5884	ACGCAGAAAGACTGCAGAGGC
AF172265	AF172265	5884	ACGCAGAAAGACTGCAGAGGC
AF172266	AF172266	5884	ACGCAGAAAGACTGCAGAGGC
AF172267	AF172267	5884	ACGCAGAAAGACTGCAGAGGC
AF172268	AF172268	5884	ACGCAGAAAGACTGCAGAGGC
AF172269	AF172269	5884	ACGCAGAAAGACTGCAGAGGC
AF172270	AF172270	5884	ACGCAGAAAGACTGCAGAGGC
AF172271	AF172271	5884	ACGCAGAAAGACTGCAGAGGC
AF172264	AF172264	5885	ACGAACGGTCAAGGCTCAACC

AF172265	AF172265	5885	ACGAACGGTCAAGGCTCAACC
AF172267	AF172267	5885	ACGAACGGTCAAGGCTCAACC
AF172269	AF172269	5885	ACGAACGGTCAAGGCTCAACC
XM_039796	KIAA0551	5885	ACGAACGGTCAAGGCTCAACC
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NM_000962	PTGS1	5887	ACGACCTGTCCCTACGTTTCC
NM_080591	PTGS1	5887	ACGACCTGTCCCTACGTTTCC
NM_000963	PTGS2	5888	ACCCCACTCCAAACACAGTGC
NM_000963	PTGS2	5889	ACTGTCTGCAGAGTTGGAAGC
NM_000963	PTGS2	5890	ACTAACGTGAAGGGCTGTCCC
NM_000963	PTGS2	5891	ACTGCAAGTTCTTCCCCTCC
NM_001718	BMP6	5892	ACGTCTTACAGGAGCATCAGC
NM_001718	BMP6	5893	ACGTGAGTGAGGTCCACGTGC
NM_001718	BMP6	5894	ACTGCCATCTCGGTTCTTTAC
NM_001718	BMP6	5895	ACACTATCTCATGCCAGTGCC
NM_001432	EREG	5896	ACGACAATCCACGTGTGGCTC
NM_001432	EREG	5897	ACGTGGGTTATACTGGTGTCC
NM_001432	EREG	5898	ACAGAGTATGTGGCTTTGACC
NM_001432	EREG	5899	ACACTTATGGGCAGGGATAAC
NM_001565	SCYB10	5900	ACTCCAGAATCGAAGGCCATC
NM_003266	TLR4	5901	ACGTTTACAGAAGCTGGTGGC
NM_138554	TLR4	5901	ACGTTTACAGAAGCTGGTGGC
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NM_138557	TLR4	5901	ACGTTTACAGAAGCTGGTGGC
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NM_138554	TLR4	5903	ACCTTGACCTTCCTGGACCTC
NM_138556	TLR4	5903	ACCTTGACCTTCCTGGACCTC
NM_138557	TLR4	5903	ACCTTGACCTTCCTGGACCTC
NM_003266	TLR4	5903	ACCTTGACCTTCCTGGACCTC
NM_138554	TLR4	5904	ACGGTGATTGTTGTGGTGTCC
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NM_138557	TLR4	5904	ACGGTGATTGTTGTGGTGTCC
NM_000584	IL8	5904	ACGGTGATTGTTGTGGTGTCC
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NM_001323	CST6	5906	ACTCTGGCAACCCTAGTCTGC
NM_000396	CTSK	5907	ACGACCAGGGTCACTGGAGAC
XM_117525	NOTCH1	5908	ACTAAGAACAACGCCTGTGGC
XM_117525	NOTCH1	5909	ACTGGCTGCAAAGGCAAGCCC
NM_024408	NOTCH1	5910	ACTTCAACGGGCTCTTGTGCC
NM_024408	NOTCH2	5911	ACTGGTGGGACTTGTGTGGCC
NM_024408	NOTCH2	5912	ACCCAGTTCTCCTGCAAATGC
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NM_000435	NOTCH3	5915	ACATGCCTAGACCTGGTGGAC
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NM_000435	NOTCH3	5918	ACTAAGGACATGCAGGATAGC
NM_004557	NOTCH4	5919	ACATGGAGGCAGCTGCCAAGC
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NM_004557	NOTCH4	5921	ACGGCATAGACGTCTCTTCCC
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NM_145159	JAG2	5923	ACCTACTGTGGCAGCCACCAC
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NM_002226	JAG2	5925	ACTGGTGGCATCTGTGTTGAC
NM_145159	JAG2	5925	ACTGGTGGCATCTGTGTTGAC
NM_002226	JAG2	5926	ACTTCACCAAAGATCCTGGCC
NM_145159	JAG2	5926	ACTTCACCAAAGATCCTGGCC
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NM_024302	MMP28	5928	ACATGGTACAAGCAGCACCTC
NM_032950	MMP28	5928	ACATGGTACAAGCAGCACCTC
NM_024302	MMP28	5929	ACATACTGCCACTCTTCCTTC
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NM_032950	MMP28	5931	ACGTCTGTCTGCCTTTGTTCC
NM_006664	SCYA27	5932	ACGCTACTGAGGAAGGTCATC
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NM_015926	ZSIG11	5934	ACGGAGTAACCCATGGCCTGC
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NM_002422	MMP3	5937	ACTCCCTCAGGAAGCTTGAAC
NM_002422	MMP3	5938	ACTGAGGTACGAGCTGGATAC
NM_005978	S100A2	5939	ACCTTCTGCACAAGGAGCTGC
NM_005978	S100A2	5940	ACCAGTGACCAGCAGGTGGAC
NM_005978	S100A2	5941	ACTGACTTCTTCCAGGGCTGC
NM_002109	HARS	5942	ACCTCCTGAAACTGAAGGCAC
NM_002109	HARS	5943	ACGGTATATCGGCGGGATAAC
NM_002109	HARS	5944	ACATCTCCTTTGACCTGAGCC
NM_002109	HARS	5945	ACGAGTGGTCAGAACAGAGCC
NM_002608	PDGFB	5946	ACCAACCGCAACGTGCAGTGC
NM_033016	PDGFB	5946	ACCAACCGCAACGTGCAGTGC
NM_002608	PDGFB	5947	ACCTCGGGTGACCATTCCGAC
NM_033016	PDGFB	5947	ACCTCGGGTGACCATTCCGAC
NM_002608	PDGFB	5948	ACGGGCAAGCACCGGAAATTC
NM_033016	PDGFB	5948	ACGGGCAAGCACCGGAAATTC
NM_002608	PDGFB	5949	ACGCACCGGAAATTCAAGCAC
NM_033016	PDGFB	5949	ACGCACCGGAAATTCAAGCAC
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NM_000785	CYP27B1	5951	ACGTTCCGACTGGAAGGCATC
NM_000785	CYP27B1	5952	ACGACTGTACCCTGTGGTACC
NM_000785	CYP27B1	5953	ACATGGCTTTGGCCCAGATCC
NM_012208	HARSL	5954	ACGGTGGAGAGCTGTTGTCCC
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NM_001878	CRABP2	5959	ACATGGTCTGTGAGCAGAAGC
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NM_001878	CRABP2	5961	ACAGACTGGCCCTCTAGCTTC
NM_004245	TGM5	5962	ACGGCAGCAAGAACTGGATCC
NM_004245	TGM5	5963	ACGCTGAAGGCTAGAAGCTTC
NM_004245	TGM5	5964	ACCATGGGCCAGGATATATGC
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NM_001264	CDSN	5966	ACTACTAAACCCTTCCCAGCC
NM_001264	CDSN	5967	ACAGCGTCAGCTCCAACCAGC
NM_001264	CDSN	5968	ACAGAGAACCCTGTGAAAGGC
NM_001264	CDSN	5969	ACGGAGAGTTACTCGACAGTC
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NM_144505	KLK8	5970	ACCTACTCTGTGGCGGTGTCC
NM_007196	KLK8	5971	ACCTGGGTCCTTACAGCTGCC
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NM_007196	KLK8	5973	ACCAGCAGCGATGTGGAGGAC
NM_144505	KLK8	5973	ACCAGCAGCGATGTGGAGGAC
NM_003467	CXCR4	5974	ACTGGATTGGTCATCCTGGTC
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NM_003467	CXCR4	5976	ACCGTCAGTGAGGCAGATGAC
NM_003467	CXCR4	5977	ACGCTGTCACACTCCAAGGGC
NM_004591	SCYA20	5978	ACTTGGACATAGCCCCAAGAAC
NM_004900	APOBEC3B	5979	ACTTATGCATTCTCTGCACCGC
NM_004900	APOBEC3B	5980	ACCGAGGCTAAGAATCTTCTC
NM_004900	APOBEC3B	5981	ACATGCAAACGAGCCGTTAC
NM_005547	IVL	5982	ACATGAAACAGCCAACTCCAC
NM_005547	IVL	5983	ACACACAAAGGGATCAGCAGC
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NM_002733	PRKAG1	5985	ACGCGCATTCTGAAGTTCCTC
NM_002733	PRKAG1	5986	ACGCCTTGCAACATCGATCAC
NM_002743	PRKCSH	5987	ACCGATGACTATTGCGACTGC
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NM_002743	PRKCSH	5989	ACGCTTGTCTCGCAGAAACCC
NM_002822	PTK9	5990	ACAGAGGATTCCCAAGGATTC
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NM_002969	MAPK12	5996	ACGAAGCTGTATCGGCCCTTC
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NM_002969	MAPK12	5998	ACGAGGTGCTCAGCTTCAAGC
NM_002977	SCN9A	5999	ACGATGATGATGAAGAAGCCC
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NM_003045	SLC7A1	6002	ACTGCAGGCCCTGCCATTGTC
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NM_003045	SLC7A1	6004	ACGCTCTCATTTAAGGTTCCC
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NM_003160	STK13	6011	ACATTGAGATCCAGGCTCATC
NM_003160	STK13	6012	ACCTATTTCCATGATGCACGC
NM_003160	STK13	6013	ACTAGAGGAAGTTGCAGATGC
NM_003180	SYT5	6014	ACCCACCATCAAGAAGAACAC
NM_003180	SYT5	6015	ACGCTTTCAGCTTCGAGGTGC
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NM_003640	IKBKAP	6024	ACCCTGTGTTTCAGCTCTGGAC
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NM_003690	PRKRA	6027	ACCCTGCACAGGTGAAGGTAC
NM_003885	CDK5R1	6028	ACCAGCAAGAACGCCAAGGAC
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NM_003885	CDK5R1	6030	ACTGCCGACCCACACTACTTC
NM_004080	DGKB	6031	ACTTCCATGGTAATGGTGTGC
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NM_004274	AKAP6	6034	ACCGTGATAGTGGACATCCAC
NM_004274	AKAP6	6035	ACAGAATCAGCAGCCTGTTCC
NM_004274	AKAP6	6036	ACGCCTGAGATGAGCAGAAGC
NM_004327	BCR	6037	ACGCCCTTCTACGTGAACGTC
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NM_004327	BCR	6038	ACTGAGAACCTCACCTCCAGC
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NM_004327	BCR	6039	ACCCTGAGAGCCAGAAGCAAC
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NM_004421	DVL1	6040	ACCATCATCACGGTCACCTCTC
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NM_004423	DVL3	6042	ACCCTGTCTCTCCACGATCAC
NM_004579	MAP4K2	6043	ACTGTGGTGGCCTACATTGGC
SK048	GCK	6043	ACTGTGGTGGCCTACATTGGC
NM_004579	MAP4K2	6044	ACGATTCTTGACACCAAAGGC
SK048	GCK	6044	ACGATTCTTGACACCAAAGGC
NM_004579	MAP4K2	6045	ACACAAGGATCTTCCGAGTGC
SK048	GCK	6045	ACACAAGGATCTTCCGAGTGC
NM_004850	ROCK2	6046	ACCAGAGTCTGATACTGCAGC
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NM_004850	ROCK2	6048	ACGCACAGTTTGAGAAGCAGC
NM_005340	HINT1	6049	ACTGTGCTGCTGATCTGGGCC
NM_005340	HINT1	6050	ACTGGTGGTGAATGAAGGTTT
NM_005399	PRKAB2	6051	ACTATTTCTTGTGACCCAGCC
NM_005451	ENIGMA	6052	ACACGAGCACAGTGCTGACCC
NM_005451	ENIGMA	6053	ACGAAGATTACAGGCGAGATC
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NM_005649	TCF17	6058	ACGTGATCTCCCTGTTGCAGC
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NM_005732	RAD50	6061	ACCTCTGGAAGGAGTCATTAC
NM_005732	RAD50	6062	ACGCTTGTGAGATTTCGTGATC
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NM_005806	OLIG2	6065	ACGCTAGGAGGCAGTGGCTTC
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NM_006253	PRKAB1	6071	ACGGATGGAGTGATGGTGCTC
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NM_006384	CIB1	6076	ACTCTGCAGGGTCTTCTCCAC
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NM_006623	PHGDH	6079	ACGAGGAGCTGATAGCGGAGC
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NM_006712	FASTK	6082	ACCAGCAGTTTATGCCCTGCC
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SK139	FASTK	6082	ACCAGCAGTTTATGCCCTGCC
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NM_007181	MAP4K1	6091	ACGATCCAGGACACCAAAGGC
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AL121939	HSDJ223E3	6092	ACTTCTCCTGCCTCAGCCTCC
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NG_000955	NG_000955	6092	ACTTCTCCTGCCTCAGCCTCC
NG_001019	NG_001019	6092	ACTTCTCCTGCCTCAGCCTCC
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NG_001028	NG_001028	6092	ACTTCTCCTGCCTCAGCCTCC
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NM_018177	N4BP2	6139	ACGAGGAACTCAGAGCAGGC
NM_018254	FLJ10876	6140	ACTGTGGAACAGGCACTTGGC
NM_018254	FLJ10876	6141	ACTTAATGCCCGTTGGACCAC
NM_018254	FLJ10876	6142	ACCTACAGGCGTCGGTTTAAC
NM_018690	APOB48R	6143	ACGATTGTAGAGGAGGAAGCC
NM_018690	APOB48R	6144	ACGAAGAGGCTGTTGGATGGC
NM_018690	APOB48R	6145	ACGGAGACTGAGCCAGAAAGC
NM_020247	CABC1	6146	ACGGGCTCAGCCAGGAGATTC
SK609	ADCK3	6146	ACGGGCTCAGCCAGGAGATTC
NM_020247	CABC1	6147	ACCGCGGGAATATGACAGATC
SK609	ADCK3	6147	ACCGCGGGAATATGACAGATC
NM_020247	CABC1	6148	ACGATCCACAACCTGATTCCC
SK609	ADCK3	6148	ACGATCCACAACCTGATTCCC
NM_020356	C20orf32	6149	ACGAAGAGGCGGTTACAGCAC
NM_020356	C20orf32	6150	ACTTCGGGACCAGATGCAGAC
NM_020356	C20orf32	6151	ACGAATGCCCGTGCTCACATAC
NM_020824	ARHGAP10	6152	ACACATTCTCCTGGCCAGGTC
NM_020824	ARHGAP10	6153	ACTACAAGTGCCTCCATCACC
NM_020824	ARHGAP10	6154	ACGAAGTGCATCTCAAGGAGC
NM_021830	C10orf2	6155	ACGCTCCTAGAGGCTAAATGC

NM_021830	C10orf2	6156	ACTATGATCACTGGGCTGACC
NM_021830	C10orf2	6157	ACGAACTCCCTCACCTTCTCC
NM_021972	SPHK1	6158	ACCTGCACGCTATTGCTGTGC
NM_021972	SPHK1	6159	ACGAGTGGGTTCGAAGACACC
NM_021972	SPHK1	6160	ACCTACTTCTGGATGGTCAGC
NM_022766	cerk	6161	ACACAGACGTTACGGGAAAC
NM_022766	cerk	6162	ACTCATTTCCCGCAGGGTCAAC
NM_022766	cerk	6163	ACGCACATGGAGGATGAGGAC
NM_024652	FLJ23119	6164	ACGATCCTCGCCGTCAGAGAC
NM_024652	FLJ23119	6165	ACAGGACACTGTTGTGTGCAC
NM_024652	FLJ23119	6166	ACACACAGAGTGGTGCCTGGC
NM_024657	FLJ11565	6167	ACCTGTAGCCAGGCCAATACC
NM_024657	FLJ11565	6168	ACGCAGTTGAATCCTGGAACC
NM_024657	FLJ11565	6169	ACCAGGAGAGGAATCACTGGC
NM_024717	FLJ22344	6170	ACCCAGTAATGCAGAAGTCCC
NM_024717	FLJ22344	6171	ACACAGGCCACAGATGTGAC
NM_024717	FLJ22344	6172	ACAGCTTCGGAGTCCATATGC
NM_024800	NEK11	6173	ACGGTGACACACCTTCTCTCC
SK574	NEK11	6173	ACGGTGACACACCTTCTCTCC
NM_024800	NEK11	6174	ACACGCATGAGGGAATCAGCC
SK574	NEK11	6174	ACACGCATGAGGGAATCAGCC
NM_024800	NEK11	6175	ACTGCTAGCGAAGCAGAGATC
SK574	NEK11	6175	ACTGCTAGCGAAGCAGAGATC
NM_024867	FLJ23577	6176	ACAGGAAGAACACCTTGCTGC
NM_024867	FLJ23577	6177	ACAGACCTCCTCAACTGATGC
NM_024867	FLJ23577	6178	ACCCTGGAGCCAATTGAAGTC
NM_025144	FLJ22670	6179	ACGTGGCAGTACAAACAAGCC
SK755	AlphaK3	6179	ACGTGGCAGTACAAACAAGCC
NM_025144	FLJ22670	6180	ACGTCAGCTCTGTAAGGAAGC
SK755	AlphaK3	6180	ACGTCAGCTCTGTAAGGAAGC
NM_025144	FLJ22670	6181	ACCAGGAGTCTGCATCACTGC
SK755	AlphaK3	6181	ACCAGGAGTCTGCATCACTGC
NM_025164	KIAA0999	6182	ACGGTTGCCATGACAGCCCTC
NM_025164	KIAA0999	6183	ACCTTGCCAGGAATGAGTCTC
NM_025164	KIAA0999	6184	ACGTCTCCTTCAGCATGGAGC
NM_031464	MGC11287	6185	ACATTACCAAATACCTGCGGC
SK473	RSKL2	6185	ACATTACCAAATACCTGCGGC
NM_031464	MGC11287	6186	ACCTGCTGACGGGAATGGCAC
SK473	RSKL2	6186	ACCTGCTGACGGGAATGGCAC
NM_031464	MGC11287	6187	ACCTATCCATGGCTCTTAGCC
SK473	RSKL2	6187	ACCTATCCATGGCTCTTAGCC
NM_032130	DKFZP434J0113	6188	ACGGAGAAGCACCTGTATGAC
NM_032130	DKFZP434J0113	6189	ACGAGGCATCGAGTCACTCAC
NM_032130	DKFZP434J0113	6190	ACAGCAGAGACCTATGAGTTC
NM_032807	FBH1	6191	ACCCTCATACGATACACAGCC
NM_032807	FBH1	6192	ACCACCCCTTCATGGTCAACTC

NM_032807	FBH1	6193	ACGGAGCTTGAAGCCAAGATC
NM_033066	MPP4	6194	ACCTAGTTCCTGCCACACCAC
NM_033066	MPP4	6195	ACCGGGAATTCTGGTGGTCTC
NM_033066	MPP4	6196	ACGTACCGCCTCATAGTGCTC
NM_033116	NEK9	6197	ACGAGATGGTGGTGTGGTACC
NM_033116	NEK9	6198	ACAGAGACCAAGGTCAAGCAC
NM_033116	NEK9	6199	ACGAAGCGTCTGGGAATCAAC
NM_033116	NEK9	6200	ACGACCATCCGTTCCAATAGC
NM_033116	NEK9	6201	ACGTAGAAGCCTCGTCACCTC
NM_052858	LOC91862	6202	ACCTTGCTGATCCTGGCCTGC
NM_052858	LOC91862	6203	ACCTGGATGTCCAGTTCTACC
NM_052858	LOC91862	6204	ACAGGCTACAGCGGTTTCGGC
NM_078471	TIAF1	6205	ACTGTGACTGGCTGGCTGAAC
NM_078471	TIAF1	6206	ACGGAAGTGCAGACCCAGTAC
NM_078471	TIAF1	6207	ACGGATGAGGCTTCTCTGGCC
NM_080836	STK35	6208	ACCAAGAGCTCGCAGCTTTAC
NM_080836	STK35	6209	ACGCCAGACAACATCCTCATC
NM_080836	STK35	6210	ACAGATGGAGTTGCACATCCC
NM_133494	NEK7	6211	ACTGGATGCCAAAGCACGTGC
NM_133494	NEK7	6212	ACAGCACGTGCTGATTGCATC
NM_133494	NEK7	6213	ACCTAGCAGATGCTGGCGACC
NM_133494	NEK7	6214	ACCAAGTGTGACTACCCACCTC
NM_133494	NEK7	6215	ACAGAGGATGCATGCATGCAC
NM_004178	TARBP2	6216	ACTTTTCACCTTCCGGGTCACC
NM_134323	TARBP2	6216	ACTTTTCACCTTCCGGGTCACC
NM_134324	TARBP2	6216	ACTTTTCACCTTCCGGGTCACC
NM_000051	ATM	6217	ACGTAGAAGGAACCAGTTACC
NM_138292	ATM	6217	ACGTAGAAGGAACCAGTTACC
SK038	ATM	6217	ACGTAGAAGGAACCAGTTACC
NM_000051	ATM	6218	ACTCCTTCCTACTCCTGAGAC
NM_138292	ATM	6218	ACTCCTTCCTACTCCTGAGAC
SK038	ATM	6218	ACTCCTTCCTACTCCTGAGAC
NM_138316	PANK	6219	ACCCTGACCATGTGTGGACGC
NM_138316	PANK	6220	ACCTTCTCTAGCCTTCACACC
NM_138316	PANK	6221	ACCTGGATGAAGTGGACTGTC
NM_002570	PACE4	6222	ACCCTTGAGTAGCAGAGGCCC
NM_138319	PACE4	6222	ACCCTTGAGTAGCAGAGGCCC
NM_138320	PACE4	6222	ACCCTTGAGTAGCAGAGGCCC
NM_138321	PACE4	6222	ACCCTTGAGTAGCAGAGGCCC
NM_138322	PACE4	6222	ACCCTTGAGTAGCAGAGGCCC
NM_138323	PACE4	6222	ACCCTTGAGTAGCAGAGGCCC
NM_138324	PACE4	6222	ACCCTTGAGTAGCAGAGGCCC
NM_002570	PACE4	6223	ACTTCCTACTGCATCGTGGGC
NM_138319	PACE4	6223	ACTTCCTACTGCATCGTGGGC
NM_138320	PACE4	6223	ACTTCCTACTGCATCGTGGGC
NM_138321	PACE4	6223	ACTTCCTACTGCATCGTGGGC

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NM_138322	PACE4	6223	ACTTCCTACTGCATCGTGGGC
NM_138323	PACE4	6223	ACTTCCTACTGCATCGTGGGC
NM_138324	PACE4	6223	ACTTCCTACTGCATCGTGGGC
NM_138325	PACE4	6223	ACTTCCTACTGCATCGTGGGC
NM_002570	PACE4	6224	ACGCAGGCTTTTCGAGTATGGC
NM_138319	PACE4	6224	ACGCAGGCTTTTCGAGTATGGC
NM_138320	PACE4	6224	ACGCAGGCTTTTCGAGTATGGC
NM_138321	PACE4	6224	ACGCAGGCTTTTCGAGTATGGC
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NM_138323	PACE4	6224	ACGCAGGCTTTTCGAGTATGGC
NM_138324	PACE4	6224	ACGCAGGCTTTTCGAGTATGGC
NM_138325	PACE4	6224	ACGCAGGCTTTTCGAGTATGGC
NM_138325	PACE4	6225	ACGAGAGGTTTCGTTTCCACAC
AL121939	HSDJ223E3	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000080218	ENSG00000080218	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000090030	ENSG00000090030	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000115257	ENSG00000115257	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000139130	ENSG00000139130	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000154195	ENSG00000154195	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000159481	ENSG00000159481	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000170507	ENSG00000170507	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000170615	ENSG00000170615	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000170896	ENSG00000170896	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000172416	ENSG00000172416	6226	ACTCGCTTGAACCCAGGAGGC
ENSG00000174931	ENSG00000174931	6226	ACTCGCTTGAACCCAGGAGGC
NG_000002	NG_000002	6226	ACTCGCTTGAACCCAGGAGGC
NG_000004	NG_000004	6226	ACTCGCTTGAACCCAGGAGGC
NG_000006	NG_000006	6226	ACTCGCTTGAACCCAGGAGGC
NG_000008	NG_000008	6226	ACTCGCTTGAACCCAGGAGGC
NG_000009	NG_000009	6226	ACTCGCTTGAACCCAGGAGGC
NG_000012	NG_000012	6226	ACTCGCTTGAACCCAGGAGGC
NG_000013	NG_000013	6226	ACTCGCTTGAACCCAGGAGGC
NG_000016	NG_000016	6226	ACTCGCTTGAACCCAGGAGGC
NG_000017	NG_000017	6226	ACTCGCTTGAACCCAGGAGGC
NG_000827	NG_000827	6226	ACTCGCTTGAACCCAGGAGGC
NG_000881	NG_000881	6226	ACTCGCTTGAACCCAGGAGGC
NG_000887	NG_000887	6226	ACTCGCTTGAACCCAGGAGGC
NG_001332	NG_001332	6226	ACTCGCTTGAACCCAGGAGGC
NG_001333	NG_001333	6226	ACTCGCTTGAACCCAGGAGGC
NG_001334	NG_001334	6226	ACTCGCTTGAACCCAGGAGGC
NG_001337	NG_001337	6226	ACTCGCTTGAACCCAGGAGGC
NM_000415	IAPP	6226	ACTCGCTTGAACCCAGGAGGC
NM_001218	CA12	6226	ACTCGCTTGAACCCAGGAGGC
NM_002433	MOG	6226	ACTCGCTTGAACCCAGGAGGC
NM_003035	SIL	6226	ACTCGCTTGAACCCAGGAGGC
NM_003417	ZNF264	6226	ACTCGCTTGAACCCAGGAGGC

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NM_003842	TNFRSF10B	6226	ACTCGCTTGAACCCAGGAGGC
NM_004367	CCR6	6226	ACTCGCTTGAACCCAGGAGGC
NM_004605	SULT2B1	6226	ACTCGCTTGAACCCAGGAGGC
NM_004863	SPTLC2	6226	ACTCGCTTGAACCCAGGAGGC
NM_005513	GTF2E1	6226	ACTCGCTTGAACCCAGGAGGC
NM_006663	RAI	6226	ACTCGCTTGAACCCAGGAGGC
NM_006915	RP2	6226	ACTCGCTTGAACCCAGGAGGC
NM_017614	BHMT2	6226	ACTCGCTTGAACCCAGGAGGC
NM_017723	FLJ20245	6226	ACTCGCTTGAACCCAGGAGGC
NM_017849	FLJ20507	6226	ACTCGCTTGAACCCAGGAGGC
NM_017962	FLJ20825	6226	ACTCGCTTGAACCCAGGAGGC
NM_018097	FLJ10460	6226	ACTCGCTTGAACCCAGGAGGC
NM_018313	PB1	6226	ACTCGCTTGAACCCAGGAGGC
NM_018891	LAMC2	6226	ACTCGCTTGAACCCAGGAGGC
NM_021624	HRH4	6226	ACTCGCTTGAACCCAGGAGGC
NM_022129	MAWBP	6226	ACTCGCTTGAACCCAGGAGGC
NM_023071	FLJ13117	6226	ACTCGCTTGAACCCAGGAGGC
NM_024500	POLYDOM	6226	ACTCGCTTGAACCCAGGAGGC
NM_031409	CCR6	6226	ACTCGCTTGAACCCAGGAGGC
NM_032158	WBSCR20	6226	ACTCGCTTGAACCCAGGAGGC
NM_032782	TIM3	6226	ACTCGCTTGAACCCAGGAGGC
NM_032785	FLJ14442	6226	ACTCGCTTGAACCCAGGAGGC
NM_032790	FLJ14466	6226	ACTCGCTTGAACCCAGGAGGC
NM_054110	GALNT7	6226	ACTCGCTTGAACCCAGGAGGC
NM_058166	TRIM6	6226	ACTCGCTTGAACCCAGGAGGC
NM_138413	LOC112817	6226	ACTCGCTTGAACCCAGGAGGC
NM_138572	LOC135763	6226	ACTCGCTTGAACCCAGGAGGC
NM_138687	PIP5K2B	6226	ACTCGCTTGAACCCAGGAGGC
NM_138764	BAX	6226	ACTCGCTTGAACCCAGGAGGC
NM_144724	FLJ30532	6226	ACTCGCTTGAACCCAGGAGGC
NM_145241	LOC114987	6226	ACTCGCTTGAACCCAGGAGGC
NM_145645	WBSCR20B	6226	ACTCGCTTGAACCCAGGAGGC
U63721	HSU63721	6226	ACTCGCTTGAACCCAGGAGGC
XM_072244	LOC130535	6226	ACTCGCTTGAACCCAGGAGGC
XM_166402	LOC219627	6226	ACTCGCTTGAACCCAGGAGGC
Z84476	HS25J6	6226	ACTCGCTTGAACCCAGGAGGC
Z98744	HS193B12	6226	ACTCGCTTGAACCCAGGAGGC
NM_138733	PGK2	6227	ACACAACCAGAGGATCAAGGC
NM_138733	PGK2	6228	ACTAGAAGCCTTCCGAGCATC
NM_138733	PGK2	6229	ACGTTGTGGCTCAAGCAAGGC
NM_033401	CASPR4	6230	ACTCGAAGTGTTTCGGATGTGC
NM_138994	CASPR4	6230	ACTCGAAGTGTTTCGGATGTGC
NM_033401	CASPR4	6231	ACCTTCACAGTGGACGAACAC
NM_138994	CASPR4	6231	ACCTTCACAGTGGACGAACAC
NM_033401	CASPR4	6232	ACCTTCAGGCCACTATTAACC
NM_138994	CASPR4	6232	ACCTTCAGGCCACTATTAACC

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NM_139021	ERK8	6233	ACTGTGCTCCTGGATGCCAAC
SK465	Erk7	6233	ACTGTGCTCCTGGATGCCAAC
NM_003069	SMARCA1	6234	ACCTCTTCTGGCAAGATGGAC
NM_139035	SMARCA1	6234	ACCTCTTCTGGCAAGATGGAC
NM_003069	SMARCA1	6235	ACCTACGCAGTGGATGCCTAC
NM_139035	SMARCA1	6235	ACCTACGCAGTGGATGCCTAC
NM_003069	SMARCA1	6236	ACTTGCAAGATAACAAGGCTCC
NM_139035	SMARCA1	6236	ACTTGCAAGATAACAAGGCTCC
NM_139209	GPRK7	6237	ACGCTGTCCCTGAACTTCCAC
NM_139209	GPRK7	6238	ACCACTGGGAAGATGTATGCC
NM_139209	GPRK7	6239	ACCCAATGGTTACATGGCTCC
NM_003404	YWHAB	6240	ACTCTGCTCTCTGTTGCCTAC
NM_139323	YWHAB	6240	ACTCTGCTCTCTGTTGCCTAC
NM_003404	YWHAB	6241	ACACCACTGTGTGCGAACTCCC
NM_139323	YWHAB	6241	ACACCACTGTGTGCGAACTCCC
NM_003404	YWHAB	6242	ACGAAATGCAGCCTACACACC
NM_139323	YWHAB	6242	ACGAAATGCAGCCTACACACC
NM_144610	FLJ25006	6243	ACGGCTCCTTTGGAAGTGTCC
SK491	SgK494	6243	ACGGCTCCTTTGGAAGTGTCC
NM_144610	FLJ25006	6244	ACGAGGAGGTTAGCATCCAGC
SK491	SgK494	6244	ACGAGGAGGTTAGCATCCAGC
NM_144624	KIS	6245	ACTGTACCTCAGCTGTTGATC
SK661	KIS	6245	ACTGTACCTCAGCTGTTGATC
NM_144648	FLJ32786	6246	ACAGGCAGCTCTAACATAGCC
NM_144648	FLJ32786	6247	ACGTGGTTGCAGCTCAAGACC
NM_144648	FLJ32786	6248	ACCACAGACAACACTCGGTCC
NM_144685	FLJ32818	6249	ACGATCCTCAAGAATGACGCC
SK582	HIPK4	6249	ACGATCCTCAAGAATGACGCC
NM_144685	FLJ32818	6250	ACGGTGATTGACTTCGGATCC
SK582	HIPK4	6250	ACGGTGATTGACTTCGGATCC
NM_144685	FLJ32818	6251	ACGTCCGACTCCAACCTTCAGC
SK582	HIPK4	6251	ACGTCCGACTCCAACCTTCAGC
NM_145001	MGC22688	6252	ACCTCCAGATCATGCAGGGTC
SK624	YANK1	6252	ACCTCCAGATCATGCAGGGTC
NM_145001	MGC22688	6253	ACGGAAGAAACAGTGAAGCTC
SK624	YANK1	6253	ACGGAAGAAACAGTGAAGCTC
NM_145025	MGC26954	6254	ACTGTTGGAGAAGCTCAACTC
NM_145025	MGC26954	6255	ACTAAACCAGCAGAGGAGCTC
NM_145025	MGC26954	6256	ACGCTCCCACATGTGAATATC
NM_145059	FUK	6257	ACTCCTGGTATCAGCTGGGAC
NM_145059	FUK	6258	ACCGTGCCCTGGAGTGAATTC
NM_145059	FUK	6259	ACCTCCAGCTGAGTGAGCAGC
NM_145203	MGC33182	6260	ACGCTGGAATCTCAGAAGGTC
NM_145203	MGC33182	6261	ACGTACAGAGACAACAGGACC
NM_145259	ALK7	6262	ACCACTGCACCTTCCAACAGC
SK405	ALK7	6262	ACCACTGCACCTTCCAACAGC

NM_145259	ALK7	6263	ACCCACTCTCTGAGTGCAATC
SK405	ALK7	6263	ACCCACTCTCTGAGTGCAATC
NM_145259	ALK7	6264	ACCCAAGAGGTATATGGCTCC
SK405	ALK7	6264	ACCCAAGAGGTATATGGCTCC
XM_027237	MAP3K9	6265	ACTATCCTGGACCAGCTAACC
SK641	Wnk3	6266	ACACAGTACCTTCTCTGCTTC
XM_029183	PRKWINK3	6266	ACACAGTACCTTCTCTGCTTC
SK345	MAST1	6267	ACCTCCTATGACGAGGATGAC
XM_032034	SAST	6267	ACCTCCTATGACGAGGATGAC
SK205	KSR1	6268	ACGAGGTGATGAACTACCGGC
XM_034172	KSR	6268	ACGAGGTGATGAACTACCGGC
SK205	KSR1	6269	ACGCGTGTCTGACTTCTGTCTC
XM_034172	KSR	6269	ACGCGTGTCTGACTTCTGTCTC
XM_034551	DYRK4	6270	ACAGGTGACTCTGACAGCGGC
XM_034551	DYRK4	6271	ACGAAGGACAAAGACAACACC
SK196	MAST3	6272	ACGTCTGGCGAGAACCTCGTC
XM_038150	KIAA0561	6272	ACGTCTGGCGAGAACCTCGTC
SK196	MAST3	6273	ACCCTCTATGAGGGCCACATC
XM_038150	KIAA0561	6273	ACCCTCTATGAGGGCCACATC
SK196	MAST3	6274	ACTGCCCCAAGTTTGCCTTCTC
XM_038150	KIAA0561	6274	ACTGCCCCAAGTTTGCCTTCTC
SK460	SgK493	6275	ACCGTGCTGCAGCTCTATGGC
XM_038576	LOC91461	6275	ACCGTGCTGCAGCTCTATGGC
SK460	SgK493	6276	ACGCGGAACCTCTATAATGCC
XM_038576	LOC91461	6276	ACGCGGAACCTCTATAATGCC
XM_042066	MAP3K1	6277	ACGTCAGCTGTCCATATCAAC
XM_043865	PIK3R1	6278	ACGAATATACCCGCACATCCC
SK510	PAK5	6279	ACATGGACCTCCGGAAGCAAC
XM_045653	PAK7	6279	ACATGGACCTCCGGAAGCAAC
XM_047620	PIP5K1C	6280	ACCCACCTACAAGAAGACCAC
XM_047620	PIP5K1C	6281	ACGTTCTATGGGCTGTACTGC
SK397	ZAP70	6282	ACGCTCATTGCTACGACGGCC
XM_047776	ZAP70	6282	ACGCTCATTGCTACGACGGCC
SK397	ZAP70	6283	ACGTACCTGGAGGAGAAGAAC
XM_047776	ZAP70	6283	ACGTACCTGGAGGAGAAGAAC
SK397	ZAP70	6284	ACGATGAAAGGGCCGGAGGTC
XM_047776	ZAP70	6284	ACGATGAAAGGGCCGGAGGTC
SK250	NEK1	6285	ACCAAGGATGGAGAAATGTGC
XM_048605	LOC257463	6285	ACCAAGGATGGAGAAATGTGC
SK250	NEK1	6286	ACTTCTGCCTGGAGTTTCGTCC
XM_048605	LOC257463	6286	ACTTCTGCCTGGAGTTTCGTCC
XM_055866	KIAA1883	6287	ACAGAGCGAGGACAAGGTGTC
XM_059051	LOC126520	6288	ACATGGGTGGATTATTCCAGC
XM_059051	LOC126520	6289	ACTGGGATGGTGCAGGTGAGC
XM_060051	LOC139728	6290	ACATCCAGGCTGGGAACATGC
XM_061154	LOC118800	6291	ACGGATAATCTTACGGATGCC

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XM_061154	LOC118800	6292	ACCTCACCAAAGCGACATGAC
XM_061691	LOC119794	6293	ACTGCAGAATCATGCGTGAAC
XM_062966	LOC122134	6294	ACATGAGTGGCTTCCCTAGCC
XM_062966	LOC122134	6295	ACACTCAACCAGGTGATTGGC
XM_064804	LOC125806	6296	ACGGGAATCCTACACAAGGAC
XM_065861	LOC130736	6297	ACTGGTATGGATTCTGACAGC
XM_065861	LOC130736	6298	ACTGGGCCAATATTGCAGAAC
XM_066534	LOC139189	6299	ACGTCACCTCTGGACATCCTC
XM_068965	LOC134692	6300	ACGATCTCGAACTCCATGATC
XM_068965	LOC134692	6301	ACGTGAAGATGATCTTCAGGC
XM_068965	LOC134692	6302	ACGTGGATGTCTGGTTCATAC
XM_069683	LOC136062	6303	ACTCCAGAGACCTATGGCGTC
XM_069683	LOC136062	6304	ACATGTGCCATCCAGTTGTGC
SK452	CLIK1L	6305	ACACTAACACCAGCTTCATGC
XM_086530	LOC149420	6305	ACACTAACACCAGCTTCATGC
SK452	CLIK1L	6306	ACGTTTGTTCAGCCTCTGGGC
XM_086530	LOC149420	6306	ACGTTTGTTCAGCCTCTGGGC
SK452	CLIK1L	6307	ACATGCTGGCTGCAAACCCTC
XM_086530	LOC149420	6307	ACATGCTGGCTGCAAACCCTC
XM_090537	LOC160851	6308	ACGGAGATGGAGGATTGGATC
XM_090537	LOC160851	6309	ACATGCCGTTGTAGCTGATGC
XM_090537	LOC160851	6310	ACGAAAGCAGTGAGGCAAGTC
XM_090977	LOC161559	6311	ACGGAATCATCCACCCGTTCC
XM_090977	LOC161559	6312	ACGGAATCATCCGCCCGTTC
SK527	DCAMKL2	6313	ACGTCTTTGAAACTGGGAGAC
XM_093975	LOC166614	6313	ACGTCTTTGAAACTGGGAGAC
SK527	DCAMKL2	6314	ACCAATCTCCAGGAAGATCTC
XM_093975	LOC166614	6314	ACCAATCTCCAGGAAGATCTC
SK527	DCAMKL2	6315	ACTGTTGAAGCTCGGTGTACC
XM_093975	LOC166614	6315	ACTGTTGAAGCTCGGTGTACC
SK449	NIM1	6316	ACTACTTGTGTGAAGGTGGGC
XM_094437	LOC167359	6316	ACTACTTGTGTGAAGGTGGGC
SK449	NIM1	6317	ACATAACCAAGGGAGAGATGC
XM_094437	LOC167359	6317	ACATAACCAAGGGAGAGATGC
SK449	NIM1	6318	ACGAAGGCTTTGGAAAGTGTC
XM_094437	LOC167359	6318	ACGAAGGCTTTGGAAAGTGTC
XM_095626	LOC169315	6319	ACGGAGAACTGATCCCTCCAC
XM_095626	LOC169315	6320	ACGTCTCAGATAGAGGAGGGC
XM_095626	LOC169315	6321	ACTGAGGCCTATGGGCGAATC
XM_095699	LOC169457	6322	ACAGACAGAAGGTCACAGTCC
XM_095699	LOC169457	6323	ACGCATGGGATCTCTGGTTAC
XM_095787	LOC158067	6324	ACGGATGCTGAAGAGCAGGTC
SK252	NEK3	6325	ACGGCTTCCCAAGTCTTTCTC
XM_166264	LOC220114	6325	ACGGCTTCCCAAGTCTTTCTC
SK252	NEK3	6326	ACGGGTGCATCAGTCCACTGC
XM_166264	LOC220114	6326	ACGGGTGCATCAGTCCACTGC

SK252	NEK3	6327	ACGCAGTGGCTCAAAGAGACC
XM_166264	LOC220114	6327	ACGCAGTGGCTCAAAGAGACC
SK526	TTBK1	6328	ACGAAGTTGCAAGGGAAGGAC
XM_166453	KIAA1855	6328	ACGAAGTTGCAAGGGAAGGAC
SK526	TTBK1	6329	ACGGAACAGGTAGGGATGATC
XM_166453	KIAA1855	6329	ACGGAACAGGTAGGGATGATC
SK526	TTBK1	6330	ACAGAGTGGGTCAATCATCGAC
XM_166453	KIAA1855	6330	ACAGAGTGGGTCAATCATCGAC
SK262	PIK3R4	6331	ACAGTTGCTCGAGCCAAGCAC
XM_030812	PIK3R4	6331	ACAGTTGCTCGAGCCAAGCAC
Y08991	HSP150	6331	ACAGTTGCTCGAGCCAAGCAC
SK262	PIK3R4	6332	ACTGGTTCTCTTCCCGACTGC
XM_030812	PIK3R4	6332	ACTGGTTCTCTTCCCGACTGC
Y08991	HSP150	6332	ACTGGTTCTCTTCCCGACTGC
SK262	PIK3R4	6333	ACTTGGAGGACGAGTCAAGAC
XM_030812	PIK3R4	6333	ACTTGGAGGACGAGTCAAGAC
Y08991	HSP150	6333	ACTTGGAGGACGAGTCAAGAC
NM_001798	CDK2	6337	ACGATCGGAGAGGGCACGTAC
NM_052827	CDK2	6337	ACGATCGGAGAGGGCACGTAC
NM_003150	STAT3	6340	ACAGTGCCTTTGTGGTGGAGC
NM_139276	STAT3	6340	ACAGTGCCTTTGTGGTGGAGC
NM_003150	STAT3	6341	ACGATTGACCTAGAGACCCAC
NM_139276	STAT3	6341	ACGATTGACCTAGAGACCCAC
NM_003150	STAT3	6342	ACCGAAGGGTACATCATGGGC
NM_139276	STAT3	6342	ACCGAAGGGTACATCATGGGC
NM_000435	NOTCH3	6352	ACGTGAACGTGGACGACTGTC
NM_000435	NOTCH3	6353	ACCATTGACGACTGTGCCAGC
NM_004557	NOTCH4	6355	ACAGGCACCTCCTGCCATAAC
NM_000245	MET	6358	ACAGAGGCACTAGCAAAGTCC
NM_000245	MET	6359	ACCATGGCTCTAGTTGTGCAC
NM_000245	MET	6360	ACATGCCTCTGGAGTGTATTC
NM_003618	MAP4K3	6361	ACGACTTTGCAGTTGTGCAGC
NM_003618	MAP4K3	6362	ACCTTGACAGAGCTTCAGCCTC
NM_003618	MAP4K3	6363	ACCACAACATTTGACACGGTC
NM_001274	CHEK1	6364	ACTCTCAGACTTTGGCTTGGC
NM_001274	CHEK1	6365	ACTGCTCGCTGGAGAATTGCC
NM_001274	CHEK1	6366	ACTCGATTCTGCTCCTCTAGC
NM_002110	HCK	6367	ACCAGCAACACACCAGGAATC
NM_002110	HCK	6368	ACCTATGTGCGCCGCGTTGAC
NM_002110	HCK	6369	ACGCCTTGGGAGAAAGATGCC
NM_002612	PDK4	6370	ACATTGATATCCTCCCGACCC
NM_002612	PDK4	6371	ACGATGCCTGTACAGTTGACC
NM_002612	PDK4	6372	ACATCAGCCTTCCCTTACACC
NM_002611	PDK2	6373	ACAACCTCCTTCACCTTCCTC
NM_002611	PDK2	6374	ACACACATCGGCAGCATCGAC
NM_002611	PDK2	6375	ACGATTGAGCGACTCTTCAGC

NM_002645	PIK3C2A	6376	ACAAGCTCACCCAAGCTGAAC
NM_002645	PIK3C2A	6377	ACAATCCCTTTCTGTGGCAAC
NM_002645	PIK3C2A	6378	ACGCCCAGGGCCATATATCTC
NM_002651	PIK4CB	6379	ACGCTACGGAAGCTGATCCTC
NM_002651	PIK4CB	6380	ACCTTTGACACCACCAGTGTC
NM_002651	PIK4CB	6381	ACCAGTCACAGCTCTCCTTGC
NM_002754	MAPK13	6382	ACGCACATGCAGCATGAGAAC
NM_002754	MAPK13	6383	ACCCTGGCTGTGAATGAGGAC
NM_002754	MAPK13	6384	ACAGCGGCCAAATCCTACATC
NM_003138	SRPK2	6385	ACAGACATGGTGGTCCAGCTC
SK359	SRPK2	6385	ACAGACATGGTGGTCCAGCTC
NM_003138	SRPK2	6386	ACGTACTTGGCCACCATCTCC
SK359	SRPK2	6386	ACGTACTTGGCCACCATCTCC
XM_172741	LOC253939	6386	ACGTACTTGGCCACCATCTCC
NM_003138	SRPK2	6387	ACTCCAACATCAAGGCCTCC
SK359	SRPK2	6387	ACTCCAACATCAAGGCCTCC
NM_003565	ULK1	6388	ACGCACGATTTGGAGGTCGCC
NM_004755	RPS6KA5	6389	ACGTCTTGGAACACATTAGGC
NM_004755	RPS6KA5	6390	ACAGAGAGCGTTTCACAGAGC
NM_004755	RPS6KA5	6391	ACTTGGGATGATTTAGCCGCC
NM_004760	STK17A	6392	ACTCTTTGACCAGTGTGTTGC
NM_004760	STK17A	6393	ACGAAACCTGAAGATCGAGCC
NM_004760	STK17A	6394	ACCCGAGGAATCCATTGTAAC
NM_004834	MAP4K4	6395	ACTGGCACCTATGGACAAGTC
NM_145686	MAP4K4	6395	ACTGGCACCTATGGACAAGTC
NM_145687	MAP4K4	6395	ACTGGCACCTATGGACAAGTC
SK437	ZC1/HGK	6395	ACTGGCACCTATGGACAAGTC
NM_004834	MAP4K4	6396	ACCACCAAAGGGAACACACTC
NM_145686	MAP4K4	6396	ACCACCAAAGGGAACACACTC
NM_145687	MAP4K4	6396	ACCACCAAAGGGAACACACTC
SK437	ZC1/HGK	6396	ACCACCAAAGGGAACACACTC
NM_004834	MAP4K4	6397	ACGAGGAGGAAGTGCCTGAAC
NM_145686	MAP4K4	6397	ACGAGGAGGAAGTGCCTGAAC
NM_145687	MAP4K4	6397	ACGAGGAGGAAGTGCCTGAAC
SK437	ZC1/HGK	6397	ACGAGGAGGAAGTGCCTGAAC
XM_038748	MAP4K4	6397	ACGAGGAGGAAGTGCCTGAAC
NM_005391	PDK3	6398	ACATAAGAGCCCTGAGGATCC
NM_005391	PDK3	6399	ACGCGCCAGACAAACCTATTC
NM_005391	PDK3	6400	ACGCCGATGATTGGAGCAATC
NM_005417	SRC	6401	ACGCTGTTTCGGAGGCTTCAAC
SK357	SRC	6401	ACGCTGTTTCGGAGGCTTCAAC
NM_005417	SRC	6402	ACGTGAGACCACGAAAGGTGC
SK357	SRC	6402	ACGTGAGACCACGAAAGGTGC
NM_005417	SRC	6403	ACCATCCTGGTGGGAGAGAAC
SK357	SRC	6403	ACCATCCTGGTGGGAGAGAAC
NM_005881	BCKDK	6404	ACCTTCCAGTGAGGATTGCTC

NM_005881	BCKDK	6405	ACTGGAGAGTCACCTAGACAC
NM_005881	BCKDK	6406	ACTGTCCCAGATGTGGTCATC
NM_005990	STK10	6407	ACACGAGATTTCCTTCATCGGC
NM_005990	STK10	6408	ACAGACACGCCCTACGACTAC
NM_005990	STK10	6409	ACGCCTCAATGCTGACAAGCC
NM_006035	CDC42BPB	6410	ACTGGTGCTGGCCATTGACTC
NM_006035	CDC42BPB	6411	ACATACGGGCGCTGAGTGTGAC
NM_006035	CDC42BPB	6412	ACGAAGCGAAGGACCTCATCC
NM_006206	PDGFRA	6413	ACTGAGCTTGAAGGCAGGCAC
NM_006206	PDGFRA	6414	ACAGAAGTTCCAGACCATCCC
NM_006206	PDGFRA	6415	ACATCAAACCCACCTTCAGCC
NM_000142	FGFR3	6416	ACGGAGCTAGAGGTTCTCTCC
NM_000142	FGFR3	6417	ACCGTCACCTTTGAGGACGCC
NM_000142	FGFR3	6418	ACGATCTCCCGCTTCCCGCTC
NM_001261	CDK9	6419	ACGTTACGCTGTCTGAGATC
NM_001261	CDK9	6420	ACCAAGATCCTGCATAGGGAC
NM_001315	MAPK14	6421	ACAAACGGGGTTACGTGTGGC
NM_139012	MAPK14	6421	ACAAACGGGGTTACGTGTGGC
NM_139013	MAPK14	6421	ACAAACGGGGTTACGTGTGGC
NM_139014	MAPK14	6421	ACAAACGGGGTTACGTGTGGC
NM_001315	MAPK14	6422	ACGTCATCAGCTTTGTGCCAC
NM_139012	MAPK14	6422	ACGTCATCAGCTTTGTGCCAC
NM_139014	MAPK14	6422	ACGTCATCAGCTTTGTGCCAC
NM_001315	MAPK14	6423	ACGAGATGGAGTCCTGAGCAC
NM_139012	MAPK14	6423	ACGAGATGGAGTCCTGAGCAC
NM_139014	MAPK14	6423	ACGAGATGGAGTCCTGAGCAC
AF346607	AF346607	6424	ACGTTGCCATCCTCAGCCTCC
NM_001569	IRAK1	6424	ACGTTGCCATCCTCAGCCTCC
AF346607	AF346607	6425	ACCATTGTGGACTTTGCTGGC
NM_001569	IRAK1	6425	ACCATTGTGGACTTTGCTGGC
AF346607	AF346607	6426	ACAAGGAGGCCCTCCTATGACC
NM_001569	IRAK1	6426	ACAAGGAGGCCCTCCTATGACC
NM_001626	AKT2	6427	ACCTTCTCCGTAGCAGAATGC
SK019	AKT2	6427	ACCTTCTCCGTAGCAGAATGC
NM_001626	AKT2	6428	ACCACCTTTGTGCATACGCTGC
SK019	AKT2	6428	ACCACCTTTGTGCATACGCTGC
NM_001626	AKT2	6429	ACACTCCTTGGCAAGGGAACC
SK019	AKT2	6429	ACACTCCTTGGCAAGGGAACC
NM_001799	CDK7	6430	ACGGCCAGAGATAAGAATACC
SK055	CDK7	6430	ACGGCCAGAGATAAGAATACC
NM_001799	CDK7	6431	ACGCCTACATGTTGATGACTC
SK055	CDK7	6431	ACGCCTACATGTTGATGACTC
NM_001799	CDK7	6432	ACCACCTGGATGTCAGCTGCC
SK055	CDK7	6432	ACCACCTGGATGTCAGCTGCC
NM_001982	ERBB3	6433	ACCCAATACCAGACACTGTAC
NM_001982	ERBB3	6434	ACTGGTCACTGCTTTGGGCCC

NM_001982	ERBB3	6435	ACCCTGGACTTTCTGATCACC
NM_002253	KDR	6436	ACCAGAATTTCTTGGGACAGC
NM_002253	KDR	6437	ACGGGCTTTACTATTCCCAGC
NM_002253	KDR	6438	ACTACCCCTTCTTCGAAGCATC
NM_002497	NEK2	6439	ACTATTGTGAAGGAGGGGATC
NM_002497	NEK2	6440	ACAAATCGCAGGATTCCAGCC
NM_002497	NEK2	6441	ACAATCGCAGGATTCCAGCCC
NM_002595	PCTK2	6442	ACCGTCTCACAGTATGCATTC
NM_002595	PCTK2	6443	ACATAAGCGGTTATCACTGCC
NM_002595	PCTK2	6444	ACCCAATGAGTCGAAGGTCTC
NM_002609	PDGFRB	6445	ACCGGCTCTACATCTTTGTGC
NM_002609	PDGFRB	6446	ACCGCAGTGCAGACTGTGGTC
NM_002609	PDGFRB	6447	ACCATCACCGTGGTTGAGAGC
NM_002731	PRKACB	6448	ACTTGGAAGGTTCACTGAGCC
NM_002731	PRKACB	6449	ACCTCCAGAGTATTTGGCTCC
NM_002731	PRKACB	6450	ACGGTCCGATTCCCATCCCAC
NM_002752	MAPK9	6451	ACACCAATTGGCTCTGGGGCC
NM_139068	MAPK9	6451	ACACCAATTGGCTCTGGGGCC
NM_139069	MAPK9	6451	ACACCAATTGGCTCTGGGGCC
NM_139070	MAPK9	6451	ACACCAATTGGCTCTGGGGCC
SK189	JNK2	6451	ACACCAATTGGCTCTGGGGCC
NM_002752	MAPK9	6452	ACCTTCATGATGACCCCTTAC
NM_139068	MAPK9	6452	ACCTTCATGATGACCCCTTAC
NM_139069	MAPK9	6452	ACCTTCATGATGACCCCTTAC
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SK189	JNK2	6453	ACGTAGCAACGCCACTCCTTC
NM_002753	MAPK10	6454	ACAGCCTATTGGCTCTGGGGC
NM_138980	MAPK10	6454	ACAGCCTATTGGCTCTGGGGC
NM_138982	MAPK10	6454	ACAGCCTATTGGCTCTGGGGC
NM_002753	MAPK10	6455	ACTCCTGGACTTTGGACTGGC
NM_138980	MAPK10	6455	ACTCCTGGACTTTGGACTGGC
NM_138981	MAPK10	6455	ACTCCTGGACTTTGGACTGGC
NM_138982	MAPK10	6455	ACTCCTGGACTTTGGACTGGC
NM_002753	MAPK10	6456	ACACTATGTGGAGAATCGGCC
NM_138980	MAPK10	6456	ACACTATGTGGAGAATCGGCC
NM_138981	MAPK10	6456	ACACTATGTGGAGAATCGGCC
NM_138982	MAPK10	6456	ACACTATGTGGAGAATCGGCC
NM_002880	RAF1	6457	ACCAAGCAAAGAACAGTGGTC
NM_002880	RAF1	6458	ACCTTTGCTCGGAAGACGTTT
NM_002880	RAF1	6459	ACTGTCCACATGGTCAGCACC
NM_002958	RYK	6460	ACGCTGGGATTCCAAGTGGAC

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SK340	RYK	6460	ACGCTGGGATTCCAAGTGGAC
NM_002958	RYK	6461	ACCAATGCAACTCCTATCACC
SK340	RYK	6461	ACCAATGCAACTCCTATCACC
NM_002958	RYK	6462	ACGAACGACTTGAGAAGTGTC
SK340	RYK	6462	ACGAACGACTTGAGAAGTGTC
NM_003242	TGFBR2	6463	ACGCCTGGTGAGACTTTCTTC
NM_003242	TGFBR2	6464	ACGGCCAAGCTGAAGCAGAAC
NM_003691	STK16	6465	ACTCACCCTAACATCCTTCGC
SK506	MPSK1	6465	ACTCACCCTAACATCCTTCGC
NM_003691	STK16	6466	ACGGGTTATGCCCACAGAGAC
SK506	MPSK1	6466	ACGGGTTATGCCCACAGAGAC
NM_003691	STK16	6467	ACCTCAGCATCCCACAAAGCC
SK506	MPSK1	6467	ACCTCAGCATCCCACAAAGCC
NM_003674	CDK10	6468	ACCACAGGCTGGGACGATGCC
NM_003948	CDKL2	6469	ACGATTGCAATGCGAGAAATC
NM_003948	CDKL2	6470	ACCCCGATGGTACAGAGCTCC
NM_003948	CDKL2	6471	ACGGCTGTTGATGTGTGGGCC
NM_004196	CDKL1	6472	ACATTGCCCTTCGGGAAATCC
NM_004196	CDKL1	6473	ACCTTGGCAGACACTGCAAGC
NM_004196	CDKL1	6474	ACAGGCTGACATGTGAACAGC
NM_001721	BMX	6475	ACCACAGAGTTCCCACCTTCC
SK417	BMX	6475	ACCACAGAGTTCCCACCTTCC
NM_002019	FLT1	6476	ACGGAAAGCGAAAGGCTGAGC
NM_002019	FLT1	6477	ACCACAGCTCAAGCAAACCAC
NM_002019	FLT1	6478	ACGGAAGGGAGCTCGTCATT
NM_002227	JAK1	6479	ACCCTCTTTGCCCTGTATGAC
SK185	JAK1	6479	ACCCTCTTTGCCCTGTATGAC
NM_002227	JAK1	6480	ACTTGGCATGGAACCAACGAC
SK185	JAK1	6480	ACTTGGCATGGAACCAACGAC
NM_002227	JAK1	6481	ACAGATTCCAGATGCAACCCC
SK185	JAK1	6481	ACAGATTCCAGATGCAACCCC
NM_002750	MAPK8	6482	ACAACCTATAGGCTCAGGAGC
NM_139046	MAPK8	6482	ACAACCTATAGGCTCAGGAGC
NM_139047	MAPK8	6482	ACAACCTATAGGCTCAGGAGC
NM_139049	MAPK8	6482	ACAACCTATAGGCTCAGGAGC
NM_002750	MAPK8	6483	ACCAGCTTGGAACACCATGTC
NM_139046	MAPK8	6483	ACCAGCTTGGAACACCATGTC
NM_139047	MAPK8	6483	ACCAGCTTGGAACACCATGTC
NM_139049	MAPK8	6483	ACCAGCTTGGAACACCATGTC
NM_002750	MAPK8	6484	ACGCTCCACCACCAAAGATCC
NM_139046	MAPK8	6484	ACGCTCCACCACCAAAGATCC
NM_139047	MAPK8	6484	ACGCTCCACCACCAAAGATCC
NM_139049	MAPK8	6484	ACGCTCCACCACCAAAGATCC
NM_004935	CDK5	6485	ACCATCGTCAGGCTTCATGAC
NM_004935	CDK5	6486	ACGCTGTACTCCACGTCCATC
NM_004935	CDK5	6487	ACGCTGCCAGACTATAAGCCC

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NM_002082	GPRK6	6488	ACGAAATGGCGGCAGATGCTC
XM_169341	LOC222456	6488	ACGAAATGGCGGCAGATGCTC
NM_002082	GPRK6	6489	ACCATCTTGCTGGATGACCAC
XM_169341	LOC222456	6489	ACCATCTTGCTGGATGACCAC
NM_002082	GPRK6	6490	ACTGAACGGTACACGTTTCAGC
NM_005228	EGFR	6491	ACCAAGCTCACGCAGTTGGGC
NM_005228	EGFR	6492	ACACCGGACTGAAGGAGCTGC
NM_005228	EGFR	6493	ACAGTGTGATCCAAGCTGTCC
NM_005235	ERBB4	6494	ACCTGAGCTCTCTCTCTGACC
XM_172034	LOC254337	6494	ACCTGAGCTCTCTCTCTGACC
NM_005235	ERBB4	6495	ACGTCTGTACTGGCCGTTGC
NM_005235	ERBB4	6496	ACACCTTGCACTGACATTTGC
NM_005255	GAK	6497	ACAATGGAATCTCGAGGCCCC
NM_005255	GAK	6498	ACGATCTTCTACCAGACGTGC
NM_005255	GAK	6499	ACTGGGAAGTACTCGATCCCC
NM_000208	INSR	6500	ACAACGAGGCCCGAAGATTTTC
NM_000208	INSR	6501	ACACGAGGCCCGAAGATTTCC
NM_000208	INSR	6502	ACCGAGGAGTGTGGAGACATC
NM_000215	JAK3	6503	ACGTCTGTGTACAGGATTC
NM_001616	ACVR2	6504	ACAGATGGCCACAAACCTGCC
L03718	HUMGPRKLG	6505	ACACCCACTCTAAAGAGGCAC
NM_005307	GPRK2L	6505	ACACCCACTCTAAAGAGGCAC
SK156	GPRK4	6505	ACACCCACTCTAAAGAGGCAC
U33054	HSU33054	6505	ACACCCACTCTAAAGAGGCAC
U33055	HSU33055	6505	ACACCCACTCTAAAGAGGCAC
U33056	HSU33056	6505	ACACCCACTCTAAAGAGGCAC
X75897	HSGRK4	6505	ACACCCACTCTAAAGAGGCAC
X97879	HSGRK4B	6505	ACACCCACTCTAAAGAGGCAC
X97880	HSGRK4C	6505	ACACCCACTCTAAAGAGGCAC
X97881	HSGRK4D	6505	ACACCCACTCTAAAGAGGCAC
X98118	HSGRK4AGE	6505	ACACCCACTCTAAAGAGGCAC
L03718	HUMGPRKLG	6506	ACTGGAAATGGCTGGAAAGGC
NM_005307	GPRK2L	6506	ACTGGAAATGGCTGGAAAGGC
SK156	GPRK4	6506	ACTGGAAATGGCTGGAAAGGC
U33054	HSU33054	6506	ACTGGAAATGGCTGGAAAGGC
U33055	HSU33055	6506	ACTGGAAATGGCTGGAAAGGC
U33056	HSU33056	6506	ACTGGAAATGGCTGGAAAGGC
X97879	HSGRK4B	6506	ACTGGAAATGGCTGGAAAGGC
X97880	HSGRK4C	6506	ACTGGAAATGGCTGGAAAGGC
X97881	HSGRK4D	6506	ACTGGAAATGGCTGGAAAGGC
X98118	HSGRK4AGE	6506	ACTGGAAATGGCTGGAAAGGC
L03718	HUMGPRKLG	6507	ACTGATTCAGGGACATTCTCC
NM_005307	GPRK2L	6507	ACTGATTCAGGGACATTCTCC
SK156	GPRK4	6507	ACTGATTCAGGGACATTCTCC
U33054	HSU33054	6507	ACTGATTCAGGGACATTCTCC
U33055	HSU33055	6507	ACTGATTCAGGGACATTCTCC

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U33056	HSU33056	6507	ACTGATTTCAGGGACATTCTCC
X97879	HSGRK4B	6507	ACTGATTTCAGGGACATTCTCC
X97880	HSGRK4C	6507	ACTGATTTCAGGGACATTCTCC
X97881	HSGRK4D	6507	ACTGATTTCAGGGACATTCTCC
X98118	HSGRK4AGE	6507	ACTGATTTCAGGGACATTCTCC
NM_005308	GPRK5	6508	ACGAAATCCTGAAGTTCCCTC
NM_005308	GPRK5	6509	ACGTACCTCACCCCAAAGTCC
NM_005308	GPRK5	6510	ACAAAGAGGAAAGGGGAGTCC
NM_005923	MAP3K5	6511	ACACTCGACTTTTGAGAAACC
SK225	MAP3K5	6511	ACACTCGACTTTTGAGAAACC
NM_005923	MAP3K5	6512	ACAGTCTACTGCTGTGACAGC
SK225	MAP3K5	6512	ACAGTCTACTGCTGTGACAGC
NM_005923	MAP3K5	6513	ACGCGAAGGACAAGTTGCTTC
SK225	MAP3K5	6513	ACGCGAAGGACAAGTTGCTTC
NM_006301	MAP3K12	6514	ACAGCCTACTCCACTGAGCAC
SK110	DLK	6514	ACAGCCTACTCCACTGAGCAC
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SK110	DLK	6515	ACACCGACATCAAGCACTTGC
NM_006301	MAP3K12	6516	ACGGAGCTGAGTGACAAGAGC
SK110	DLK	6516	ACGGAGCTGAGTGACAAGAGC
NM_012119	CCRK	6517	ACCTGAAGGCTGTGTTCCAC
SK483	CCRK	6517	ACCTGAAGGCTGTGTTCCAC
XM_005420	CCRK	6517	ACCTGAAGGCTGTGTTCCAC
NM_012119	CCRK	6518	ACACCTGCCAACCTGCTCATC
SK483	CCRK	6518	ACACCTGCCAACCTGCTCATC
XM_005420	CCRK	6518	ACACCTGCCAACCTGCTCATC
NM_012119	CCRK	6519	ACGGCTCTCCTCCATCAGTAC
SK483	CCRK	6519	ACGGCTCTCCTCCATCAGTAC
XM_005420	CCRK	6519	ACGGCTCTCCTCCATCAGTAC
NM_012395	PFTK1	6520	ACGATGTCTACACGGAAGTGC
NM_012395	PFTK1	6521	ACAGTTAGGCGGCACTCCAGC
NM_012395	PFTK1	6522	ACACCACAGAACCTTCTGATC
NM_014432	IL20RA	6523	ACTGGACTCCACCAGAGGGTC
NM_014432	IL20RA	6524	ACGACCTTCCTGTTTCCATGC
NM_014432	IL20RA	6525	ACTCAAACAGAACGTGGTCCC
NM_014911	AAK1	6526	ACGCAATGGGATGAAATGTGC
SK422	AAK1	6526	ACGCAATGGGATGAAATGTGC
NM_014911	AAK1	6527	ACAACATCCTCTTGTCATGACC
SK422	AAK1	6527	ACAACATCCTCTTGTCATGACC
NM_014911	AAK1	6528	ACTCCACAAACTGAGGGAGTC
SK422	AAK1	6528	ACTCCACAAACTGAGGGAGTC
NM_016507	CRK7	6529	ACACATCGTCCACCACCAGCAC
SK485	CRK7	6529	ACACATCGTCCACCACCAGCAC
NM_016507	CRK7	6530	ACAAGCCAAGAAGTCTCCAGC
SK485	CRK7	6530	ACAAGCCAAGAAGTCTCCAGC
NM_016507	CRK7	6531	ACTCCAGGTCATCCAAGCTCC

SK485	CRK7	6531	ACTCCAGGTCATCCAAGCTCC
NM_003565	ULK1	6532	ACAGGCATCATCCACCGCGAC
NM_003565	ULK1	6533	ACCATCCTGCTGTCCAACCCC
NM_003582	DYRK3	6534	ACCAGTTCATCCAAGGCACCC
SK488	DYRK3	6534	ACCAGTTCATCCAAGGCACCC
NM_003582	DYRK3	6535	ACACTTCGACAGTACGTGGCC
SK488	DYRK3	6535	ACACTTCGACAGTACGTGGCC
NM_003582	DYRK3	6536	ACATGGTGCGCAATGAGAAGC
SK488	DYRK3	6536	ACATGGTGCGCAATGAGAAGC
NM_003668	MAPKAPK5	6537	ACGCCAGCCAAGTAACAAAGC
NM_139078	MAPKAPK5	6537	ACGCCAGCCAAGTAACAAAGC
NM_003668	MAPKAPK5	6538	ACGAGCTGTGACTTGTGGTCC
NM_139078	MAPKAPK5	6538	ACGAGCTGTGACTTGTGGTCC
NM_003668	MAPKAPK5	6539	ACCTCCGAGATGTGATTGCTC
NM_139078	MAPKAPK5	6539	ACCTCCGAGATGTGATTGCTC
NM_003942	RPS6KA4	6540	ACGGTGAGCGTGGAGAAGTTC
NM_003942	RPS6KA4	6541	ACAGAGCGGACCTTCTCCTTC
NM_003942	RPS6KA4	6542	ACTCTGCACGAGGTGCATCAC
NM_003684	MKNK1	6543	ACAGTTCAGGTGCCGTGAGC
SK235	MNK1	6543	ACAGTTCAGGTGCCGTGAGC
NM_003684	MKNK1	6544	ACGGAGGTTCCATCTTAGCCC
SK235	MNK1	6544	ACGGAGGTTCCATCTTAGCCC
NM_003684	MKNK1	6545	ACCTGAACAACCTCCTGTACCC
SK235	MNK1	6545	ACCTGAACAACCTCCTGTACCC
NM_003821	RIPK2	6546	ACTATCCTGATGTTGCTTGGC
NM_003821	RIPK2	6547	ACTCAAGGGCCAGTATCAAGC
NM_003821	RIPK2	6548	ACGATGTCACCAATCCTTTGC
NM_003831	SUDD	6549	ACCAGCTGGCCAAAGAATTGC
NM_003831	SUDD	6550	ACGTTGCTGTTGCTGAAGGAC
NM_003831	SUDD	6551	ACTATGATGCACAGCTTAGGC
NM_003952	RPS6KB2	6552	ACTGCCAAGGACACAGCACAC
SK266	p70S6Kb	6552	ACTGCCAAGGACACAGCACAC
NM_003952	RPS6KB2	6553	ACGCCCCGAGAACATCATGCTC
SK266	p70S6Kb	6553	ACGCCCCGAGAACATCATGCTC
NM_003952	RPS6KB2	6554	ACGGAGTCTATCCATGAGGGC
SK266	p70S6Kb	6554	ACGGAGTCTATCCATGAGGGC
NM_004119	FLT3	6555	ACCATTTCTGTCTCTGGGTC
NM_004119	FLT3	6556	ACGCACAGCTCCCTGAATTGC
NM_004119	FLT3	6557	ACTGGGTGCTTTGCGATTAC
NM_004203	PKMYT1	6558	ACGCGTTCCATGTACCATTTC
SK248	MYT1	6558	ACGCGTTCCATGTACCATTTC
NM_004203	PKMYT1	6559	ACGTGACATCAACTCAGAGCC
SK248	MYT1	6559	ACGTGACATCAACTCAGAGCC
NM_004203	PKMYT1	6560	ACCTCCCATGGTCTTCTCTGC
SK248	MYT1	6560	ACCTCCCATGGTCTTCTCTGC
NM_004217	STK12	6561	ACAGCCATTTATCGTGGCGC

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NM_004217	STK12	6562	ACCATCCTGCGTCTCTACAAC
NM_004217	STK12	6563	ACGGTGGACCTAAAGTTCCCC
NM_004226	STK17B	6564	ACTTGGCAAAGTCTTGTCCCC
NM_004226	STK17B	6565	ACATAGGGCATGCGTGTGAAC
NM_004226	STK17B	6566	ACGGTCCTCTGAAGACAAGAC
NM_004570	PIK3C2G	6567	ACAGAATGCTCCTGGGGAAGC
NM_004570	PIK3C2G	6568	ACGCAGCAATACGAGTCTGGC
NM_004570	PIK3C2G	6569	ACTTCTGGGAAGATCTGGAGC
NM_004690	LATS1	6570	ACATGTCAACCGAAGATCCTC
NM_004690	LATS1	6571	ACTCCTTAGTTCTCAGAGGC
NM_004690	LATS1	6572	ACATGTTGTCCCTGCTGGCAC
NM_004717	DGKI	6573	ACTGCCGTGAATGGAGAACAC
NM_004717	DGKI	6574	ACACCCATCTCTTCTCCTCTC
NM_004717	DGKI	6575	ACTGACCTGGCTCGAACTCTC
NM_004734	DCAMKL1	6576	ACACGGCTCATTCCTTTGAGC
SK063	DCAMKL1	6576	ACACGGCTCATTCCTTTGAGC
NM_004734	DCAMKL1	6577	ACATGTCGAGGCAAAGAGCAC
SK063	DCAMKL1	6577	ACATGTCGAGGCAAAGAGCAC
NM_004734	DCAMKL1	6578	ACCATCGTCCACCGTGATATC
SK063	DCAMKL1	6578	ACCATCGTCCACCGTGATATC
NM_000875	IGF1R	6579	ACCTCTTCTACAACCTACGCCC
NM_000875	IGF1R	6580	ACTGCTGACCTCTGTTACCTC
NM_000875	IGF1R	6581	ACTGAGTACAACCTACCGCTGC
NM_001258	CDK3	6582	ACGGAACCTGAAGCACCCCAAC
NM_001258	CDK3	6583	ACGAAGTACATGGACTCCACC
NM_001258	CDK3	6584	ACAGCCCTGTTTCCTGGTGAC
NM_001259	CDK6	6585	ACGGCCCGCGACTTGAAGAAC
NM_001259	CDK6	6586	ACCATTCTGGTGACCAGCAGC
NM_001259	CDK6	6587	ACAACCTGGATTCCCACCTGC
NM_001277	CHK	6588	ACCATGCTGTTCCAGTGCTCC
NM_001277	CHK	6589	ACGAGGGATCCGAACAAGCTC
NM_001277	CHK	6590	ACCTCTATGGCATCTTTCCCC
NM_001260	CDK8	6591	ACCTGGGATCTCTATGTCGGC
NM_001260	CDK8	6592	ACGGTGTGGCTTCTGTTTGAC
NM_001260	CDK8	6593	ACCTACTTCTTGGAGCAAGGC
NM_001261	CDK9	6594	ACAACGAGAAGGAGGGGTTCC
NM_004445	EPHB6	6595	ACGGCTCAGCACTCATGCTAC
SK132	EphB6	6595	ACGGCTCAGCACTCATGCTAC
NM_004445	EPHB6	6596	ACCATCCTGGACTATCAGCTC
SK132	EphB6	6596	ACCATCCTGGACTATCAGCTC
NM_004445	EPHB6	6597	ACGTATTACATCGACCCCTCC
SK132	EphB6	6597	ACGTATTACATCGACCCCTCC
NM_004448	ERBB2	6598	ACGAACAACCAGCTGGCTCTC
NM_004448	ERBB2	6599	ACCACAGACACGTTTGAGTCC
NM_004448	ERBB2	6600	ACGTAATCCGGGGACGAATTC
NM_005163	AKT1	6601	ACTGATGGCACCTTCATTGGC

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NM_005163	AKT1	6602	ACCACCTTCATCATCCGCTGC
NM_005163	AKT1	6603	ACGAAGGAAGTCATCGTGGCC
NM_005198	CHKL	6604	ACAGCGTGATGTTTCGCCATAC
NM_005198	CHKL	6605	ACCAGTACATCCCAAGTCGGC
NM_005198	CHKL	6606	ACGGATGAGATGGGCAACCTC
NM_005465	AKT3	6607	ACTCAGATGTCTCCAGTGGAC
NM_005465	AKT3	6608	ACGGGAAGAATGGACAGAAGC
NM_005465	AKT3	6609	ACAGGATGAAGTGGCACACAC
NM_004920	AATK	6610	ACCAATTTCTGTGCACAGCGAC
SK413	LMR1	6610	ACCAATTTCTGTGCACAGCGAC
NM_004920	AATK	6611	ACGCAGAGGAGGAGTTTGAAC
SK413	LMR1	6611	ACGCAGAGGAGGAGTTTGAAC
NM_004920	AATK	6612	ACCGTGTCTAGCCAACAACAAC
SK413	LMR1	6612	ACCGTGTCTAGCCAACAACAAC
NM_001721	BMX	6613	ACAGAGATAAGGGGTAAACCCC
SK417	BMX	6613	ACAGAGATAAGGGGTAAACCCC
NM_001721	BMX	6614	ACACACAGAGTTCCCACCTTC
SK417	BMX	6614	ACACACAGAGTTCCCACCTTC
NM_000215	JAK3	6615	ACGACTGTCTAGCTACAAGGCC
NM_000215	JAK3	6616	ACGTCCAACCTGATCGTGGTC
NM_001106	ACVR2B	6617	ACGGGCTGCTGGCTAGATGAC
SK011	ACTR2B	6617	ACGGGCTGCTGGCTAGATGAC
NM_001106	ACVR2B	6618	ACGGCCCAGCTCATGAATGAC
SK011	ACTR2B	6618	ACGGCCCAGCTCATGAATGAC
NM_001106	ACVR2B	6619	ACCGGGAGATCTTCAGCACAC
SK011	ACTR2B	6619	ACCGGGAGATCTTCAGCACAC
NM_001203	BMPR1B	6620	ACGAGGATGACTCTGGGTTGC
NM_001203	BMPR1B	6621	ACGACCTACACCTTACACTGC
NM_001203	BMPR1B	6622	ACGTTTGGATGGGAAAGTGGC
NM_001278	CHUK	6623	ACAACAGAGAACGATGGTGCC
NM_001278	CHUK	6624	ACCACTGCAGTATCTGGCCCC
NM_001278	CHUK	6625	ACGAGATGTCTAGGAGAAGTTC
NM_001105	ACVR1	6626	ACGGTCAACCCCCAACTCTAC
NM_001105	ACVR1	6627	ACAAGGCGCAACCAAGAAGCG
NM_001105	ACVR1	6628	ACCACTGGCTCGCCAGATTAC
NM_001616	ACVR2	6629	ACATCCAGTTACACCTAAGCC
NM_001616	ACVR2	6630	ACCCATGGCTAGAGGATTGGC
NM_016653	ZAK	6631	ACATACTCAGTGTCTCTCAGTC
NM_133646	ZAK	6631	ACATACTCAGTGTCTCTCAGTC
NM_016653	ZAK	6632	ACCTTTCCCATGGATGGCTCC
NM_133646	ZAK	6632	ACCTTTCCCATGGATGGCTCC
NM_016653	ZAK	6633	ACTGACACGAGCCTTCCTGAC
NM_133646	ZAK	6633	ACTGACACGAGCCTTCCTGAC
NM_019884	GSK3A	6634	ACGAACCGAGAGCTGCAGATC
NM_019884	GSK3A	6636	ACCCCCAACTACAGGAGTTC
NM_001619	ADRBK1	6637	ACGAGTGCCACTGAGCATGTC

NM_001619	ADRBK1	6638	ACTGTGGAGCTCAACATCCAC
NM_001619	ADRBK1	6639	ACAAGCGCATCAAGATGAAGC
NM_002529	NTRK1	6640	ACCGCTCTGGAGTCTCTCTCC
NM_002529	NTRK1	6641	ACAACGTGTCAGGGCCTCTCC
NM_002529	NTRK1	6642	ACCAGGAAGAACGTGACGTGC
NM_002745	MAPK1	6643	ACAATCAGCCCCCTTTGAGCAC
NM_138957	MAPK1	6643	ACAATCAGCCCCCTTTGAGCAC
NM_002745	MAPK1	6644	ACGCCTTCCAACCTGCTGCTC
NM_138957	MAPK1	6644	ACGCCTTCCAACCTGCTGCTC
NM_002745	MAPK1	6645	ACGTAGAACAGGCTCTGGCCC
NM_138957	MAPK1	6645	ACGTAGAACAGGCTCTGGCCC
NM_000359	TGM1	6646	ACCTTCCATGTGTGGAACGAC
NM_000359	TGM1	6647	ACGATCCTCAACGTTGGGGAC
NM_000359	TGM1	6648	ACTGCAGCTGGAGATGGCACC
NM_000738	CHRM1	6649	ACCATCATGGTGCTGGTGCTC
NM_000738	CHRM1	6650	ACGCCTTCCGGGACACCTTTC
NM_000738	CHRM1	6651	ACGATGCCAATGGTGGACCCC
NM_000739	CHRM2	6652	ACCATCCTAGTCATGGTTTCC
NM_000739	CHRM2	6653	ACCAGCACTATCAACCCTGCC
NM_000739	CHRM2	6654	ACAGAAGGACAAGAAGGAGCC
NM_000740	CHRM3	6655	ACCAACAATGATGCTGCTGCC
NM_000740	CHRM3	6656	ACTCTGGGCTACTGGCTGTGC
NM_000740	CHRM3	6657	ACGCAGCTGAAGACGGTCAAC
NM_000741	CHRM4	6658	ACCAGGCAGCTGCAGACAGTC
NM_000741	CHRM4	6659	ACCCACTGCTTCATCCAGTTC
NM_000741	CHRM4	6660	ACGGACACTTCCAATGAGTCC
NM_000746	CHRNA7	6661	ACCGGGAACCTGCTGTACATC
NM_000746	CHRNA7	6662	ACGGCGAGTTCCAGAGGAAGC
NM_000746	CHRNA7	6663	ACTGGGACCTAGTGGGAATCC
NM_001287	CLCN7	6664	ACGAGCGTGGTGAGCCTCTTC
NM_001287	CLCN7	6665	ACGAGAGGCTTGAGAGGAGCTC
NM_001287	CLCN7	6666	ACCAGTGAGAACCAGCTGTTC
NM_001382	DPAGT1	6667	ACCAACATGACCCCTCATCAAC
NM_001382	DPAGT1	6668	ACCACGACCATTGTGGTGCCC
NM_001382	DPAGT1	6669	ACGGTGATTGTCCGGGATGATC
NM_001830	CLCN4	6670	ACCTTCTTCAGCAGCCTTTTC
NM_001830	CLCN4	6671	ACGGACGAGTTTACTCACC GC
NM_001830	CLCN4	6672	ACCGAGACCACTTTTGAGGAC
NM_002252	KCNS3	6673	ACCCCTCTGAACATCATTGAC
NM_002252	KCNS3	6674	ACGTGTCATGAGCTACCTTAC
NM_002252	KCNS3	6675	ACGGACTGGGACCAGAAAAGC
NM_002562	P2RX7	6676	ACGCTGGTCCTGTCCAGACAC
NM_002562	P2RX7	6677	ACGTGGTTCTTCCACGTGATC
NM_002562	P2RX7	6678	ACCTTCAGATACGCCAAGTAC
NM_002707	PPM1G	6679	ACGGCTTTAGAAGATGCCTTC
NM_002707	PPM1G	6680	ACATCTGGAGGTGGGACAGGC

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NM_002707	PPM1G	6681	ACGGCCTACACAGGCTTTTCC
NM_002768	PCOLN3	6682	ACGTGAAGAAGGCCCTTCTGC
NM_002768	PCOLN3	6683	ACCGCCATCCGCAAGAAGAAC
NM_002768	PCOLN3	6684	ACGAATATGGCCCAGGTGACC
NM_002844	PTPRK	6685	ACCTCAGTCAGAACGAGGTTTC
NM_002844	PTPRK	6686	ACTGTCAGCCTCAAGATGATC
NM_002844	PTPRK	6687	ACAAGCCAGACTTCAGCTGCC
NM_003374	VDAC1	6688	ACGCGGATAATATGTAGGCAC
NG_001223	NG_001223	6689	ACATCAAGACAGGGTACAAGC
NG_001224	NG_001224	6689	ACATCAAGACAGGGTACAAGC
NM_003374	VDAC1	6689	ACATCAAGACAGGGTACAAGC
NG_001224	NG_001224	6690	ACGAAGTTGGAGACCGCTGTC
NM_003374	VDAC1	6690	ACGAAGTTGGAGACCGCTGTC
NM_004159	PSMB8	6691	ACCACTTATGCCTACGGTGTC
NM_004159	PSMB8	6692	ACGAGGCCATGACCTTGGCC
NM_004159	PSMB8	6693	ACAGTACAGATGTCAGTGACC
NM_005046	KLK7	6694	ACGGCCTCGAAGTCATTCCGC
NM_005046	KLK7	6694	ACGGCCTCGAAGTCATTCCGC
NM_139277	KLK7	6694	ACGGCCTCGAAGTCATTCCGC
NM_139277	KLK7	6694	ACGGCCTCGAAGTCATTCCGC
NM_005046	KLK7	6695	ACGAAAGTCAGGCTGCCCTCC
NM_005046	KLK7	6695	ACGAAAGTCAGGCTGCCCTCC
NM_139277	KLK7	6695	ACGAAAGTCAGGCTGCCCTCC
NM_139277	KLK7	6695	ACGAAAGTCAGGCTGCCCTCC
NM_005046	KLK7	6696	ACTTCCATGCTGTGCGCTGGC
NM_005046	KLK7	6696	ACTTCCATGCTGTGCGCTGGC
NM_139277	KLK7	6696	ACTTCCATGCTGTGCGCTGGC
NM_139277	KLK7	6696	ACTTCCATGCTGTGCGCTGGC
NM_005151	USP14	6697	ACCTGTGTACACCAGAACTTC
NM_005151	USP14	6698	ACTGATGGGGTCAGCAGATGC
NM_005151	USP14	6699	ACGGTGAACAAGGACAGTATC
NM_006208	ENPP1	6700	ACATCTTTCTTGCCGGGAACC
NM_006208	ENPP1	6701	ACCACCATCTGTCTTCTTTCC
NM_006208	ENPP1	6702	ACCTGTGCGCTGTGATGCTGCC
NM_012114	CASP14	6703	ACGACCTGGATGCTCTGGAAC
NM_012114	CASP14	6704	ACTCTCTTCGAGGCCCTGAAC
NM_012114	CASP14	6705	ACAAGCAAGGAAAACGAACCC
NM_012125	CHRM5	6706	ACGGAACCTTCAACGAAAGGC
NM_012125	CHRM5	6707	ACCCTCTACACCACCTACATC
NM_012125	CHRM5	6708	ACGAGTCAGGGTAAGGAAAGC
NM_015127	MCLC	6709	ACTCAGTTCATGTGCTGAGAC
NM_015127	MCLC	6709	ACTCAGTTCATGTGCTGAGAC
NM_015127	MCLC	6711	ACCAAAGGCACTTGCAGTTAC
NM_016113	TRPV2	6712	ACGATCGAGATTTTCAGGCAC
NM_016113	TRPV2	6713	ACCAAGTGTGCGCACTGACAGC
NM_016113	TRPV2	6714	ACGACCAGCAAGTACCTCACC

NM_020676	LOC57406	6715	ACGACAGCCAAGCTCATAATC
NM_020676	LOC57406	6716	ACACCCTCCATCCTCATGCTC
NM_020676	LOC57406	6717	ACACCTTTCCACCTGGTAGGC
NM_022304	HRH2	6718	ACCAGCAGGAACGAGACCAGC
NM_022304	HRH2	6719	ACGAGAAACCCCTGAAGCTCC
NM_022304	HRH2	6720	ACTGTGGTGGTCTGTCTGGCC
NM_032564	DGAT2	6721	ACAGAAATGGGAGTGGCAATGC
NM_032564	DGAT2	6722	ACGCACAAGACCAAGTTCGGC
NM_032564	DGAT2	6723	ACGACACACAACCTGCTGACC
NM_033133	CNP	6724	ACGAACATGGAGGTCAGGGCC
NM_033133	CNP	6725	ACGACGCTCTTCATCTTGCGC
NM_033133	CNP	6726	ACGAAGGAGCTGCGACAATTC
NM_005046	KLK7	6729	ACCTTTCCCTTGCGGCCAACC
NM_139277	KLK7	6729	ACCTTTCCCTTGCGGCCAACC
NM_145068	TRPV3	6730	ACGTACCAACACGAAGGCTTC
NM_145068	TRPV3	6731	ACGCACATGTTCTTTCTGTCC
NM_145068	TRPV3	6732	ACAGAGTACCTCGCCTGCCTC
NM_001629	ALOX5AP	6733	ACCTGTGTAGATGCGTACCCC
NM_001629	ALOX5AP	6734	ACGACGATCTCCACCACCATC
NM_001629	ALOX5AP	6735	ACATCTATTGGCCATCTGGGC
NM_002963	S100A7	6736	ACGGAGAACTTCCCCAACTTC
NM_002963	S100A7	6737	ACGGGCACAAATTACCTCGCC
NM_003293	TPS1	6738	ACGGTCCCCATAATGGAAAAC
NM_003293	TPS1	6738	ACGGTCCCCATAATGGAAAAC
NM_003293	TPS1	6738	ACGGTCCCCATAATGGAAAAC
NM_003294	TPSB1	6738	ACGGTCCCCATAATGGAAAAC
NM_003294	TPSB1	6738	ACGGTCCCCATAATGGAAAAC
NM_003294	TPSB1	6738	ACGGTCCCCATAATGGAAAAC
NM_003294	TPSB1	6738	ACGGTCCCCATAATGGAAAAC
NM_024164	TPSB2	6738	ACGGTCCCCATAATGGAAAAC
NM_024164	TPSB2	6738	ACGGTCCCCATAATGGAAAAC
NM_024164	TPSB2	6738	ACGGTCCCCATAATGGAAAAC
NM_003293	TPS1	6741	ACTCCTCCTGAGTGCTGGACC
NM_003293	TPS1	6741	ACTCCTCCTGAGTGCTGGACC
NM_003294	TPSB1	6741	ACTCCTCCTGAGTGCTGGACC
NM_003294	TPSB1	6741	ACTCCTCCTGAGTGCTGGACC
NM_024164	TPSB2	6741	ACTCCTCCTGAGTGCTGGACC
NM_024164	TPSB2	6741	ACTCCTCCTGAGTGCTGGACC
NM_012467	TPSG1	6742	ACCTGGAGATCACTTTGTCTC
NM_003293	TPS1	6745	ACACACCACTGCTTCCTACCC
NM_003294	TPSB1	6745	ACACACCACTGCTTCCTACCC
NM_024164	TPSB2	6745	ACACACCACTGCTTCCTACCC
NM_000214	JAG1	6746	ACGTGTGCCTCAAGGAGTATC
NM_000214	JAG1	6747	ACCCTCTGTGAGCTGGACATC
NM_000214	JAG1	6748	ACCTGCTCACACCTGAAAGAC
AB047783	AB047783	6749	ACCTTCCTGCACTGCATGGCC
NM_020639	ANKRD3	6749	ACCTTCCTGCACTGCATGGCC

AB047783	AB047783	6750	ACCTGATGAAGATCCTGCAGC
NM_020639	ANKRD3	6750	ACCTGATGAAGATCCTGCAGC
AB047783	AB047783	6751	ACCCTGCAGAGCCTCAAGTTC
NM_020639	ANKRD3	6751	ACCCTGCAGAGCCTCAAGTTC
NM_004417	DUSP1	6752	ACAGGACTCAGTGTGTGATCC
NM_004417	DUSP1	6753	ACCCACAAGGCAGACATCAGC
NM_004417	DUSP1	6754	ACCGTCTCAGCCAATTGTCCC
NM_006263	PSME1	6755	ACGAGGAGCGGAAGAAACAGC
NM_006263	PSME1	6756	ACACAGCAGGAGAAGGAAGAC
NM_006263	PSME1	6757	ACGGATGTCATTGAGCAGCTC
NM_001444	FABP5	6758	ACAACCTCAGACTGTCTGCAAC
NM_001444	FABP5	6759	ACTGTCCACCTGTACTCGGATC
NM_145699	APOBEC3A	6760	ACCCAGGCTAAGAATCTTCTC
NM_000214	JAG1	6761	ACTCTCATTGCCAGCTACTAC
NM_000359	TGM1	6762	ACCCCAATGTGTATGCCAACCC
NM_000738	CHRM1	6763	ACATACAGTCAAGAGGCCGAC
NM_000739	CHRM2	6764	ACGCAGAATATTGTAGCCCGC
NM_000740	CHRM3	6765	ACGAGAGCCGGTGTGATGATC
NM_000741	CHRM4	6766	ACGAAAGCCAAGACGCTGGCC
NM_000746	CHRNA7	6767	ACTGACTCGCAACCACTCACC
NM_001287	CLCN7	6768	ACGGTCGGCGTCATTGTGGAC
NM_001629	ALOX5AP	6769	ACATGATGTCATGTCAGCTCC
NM_001830	CLCN4	6770	ACTCCCTACACACGCCAGAGC
NM_002252	KCNS3	6771	ACAGATGACCACACATCCAGC
NM_002562	P2RX7	6772	ACCCAGAAGACCTGTGAAGTC
NM_002562	P2RX7	6772	ACCCAGAAGACCTGTGAAGTC
NM_002707	PPM1G	6773	ACCTGTATTCCTGAGCTGGAC
NM_002768	PCOLN3	6774	ACCAACTCCCTGAGGCCTCTC
NM_002844	PTPRK	6775	ACGCAGCAGCAACAGAAGAAC
NM_002963	S100A7	6776	ACCTTCCTTAGTGCCCTGTGAC
NM_003293	TPS1	6777	ACTGGATCCACCACTATGTCC
NM_003294	TPSB1	6777	ACTGGATCCACCACTATGTCC
NM_024164	TPSB2	6777	ACTGGATCCACCACTATGTCC
NM_004417	DUSP1	6778	ACTACCACTACAAGAGCATCC
NM_005046	KLK7	6779	ACAATGCACAGGAGTGAGGAC
NM_139277	KLK7	6779	ACAATGCACAGGAGTGAGGAC
NM_005151	USP14	6780	ACCTTCTTCCAGTATTCCACC
NM_012114	CASP14	6783	ACAGACAGCCCCACAAACCATC
NM_015127	MCLC	6784	ACCAAGAGCCCTGAAGTGCTC
NM_016113	TRPV2	6785	ACGCAGTGGGATGTGGTAAGC
NM_020639	ANKRD3	6786	ACCCAGCGATCTGGGTACCAC
NM_020676	LOC57406	6787	ACAGAACTGCAGGGCTCTGCC
NM_022304	HRH2	6788	ACAGCCACAGTGACACTGGCC
NM_145068	TRPV3	6792	ACTGGCTGAGGAGCAGATTCC
NM_145699	APOBEC3A	6793	ACAACCAGGCTAAGAATCTTC
NM_001382	DPAGT1	6794	ACACTGGAGATGAGCTATTCC

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NM_003374	VDAC1	6795	ACTTGATGAGAGGCTCGCTGC
NM_004159	PSMB8	6796	ACGTGATGCTCATAGGAACCC
NM_012125	CHRM5	6797	ACACTACCTTCTGTCTCCAGC
NM_033133	CNP	6798	ACGATGGACTTGGTCACCTAC
NG_000002	NG_000002	6799	ACCAGTTTGATGGTGTGGCAC
NG_002377	NG_002377	6799	ACCAGTTTGATGGTGTGGCAC
NG_000002	NG_000002	6800	ACCTCCCAAGTATAAGGGTCC
NG_002377	NG_002377	6800	ACCTCCCAAGTATAAGGGTCC
NG_000002	NG_000002	6801	ACCGAAGCTGACATGGGTTTC
NG_002377	NG_002377	6801	ACCGAAGCTGACATGGGTTTC
NG_000002	NG_000002	6802	ACGTAGTTGTGTCCCTGTTGC
NG_002377	NG_002377	6802	ACGTAGTTGTGTCCCTGTTGC
NM_002836	PTPRA	6803	ACTATAACTCTGGGACCCACC
NM_080840	PTPRA	6803	ACTATAACTCTGGGACCCACC
NM_080841	PTPRA	6803	ACTATAACTCTGGGACCCACC
NM_002836	PTPRA	6804	ACTTATTGCGGTGATGGTGGC
NM_080840	PTPRA	6804	ACTTATTGCGGTGATGGTGGC
NM_080841	PTPRA	6804	ACTTATTGCGGTGATGGTGGC
NM_002836	PTPRA	6805	ACAGCCACAGCGCCTCATCAC
NM_080840	PTPRA	6805	ACAGCCACAGCGCCTCATCAC
NM_080841	PTPRA	6805	ACAGCCACAGCGCCTCATCAC
NM_002836	PTPRA	6806	ACGAAGGTGAAGGCCTGTAAC
NM_080840	PTPRA	6806	ACGAAGGTGAAGGCCTGTAAC
NM_080841	PTPRA	6806	ACGAAGGTGAAGGCCTGTAAC
NM_002836	PTPRA	6807	ACGCCCTTCTGGAGCATTATC
NM_080840	PTPRA	6807	ACGCCCTTCTGGAGCATTATC
NM_080841	PTPRA	6807	ACGCCCTTCTGGAGCATTATC
AB083587	AB083587	6808	ACGGAGCTTCTCCTTCCCTCC
AB083589	AB083589	6809	ACGGAGCTTCATACATCCTAC
XM_115681	LOC200379	6809	ACGGAGCTTCATACATCCTAC
AB083590	AB083590	6810	ACTTTGCAGCCTGCTGGCTGC
AF317653	GPR62	6810	ACTTTGCAGCCTGCTGGCTGC
AB083593	AB083593	6811	ACCGTCTATGCCAGCATCTTC
XM_060898	LOC128227	6811	ACCGTCTATGCCAGCATCTTC
AB083593	AB083593	6812	ACCCCTGTGCTGTACTGTCTC
XM_060898	LOC128227	6812	ACCCCTGTGCTGTACTGTCTC
AB083594	AB083594	6813	ACGTCATCTTTGCTTCAGAGC
AB083594	AB083594	6814	ACGTACCACACGGTCTCATAAC
XM_064062	LOC124274	6814	ACGTACCACACGGTCTCATAAC
AB083594	AB083594	6815	ACGCAACCTGTACAGTTCTAC
XM_064062	LOC124274	6815	ACGCAACCTGTACAGTTCTAC
AB083587	AB083587	6816	ACTCCCTTCAAGGAGCTTCTC
AB083601	AB083601	6817	ACCTGCAGCTCCCAGGCTATC
AB083605	AB083605	6818	ACTCACACCTTAGGCTTCATC
ENSG00000175180	ENSG00000175180	6818	ACTCACACCTTAGGCTTCATC
AB083607	AB083607	6819	ACTCCCAGAGACCATGGCAAC

AB083607	AB083607	6820	ACTATCCTGTGCTGGGCCTTC
XM_064908	LOC126022	6820	ACTATCCTGTGCTGGGCCTTC
AB083608	AB083608	6821	ACACATCCTTCTGCAAGTCAC
AB083608	AB083608	6822	ACTAAGAGGCTATCTCAGTGC
AB083609	AB083609	6823	ACGCACCTGATTGTAGCCAAC
AB083609	AB083609	6824	ACCAGAGCTACGCAGAGCATC
XM_064909	LOC126023	6824	ACCAGAGCTACGCAGAGCATC
AB083610	AB083610	6825	ACGCCACACAACCTGGTCCTGC
ENSG00000174930	ENSG00000174930	6825	ACGCCACACAACCTGGTCCTGC
AB083611	AB083611	6826	ACGATGCTTAGGAGCATCTAC
AB083614	AB083614	6827	ACCGAGACAGACACTGGCGAC
AB083616	AB083616	6828	ACCACCTTGACTGGCATTTC
AB083616	AB083616	6829	ACGAGCTCCTGTGATTCTACC
AB083616	AB083616	6830	ACCCCTCCATGGATGGAGAAC
AB083617	AB083617	6831	ACTGGGCTTGTCCTGTCTGCC
XM_167214	LOC222611	6831	ACTGGGCTTGTCCTGTCTGCC
AB083617	AB083617	6832	ACCCTGGCAAAGGCTATCTAC
XM_167214	LOC222611	6832	ACCCTGGCAAAGGCTATCTAC
AB083625	AB083625	6833	ACTGGCATTGGGTACTGCTGC
AB083625	AB083625	6834	ACGGACCAGGACTGTCTCAC
AB083625	AB083625	6835	ACTAGTGATGTGAGTTCGGCC
AF380189	TA3	6836	ACCCTTGGAATTGCTATGGC
XM_069044	LOC134860	6836	ACCCTTGGAATTGCTATGGC
AF380189	TA3	6837	ACGCGGCAAGGTCTTAAGGAC
XM_069044	LOC134860	6837	ACGCGGCAAGGTCTTAAGGAC
AF380192	TA4	6838	ACACCTCCTGGTGATGATTTC
ENSG00000146383	ENSG00000146383	6838	ACACCTCCTGGTGATGATTTC
AF411117	GPR103	6839	ACTGTTAGGCGCCTGCATTGC
AF411117	GPR103	6840	ACAGGACCAAGGACTTGTGC
AF411117	GPR103	6841	ACGATCTACACCACCTTCATC
D13305	HUMBRACHRE	6842	ACCAGCAGCAGTGTGGGCAAC
L04473	HUMCCKR	6842	ACCAGCAGCAGTGTGGGCAAC
L07746	HUMCCKBR	6842	ACCAGCAGCAGTGTGGGCAAC
L08112	HUMCCBGR	6842	ACCAGCAGCAGTGTGGGCAAC
L10822	HUMGARE	6842	ACCAGCAGCAGTGTGGGCAAC
NM_000731	CCKBR	6842	ACCAGCAGCAGTGTGGGCAAC
S70057	S70057	6842	ACCAGCAGCAGTGTGGGCAAC
D13305	HUMBRACHRE	6843	ACTCTCATGGGCACATTCATC
L04473	HUMCCKR	6843	ACTCTCATGGGCACATTCATC
L07746	HUMCCKBR	6843	ACTCTCATGGGCACATTCATC
L08112	HUMCCBGR	6843	ACTCTCATGGGCACATTCATC
L10822	HUMGARE	6843	ACTCTCATGGGCACATTCATC
NM_000731	CCKBR	6843	ACTCTCATGGGCACATTCATC
S70057	S70057	6843	ACTCTCATGGGCACATTCATC
D13305	HUMBRACHRE	6844	ACGCTGCTGGCTAAGAAGCGC
L04473	HUMCCKR	6844	ACGCTGCTGGCTAAGAAGCGC

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L07746	HUMCCKBR	6844	ACGCTGCTGGCTAAGAAGCGC
L08112	HUMCCBGR	6844	ACGCTGCTGGCTAAGAAGCGC
L10822	HUMGARE	6844	ACGCTGCTGGCTAAGAAGCGC
NM_000731	CCKBR	6844	ACGCTGCTGGCTAAGAAGCGC
S70057	S70057	6844	ACGCTGCTGGCTAAGAAGCGC
M84605	HUMOPIODRE	6845	ACCCTCGTGGTGATCTGGATC
M84605	HUMOPIODRE	6846	ACCTACTGCCGCTTCCAGAAC
NM_001059	TACR3	6846	ACCTACTGCCGCTTCCAGAAC
M84605	HUMOPIODRE	6847	ACTACATCCAGCAGGTCTACC
NM_001059	TACR3	6847	ACTACATCCAGCAGGTCTACC
NM_000024	ADRB2	6848	ACTGTGCTGGTCATCACAGCC
NM_000024	ADRB2	6849	ACGTACCAGAGCCTGCTGACC
NM_000024	ADRB2	6850	ACCTGCTGTGTGAAGACCTCC
NM_000025	ADRB3	6851	ACTTCTGCCTTCAACCCGCTC
XM_165515	LOC220846	6851	ACTTCTGCCTTCAACCCGCTC
NM_000054	AVPR2	6852	ACGTATCTGCAGATGGTGGGC
NM_000115	EDNRB	6853	ACAGCAGAGACGGGAAGTGGC
NM_003991	EDNRB	6853	ACAGCAGAGACGGGAAGTGGC
NM_000145	FSHR	6854	ACGGCCAACAACCTGCTCTAC
NM_000145	FSHR	6855	ACTCTACCTGCTGCTCATTGC
NM_000145	FSHR	6856	ACGGAATGGCCACTGCTCTTC
NM_000160	GCGR	6857	ACGTGGAAGCTCTACGGTGAC
NM_000160	GCGR	6858	ACGGAGGTGGCCAAGATGTAC
NM_000160	GCGR	6859	ACGTCCACGCTGACCCCTCATC
NM_000164	GIPR	6860	ACCGGGTCCTTCGATATGTAC
NM_000164	GIPR	6861	ACGAATGAGGCCTTTCTGGAC
NM_000164	GIPR	6862	ACGCTCGGCTTTGAGATCTTC
NM_000233	LHCGR	6863	ACTGCCTTTGACAACCTCCTC
NM_000233	LHCGR	6864	ACGCTGCGATTAAGACATGCC
NM_000233	LHCGR	6865	ACTAAGCCTTCTCAATCCACC
NM_000273	OA1	6866	ACTCCAGCCCAGGGATTTCTC
NM_000273	OA1	6867	ACTGAGGGTGACCCTGCTCTC
NM_000316	PTHR1	6868	ACTCACAAAGGCCATGCCTAC
NM_000316	PTHR1	6869	ACGTGGATCATCCAGGTGCCC
NM_000316	PTHR1	6870	ACTCTTGGAGCCGCTGGACAC
NM_000369	TSHR	6871	ACCTTACATAGACCCTGATGC
NM_000369	TSHR	6872	ACTGAGAGCAGTATGCAGAGC
NM_000369	TSHR	6873	ACGAGGATGGCTGTGTTGATC
NM_000388	CASR	6874	ACCTGCTCAGAGCACATTCCC
NM_000388	CASR	6875	ACGGGAGAAAGACTCTTCATC
NM_000388	CASR	6876	ACTTCTACGCACCAGAACTCC
NM_000406	GNRHR	6877	ACAGATCCGAGTGACGGTTAC
NM_000406	GNRHR	6878	ACAGCAACAGCAAAGTCGGAC
NM_000406	GNRHR	6879	ACTGACGGTTGCATTTGCCAC
NM_000513	OPN1MW	6880	ACGTTCAAGAAGCTGCGCCAC
NM_020061	OPN1LW	6880	ACGTTCAAGAAGCTGCGCCAC

NM_000513	OPN1MW	6881	ACCCAGGTCTATGGCTACTTC
NM_000513	OPN1MW	6882	ACGTGCCACTATCTACAACCC
NM_020061	OPN1LW	6882	ACGTGCCACTATCTACAACCC
NM_000524	HTR1A	6883	ACGTGATCACCTCTCTGCTGC
NM_000524	HTR1A	6884	ACGGATCATGGCTACACTATC
NM_000524	HTR1A	6885	ACTTGGCTGGGCTACTCCAAC
NM_000529	MC2R	6886	ACTAAGAATCTCCAGGCACCC
NM_000529	MC2R	6887	ACCGGCATGTTGATCATGTGC
NM_000539	RHO	6888	ACCTTCCTCACGCTCTACGTC
NM_000539	RHO	6889	ACGCCCATGAGCAACTTCCGC
NM_000539	RHO	6890	ACCAAGCAGTTCGGAACTGC
NM_000579	CCR5	6891	ACCATGCTGGTCATCCTCATC
NM_000579	CCR5	6892	ACCATTGTCCTTCTCCTGAAC
NM_000579	CCR5	6893	ACGCACATTGCCAAACGCTTC
NM_000621	HTR2A	6894	ACGCTGCAGAATGCCACCAAC
NM_000621	HTR2A	6895	ACGTGATCTTGGCACACGGGC
NM_000621	HTR2A	6896	ACCAAGACCTATAGGTCAGCC
NM_000623	BDKRB2	6897	ACCATCTTTGTCTCCTCAGCGTC
NM_000623	BDKRB2	6898	ACGTGTTTACCAACATGCTCC
NM_000623	BDKRB2	6899	ACCCCACTGGTGTACGTGATC
NM_000634	IL8RA	6900	ACCTCCCTGGTGATGCTGGTC
NM_000634	IL8RA	6901	ACTCTGTCCCTGCCCTTCTTC
NM_000647	CCR2	6902	ACCATGCTGGTCGTCCTCATC
NM_000648	CCR2	6902	ACCATGCTGGTCGTCCTCATC
NM_000647	CCR2	6903	ACTCCCATCATCTATGCCTTC
NM_000648	CCR2	6903	ACTCCCATCATCTATGCCTTC
NM_005284	GPR6	6903	ACTCCCATCATCTATGCCTTC
NM_000647	CCR2	6904	ACGTGACTACACAAGGACTCC
NM_000674	ADORA1	6905	ACCATTGGGCCACAGACCTAC
NM_000674	ADORA1	6906	ACGGTCATCAGCATGGAGTAC
NM_000674	ADORA1	6907	ACCTGCATCACCTCTTCTGC
NM_000675	ADORA2A	6908	ACCCTGCAGAACGTCACCAAC
NM_000675	ADORA2A	6909	ACGGGCATCATTGCCATCTGC
NM_000675	ADORA2A	6910	ACTCCCTTCATCTACGCCTAC
NM_000676	ADORA2B	6911	ACCAGTAAAGACAGTGCCACC
NM_000676	ADORA2B	6912	ACGATCTTCCTGGTGGCCTGC
NM_000676	ADORA2B	6913	ACGTGGGCAATGAATATGGCC
NM_000677	ADORA3	6914	ACACTGACCTCAGAGTACCAC
NM_000677	ADORA3	6915	ACCTCCATGATGAACCCTATC
NM_000678	ADRA1D	6916	ACTTGGCCGACTACAGCAACC
NM_000679	ADRA1B	6917	ACCCAGACCTCGAGCAACTCC
NM_000679	ADRA1B	6918	ACGGAGCTGACCCTGAGGATC
NM_000679	ADRA1B	6919	ACGGAGTTCAAGCGCGCTTTC
NM_000680	ADRA1A	6920	ACCATCCTAGTGATCCTCTCC
NM_033302	ADRA1A	6920	ACCATCCTAGTGATCCTCTCC
NM_033303	ADRA1A	6920	ACCATCCTAGTGATCCTCTCC

NM_033304	ADRA1A	6920	ACCATCCTAGTGATCCTCTCC
NM_000680	ADRA1A	6921	ACGTCTGGCCTCAAGACCGAC
NM_033302	ADRA1A	6921	ACGTCTGGCCTCAAGACCGAC
NM_033303	ADRA1A	6921	ACGTCTGGCCTCAAGACCGAC
NM_033304	ADRA1A	6921	ACGTCTGGCCTCAAGACCGAC
NM_000680	ADRA1A	6922	ACGTGACGCTCCGCATCCATC
NM_033302	ADRA1A	6922	ACGTGACGCTCCGCATCCATC
NM_033303	ADRA1A	6922	ACGTGACGCTCCGCATCCATC
NM_033304	ADRA1A	6922	ACGTGACGCTCCGCATCCATC
NM_000680	ADRA1A	6923	ACGAACCATCAAGTTCCAACC
NM_000681	ADRA2A	6924	ACGGCTTGGTGCGAGATCTAC
NM_000681	ADRA2A	6925	ACCGACCAGAAGTGGTACGTC
NM_000681	ADRA2A	6926	ACCCCGGTCATCTACACCATC
NM_000682	ADRA2B	6927	ACCCCTGTTATCTACACCATC
NM_000684	ADRB1	6928	ACTGTGCTGGTGATCGTGGCC
NM_000684	ADRB1	6929	ACGTGCTGCGACTTCGTCACC
NM_000684	ADRB1	6930	ACCGTGGTGAAGGCCTTCCAC
NM_000686	AGTR2	6931	ACGAAGAAATCCCTGGCAAGC
NM_000686	AGTR2	6932	ACGAACAGGATAACCCGTGAC
NM_000686	AGTR2	6933	ACCCGGTTCCAACAGAAGCTC
NM_000706	AVPR1A	6934	ACCAATGTCACCAAGGCCCGC
NM_000706	AVPR1A	6935	ACCATCTGGTGCAACGTCCGC
NM_000706	AVPR1A	6936	ACACCCTACCATCACCATCAC
NM_000707	AVPR1B	6937	ACGTACCTGCAGGTGCTCAGC
NM_000707	AVPR1B	6938	ACGTCAAGACACAGGCCTGGC
NM_000710	BDKRB1	6939	ACTGCTCCAGAAGCCTGGGAC
NM_000710	BDKRB1	6940	ACTCTACCTGGCCAACCTGGC
NM_000710	BDKRB1	6941	ACGACCACAGCGTGATCCTC
NM_000730	CCKAR	6942	ACGGATTTCATCTTCGGGAGC
NM_000730	CCKAR	6943	ACCCAGACCGCGAATATGTGC
NM_000730	CCKAR	6944	ACCCGCATCCGGAGTAACAGC
NM_000752	LTB4R	6945	ACGAAGAGGGAGAGATGGAGC
NM_000794	DRD1	6946	ACCATCTGGGTGGCCTTTGAC
NM_000794	DRD1	6947	ACCTGTGACTCCAGCCTCAGC
NM_000794	DRD1	6948	ACGGAGTGCAATCTGGTTTAC
NM_000795	DRD2	6949	ACCTACTATGCCACACTGCTC
NM_016574	DRD2	6949	ACCTACTATGCCACACTGCTC
NM_000795	DRD2	6950	ACTGGGAGTTTCCCAGTGAAC
NM_000795	DRD2	6951	ACCATTGAGTTCCGCAAGGCC
NM_016574	DRD2	6951	ACCATTGAGTTCCGCAAGGCC
NM_000796	DRD3	6952	ACCAGTCAGTGCAACAGTGTC
NM_033658	DRD3	6952	ACCAGTCAGTGCAACAGTGTC
NM_033659	DRD3	6952	ACCAGTCAGTGCAACAGTGTC
NM_033663	DRD3	6952	ACCAGTCAGTGCAACAGTGTC
NM_000796	DRD3	6953	ACGCGTTACTACAGCATCTGC
NM_033658	DRD3	6953	ACGCGTTACTACAGCATCTGC

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NM_033663	DRD3	6953	ACGCGTTACTACAGCATCTGC
NM_000796	DRD3	6954	ACGGCAACCCAAATGGTGGCC
NM_033658	DRD3	6954	ACGGCAACCCAAATGGTGGCC
NM_033659	DRD3	6954	ACGGCAACCCAAATGGTGGCC
NM_033660	DRD3	6954	ACGGCAACCCAAATGGTGGCC
NM_033663	DRD3	6954	ACGGCAACCCAAATGGTGGCC
NM_000798	DRD5	6955	ACCATGACCAACGTCTTCATC
NM_000798	DRD5	6956	ACGCGCAAGATGACTCAGCGC
NM_000798	DRD5	6957	ACTGCAGAGAACTGTGACTCC
NM_000823	GHRHR	6958	ACTGTGACTTCATCACCAGC
NM_000823	GHRHR	6959	ACACTGGCCTTCGAGGACATC
NM_000823	GHRHR	6960	ACGGTGCTGACATCTATGTGC
NM_000838	GRM1	6961	ACTACTTCCTGAGGGTTGTCC
NM_000838	GRM1	6962	ACCAGGCTGTGAGCCCATTCC
NM_000838	GRM1	6963	ACTGGACTCCTCATCATGAGC
NM_000839	GRM2	6964	ACGCTGAGTGACAAGTCCCGC
NM_000839	GRM2	6965	ACCCGCATTGCACGCATCTTC
NM_000839	GRM2	6966	ACGCTGCACATCATCCTCTTC
NM_000840	GRM3	6967	ACGACCGAGGGATTCAACGCC
NM_000840	GRM3	6968	ACCTTCACGGCTCCATTCAAC
NM_000840	GRM3	6969	ACCTGCATTGCCCGCATCTTC
NM_000841	GRM4	6970	ACCAGCCGCTACGACTTCTTC
NM_000841	GRM4	6971	ACGATTGCACCTGTGCTGCAC
NM_000841	GRM4	6972	ACGTCTACATCATCCTCTTCC
NM_000842	GRM5	6973	ACGCTCACAAGTCACTTGCCC
NM_000842	GRM5	6974	ACGCTCCAATCTCCCGATGTC
NM_000842	GRM5	6975	ACCATCATCAGATCTGTGTGC
NM_000843	GRM6	6976	ACCCGCAGGAACATCTGGTTC
NM_000843	GRM6	6977	ACGAAGATGGTGAAGGGCGTC
NM_000843	GRM6	6978	ACGACCAACCGTATCTACCGC
NM_000844	GRM7	6979	ACGGATCTCTGTGCTGACTAC
NM_000844	GRM7	6980	ACTCAGTAACAGCTCCCAGAC
NM_000844	GRM7	6981	ACCTACCACGCTTACAATCTC
NM_000845	GRM8	6982	ACCATCACTCTGGGTGTCCGC
NM_000845	GRM8	6983	ACTCCACGTGAACCAAGACC
NM_000845	GRM8	6984	ACAGTGAACCTCTGTGAGAGTC
NM_000861	HRH1	6985	ACCCTGTACATCGTCAGCCTC
NM_000861	HRH1	6986	ACGGTCATGACTGCCATCATC
NM_000861	HRH1	6987	ACCACAGGCCTGGATTACATC
NM_000863	HTR1B	6988	ACCTGCAGCGCCAAGGACTAC
NM_000863	HTR1B	6989	ACCACCGACCACATCCTCTAC
NM_000863	HTR1B	6990	ACCCAAGTCAAAGTGCAGATC
NM_000864	HTR1D	6991	ACCACCTCTCAGATTTCTTAC
NM_000864	HTR1D	6992	ACTCAAGCTTGCTGACAGTGC
NM_000864	HTR1D	6993	ACTTGTCCCTTTCCGGAAGGC
NM_000865	HTR1E	6994	ACTCTGTTCTCTGGCCGTGAC

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NM_000865	HTR1E	6995	ACGCACAGATAGCCAGAATTC
NM_000866	HTR1F	6996	ACGTGGTCTGTGACATTTGGC
NM_000866	HTR1F	6997	ACTGCATCATCAAGCACGACC
NM_000866	HTR1F	6998	ACGAGAACGGAAAGCAGCCAC
NM_000867	HTR2B	6999	ACCTCACGGGCTACAGCATTC
NM_000867	HTR2B	7000	ACCAGAGAGCCTCAAAGGTCC
NM_000867	HTR2B	7001	ACTGAGGCTCCGAAGTTCAAC
NM_000868	HTR2C	7002	ACCTGGCCAGCACTTTCAATC
NM_000868	HTR2C	7003	ACTTCGCGGACTAAGGCCATC
NM_000868	HTR2C	7004	ACTCCCTCCAGTGTGGTTAGC
NM_000870	HTR4	7005	ACGAGGAAGTTCAACCAGAAC
NM_000870	HTR4	7006	ACAGCAGCCAAGACCCTGTGC
NM_000870	HTR4	7007	ACCTTCTCCTTTGGTGGCTGC
NM_000871	HTR6	7008	ACCTTCTTCCTGGTGTGCTC
NM_000871	HTR6	7009	ACCATAGTCCAGGCCGTGTGC
NM_000872	HTR7	7010	ACAGTTGTGATCGGCTCCATC
NM_019859	HTR7	7010	ACAGTTGTGATCGGCTCCATC
NM_019860	HTR7	7010	ACAGTTGTGATCGGCTCCATC
NM_000872	HTR7	7011	ACCACAAGTTTCTGGCTTCC
NM_019859	HTR7	7011	ACCACAAGTTTCTGGCTTCC
NM_019860	HTR7	7011	ACCACAAGTTTCTGGCTTCC
NM_000872	HTR7	7012	ACGCGAGAACAGAAAGCAGCC
NM_019859	HTR7	7012	ACGCGAGAACAGAAAGCAGCC
NM_019860	HTR7	7012	ACGCGAGAACAGAAAGCAGCC
NM_000909	NPY1R	7013	ACCCTGGCCTTGATCATAATC
NM_000909	NPY1R	7014	ACGTACAGGTCCAGTGAAACC
NM_000909	NPY1R	7015	ACTCTGTTATTCCTGCTCTGC
NM_000910	NPY2R	7016	ACGAGCATGCGCACAGTAACC
NM_000910	NPY2R	7017	ACGATCTCCAAGCGAATCAGC
NM_000910	NPY2R	7018	ACCTCATCTTCACAGTGTTCC
NM_000911	OPRD1	7019	ACCGTGCTTGTCATGTTCCGC
NM_000911	OPRD1	7020	ACGATCTGCGTGTTCTCTTC
NM_000911	OPRD1	7021	ACCTTCAAGCGCTGCTTCCGC
NM_000912	OPRK1	7022	ACGATGAAGACAGCAACCAAC
NM_000912	OPRK1	7023	ACCATGTTCAACCAGCATCTTC
NM_000912	OPRK1	7024	ACGCGGTGTTTCCGGGACTTC
NM_000913	OPRL1	7025	ACCTGCCTTGTCATGTACGTC
NM_000913	OPRL1	7026	ACGTTCTGCTGTGCATCTGCC
NM_000914	OPRM1	7027	ACGACTGCCACCAACATCTAC
NM_000914	OPRM1	7028	ACTGTCTGCAACTGGATCCTC
NM_000914	OPRM1	7029	ACCTACGTTCCAGACTGTTTC
NM_000916	OXTR	7030	ACGCACTCGCGCCTCTTCTTC
NM_000916	OXTR	7031	ACGGCCTACATCACATGGATC
NM_000952	PTAFR	7032	ACCCAGGGCAACTGGATACTC
NM_000952	PTAFR	7033	ACCCTGGTCATCATCCGTACC
NM_000952	PTAFR	7034	ACGTGGTTGTGCCATTCAACC

NM_000955	PTGER1	7035	ACGCACAACCAGAGGCCCAAC
NM_000956	PTGER2	7036	ACTTGACCCTTGGGTCTTTGC
NM_000957	PTGER3	7037	ACGAAGTCCTTCCTGCTGTGC
NM_000957	PTGER3	7038	ACGCAGCGTTGGGAGCACATC
NM_000958	PTGER4	7039	ACCCATGCCTATTTCTACAGC
NM_000958	PTGER4	7040	ACGGACATCTTCTGCCATGTC
NM_000958	PTGER4	7041	ACTATCAGAGACCTCAGACTC
NM_000959	PTGFR	7042	ACGTGGTGTGTGCTTGTTTGC
NM_000959	PTGFR	7043	ACTGGTAATCCAGCTCCTGGC
NM_000959	PTGFR	7044	ACGGCTGTCCTTAAGAATCTC
NM_000960	PTGIR	7045	ACCGTCGTCCAAAGCAGAAGC
NM_001049	SSTR1	7046	ACATGCGTCCCAGAACGGGAC
NM_001049	SSTR1	7047	ACCATGTTCCACCAGCATCTAC
NM_001049	SSTR1	7048	ACGACTTCCAACCTGAGAACC
NM_001050	SSTR2	7049	ACGATGAAGACCATCACCAAC
NM_001050	SSTR2	7050	ACGGTGAAGTCCTCTGGAATC
NM_001050	SSTR2	7051	ACCAGCTGTGCCAACCCTATC
NM_001051	SSTR3	7052	ACCCAGTTCACCAGCATATTC
NM_001051	SSTR3	7053	ACCATCGTCAACGTGGTGTGC
XM_170447	LOC219351	7053	ACCATCGTCAACGTGGTGTGC
NM_001052	SSTR4	7054	ACGATGAAGACGGCTACCACC
NM_001052	SSTR4	7055	ACCCACGTGTCCCTTATCCTC
NM_001053	SSTR5	7056	ACGATGAAGACCGTCACCAAC
NM_001053	SSTR5	7057	ACCCAGTTCACCAGTGTCTTC
NM_001057	TACR2	7058	ACTGCCATCGTCATCTGGATC
NM_001057	TACR2	7059	ACGGCGGTTATTGCTGGCATC
NM_001057	TACR2	7060	ACGTTTCATCCAGCAAGTCTAC
NM_001058	TACR1	7061	ACGTTCCACAACCTTCTTTCCC
NM_001058	TACR1	7062	ACTGACAGGTTCCGTCTGGGC
NM_001059	TACR3	7063	ACTTCCAAATCTGCCTCCGCC
NM_001060	TBXA2R	7064	ACCCTCCAACAGGGAAGGCTC
NM_001118	ADCYAP1R1	7065	ACGAAGGAGCAAGCCATGTGC
NM_001118	ADCYAP1R1	7066	ACCTCCTTAGATCTCTCAGAC
NM_001118	ADCYAP1R1	7067	ACCCGTTACTTCGCTGTGGAC
NM_001295	CCR1	7068	ACCATGACCAGCATCTACCTC
NM_001295	CCR1	7069	ACAGCCTACGAGAGTGGAAGC
NM_001295	CCR1	7070	ACGTACCTGCGGCAGTTGTTC
NM_001296	CCBP2	7071	ACCCTCCTTCTTCTCATGGTC
NM_001296	CCBP2	7072	ACTCCCAAGGGTGTGTGGAAC
NM_001296	CCBP2	7073	ACATGACTGGCATGAATGACC
NM_001337	CX3CR1	7074	ACGAAGCCCAAGAGTGTCAAC
NM_001337	CX3CR1	7075	ACTGAATGCCTTGGTGACTAC
NM_001337	CX3CR1	7076	ACCCACAAGAAAGCCAAAGCC
NM_001400	EDG1	7077	ACGCTGAATATCAGCGCGGAC
NM_001400	EDG1	7078	ACGGGAGTATGTTTGTGGCCC
NM_001400	EDG1	7079	ACTCTACTCCTTGGTCAGGAC

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NM_001400	EDG1	7080	ACGGTGAAGACCTGTGACATC
NM_001400	EDG1	7081	ACATTCAAGCGACCCATCATC
NM_001407	CELSR3	7082	ACCGGATTGGTGCACTACAAC
NM_001407	CELSR3	7083	ACTGCTCCACAATTTGTGGCC
NM_001407	CELSR3	7084	ACCATCCAGAACGACACAGAC
NM_001408	CELSR2	7085	ACCCTCTGGCTCTACACCAGC
NM_001408	CELSR2	7086	ACCAATGGCACAGGCTGGATC
NM_001408	CELSR2	7087	ACGAAGAACGTGTGTGACAGC
NM_001462	FPRL1	7088	ACGGGCATGATTAAATCCAGC
NM_001466	FZD2	7089	ACGGTGCCATCCTATCTCAGC
NM_001466	FZD2	7090	ACGACCATCACCATCCTGGCC
NM_001466	FZD2	7091	ACATACCTCATGACGCTCATC
NM_001470	GABBR1	7092	ACGAAGTACGTCTGGTTCCTC
NM_021903	GABBR1	7092	ACGAAGTACGTCTGGTTCCTC
NM_021904	GABBR1	7092	ACGAAGTACGTCTGGTTCCTC
NM_021905	GABBR1	7092	ACGAAGTACGTCTGGTTCCTC
NM_001470	GABBR1	7093	ACGGATGATCTTTCTGGTCC
NM_021903	GABBR1	7093	ACGGATGATCTTTCTGGTCC
NM_021904	GABBR1	7093	ACGGATGATCTTTCTGGTCC
NM_021905	GABBR1	7093	ACGGATGATCTTTCTGGTCC
NM_001480	GALR1	7094	ACGAAGGCCTACGTGGTGTGC
NM_001480	GALR1	7095	ACTTCCTCCGTGAATCCTATC
NM_001504	GPR9	7096	ACCTTCTACGCAGGAGCCCTC
NM_001504	GPR9	7097	ACCGCCACCCACTGCCAATAC
NM_001505	GPR30	7098	ACCATGTACAGCAGCGTCTTC
NM_001505	GPR30	7099	ACCGTCTTCATCAGCGTGCAC
NM_001506	GPR32	7100	ACCTGCCTCCTTGTCTTCATC
NM_001506	GPR32	7101	ACCTCTGACAATGAGACTGCC
NM_001507	GPR38	7102	ACCCCAATCCTCTACAACCTC
NM_001508	GPR39	7103	ACGCTGCACACTTTCTCTTC
NM_001508	GPR39	7104	ACGCTGCTGATTGGCTTCGTC
NM_001525	HCRT1	7105	ACACAGTATGAGTGGGTCCCTC
NM_001525	HCRT1	7106	ACGATCTACCACAGTTGCTTC
NM_001525	HCRT1	7107	ACGTCCTTGTCCTTGCAGAGC
NM_001526	HCRT2	7108	ACCTCTGGTGTGACAGATCC
NM_001526	HCRT2	7109	ACGTCCTTGACCACTCAAATC
NM_001557	IL8RB	7110	ACCTCCCTCGTGATGCTGGTC
NM_001557	IL8RB	7111	ACGTTTCGCCATGGACTCCTC
NM_001702	BAI1	7112	ACGTTCTTCGGCTACTTCTCC
NM_001702	BAI1	7113	ACGGACCTGAGGGATGCATAC
NM_001702	BAI1	7114	ACGAACGAGAATGTCGCCACC
NM_001703	BAI2	7115	ACGCTCTGCAGTATGGCTGCC
NM_001703	BAI2	7116	ACTTGCCAGACCCTGGAGACC
NM_001703	BAI2	7117	ACGGAGGTCAACACTTGCAAC
NM_001704	BAI3	7118	ACGGACCTTAGCTGCTCTAAC
NM_001704	BAI3	7119	ACGCAGAGAGTGCTATAACCC

NM_001704	BAI3	7120	ACCTGTGCTTACCGATGCATC
NM_001708	OPN1SW	7121	ACGCATGCACTGACGGTGGTC
NM_001708	OPN1SW	7122	ACGCTGTTGCAGCTCAGCAGC
NM_001708	OPN1SW	7123	ACGCAGTTCCAAGCTTGATC
NM_001716	BLR1	7124	ACATCATCTCTGCCCTGCCAC
NM_032966	BLR1	7124	ACATCATCTCTGCCCTGCCAC
NM_001716	BLR1	7125	ACGAGAACCAAGCAGAAACGC
NM_032966	BLR1	7125	ACGAGAACCAAGCAGAAACGC
NM_001716	BLR1	7126	ACTACCTGCAAGCTGAATGGC
NM_032966	BLR1	7126	ACTACCTGCAAGCTGAATGGC
NM_001727	BRS3	7127	ACCTTGTGTGCCAGTGGATGC
NM_001727	BRS3	7128	ACCAAAGCCATGCCCGTAAGC
NM_001727	BRS3	7129	ACGCAGGCAGAGGACAGATTC
NM_001736	C5R1	7130	ACGCGGACCATCAATGCCATC
NM_001736	C5R1	7131	ACGGTGTGTGTGGCGTGGAC
NM_001736	C5R1	7132	ACCGTGTGTGACTGAAGAGTCC
NM_001742	CALCR	7133	ACTGCTATGACCGAATGCAGC
NM_001742	CALCR	7134	ACCGCTTGCGGTGGTATTATC
NM_001742	CALCR	7135	ACCAATGAGGTCCAAACCACC
NM_001784	CD97	7136	ACCTCCATCTTTCTGAGCCAC
NM_078481	CD97	7136	ACCTCCATCTTTCTGAGCCAC
NM_001784	CD97	7137	ACTTAAAGAAGGCGAGGGCGC
NM_078481	CD97	7137	ACTTAAAGAAGGCGAGGGCGC
NM_001837	CCR3	7138	ACTGTGGTGGTGGTGTATGATC
NM_001837	CCR3	7139	ACGAGACTCTTTGCAGTGCTC
NM_001837	CCR3	7140	ACGTACCTGCGCCACTTCTTC
NM_001838	CCR7	7141	ACAGCCTGGTTCCTCCCTATC
NM_001838	CCR7	7142	ACGCTGTCTGTGTGGGCATC
NM_001838	CCR7	7143	ACCAAGGCCATCAAGGTGATC
NM_001840	CNR1	7144	ACGGAGAATGAGGAGAACATC
NM_016083	CNR1	7144	ACGGAGAATGAGGAGAACATC
NM_033181	CNR1	7144	ACGGAGAATGAGGAGAACATC
NM_001840	CNR1	7145	ACGATAGCCGCAACGTGTTTC
NM_016083	CNR1	7145	ACGATAGCCGCAACGTGTTTC
NM_033181	CNR1	7145	ACGATAGCCGCAACGTGTTTC
NM_001840	CNR1	7146	ACACACGCAAACAATGCAGCC
NM_016083	CNR1	7146	ACACACGCAAACAATGCAGCC
NM_033181	CNR1	7146	ACACACGCAAACAATGCAGCC
NM_001841	CNR2	7147	ACCTCCATGGTCAACCCTGTC
NM_001841	CNR2	7148	ACTCACTCCGTGGCCAGATTC
NM_001883	CRHR2	7149	ACCACGACCTTGGACCAGATC
NM_001883	CRHR2	7150	ACTGAACAGTGCTGGTTTGGC
NM_001883	CRHR2	7151	ACCTCCTTCTGCACTCGTTC
NM_001957	EDNRA	7152	ACCCCACTAATTTGGTCCTAC
NM_001957	EDNRA	7153	ACATTGTCTCCATCTGGATCC
NM_001957	EDNRA	7154	ACAGTCTGATGACCTCGGTCC

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NM_001974	EMR1	7155	ACGGATCCAGGAGTGCGATGC
NM_001974	EMR1	7156	ACGAGGGAACCGCAGTGAAAC
NM_001974	EMR1	7157	ACTTACTTCAGCTCTCGCAAC
NM_001992	F2R	7158	ACCAAATGCCACCTTAGATCC
NM_001992	F2R	7159	ACTGAAGGTCAAGAAGCCGGC
NM_001992	F2R	7160	ACAGAAAGTTCCGATCCCAGC
NM_002029	FPR1	7161	ACCTTGTTCCGAAGTGTCTTC
NM_002029	FPR1	7162	ACGAAGGTGATCATTGGGCCC
NM_002030	FPRL2	7163	ACCTTGGCCCTAGCTGACTTC
NM_002030	FPRL2	7164	ACGGTCTTTCTGATCCTCCAC
NM_002030	FPRL2	7165	ACGACTGATTGCGTCTTTGCC
NM_002036	FY	7166	ACGGCTTTGCAGGCCACACAC
NM_002036	FY	7167	ACTCCTAGTTCTCTTCCCACC
NM_002062	GLP1R	7168	ACATGGCGAGAATACCGACGC
NM_002062	GLP1R	7169	ACCTGTGTTGCATCCTTCATC
NM_002062	GLP1R	7170	ACTTTCGGAAGAGCTGGGAGC
NM_002377	MAS1	7171	ACTGGGATTCTCCTCTGGTTC
NM_002377	MAS1	7172	ACGTACCAGTCGGCATTGGTC
NM_002377	MAS1	7173	ACTCAACAGTAGCGCCAACCC
NM_002386	MC1R	7174	ACCTGCACTCACCCATGTAC
NM_002386	MC1R	7175	ACCTTCAACCTCTTTCTCGCC
NM_002511	NMBR	7176	ACCTGATCCCTGTCATCCAGC
NM_002511	NMBR	7177	ACCAGATGGAAACACGGAAAC
NM_002511	NMBR	7178	ACTGCTAAGAACATGGTGACC
NM_002531	NTSR1	7179	ACGGCCAAGACCCTCATGTCC
NM_002531	NTSR1	7180	ACGCTGACCGTCATGGTACGC
NM_002531	NTSR1	7181	ACCGCACTCTTCTACGTCAGC
NM_002548	OR1D2	7182	ACTCACACAGTGCTGATTGCC
NM_002563	P2RY1	7183	ACTTTGGCTCTGGCCGACTTC
NM_002563	P2RY1	7184	ACCCATCACCTGTTACGACAC
NM_002563	P2RY1	7185	ACGAGTGAAGACATGACCCCTC
NM_002564	P2RY2	7186	ACGACCTGGAATGCGTCCACC
NM_002564	P2RY2	7187	ACCGCCATCAACATGGCCTAC
NM_002565	P2RY4	7188	ACCCAGCAACAAAGGGACCAC
NM_002565	P2RY4	7189	ACTATCGACGTCAGCTCCGTC
NM_002921	RGR	7190	ACTGGTGCCACGATCAATGC
NM_002980	SCTR	7191	ACGAGCAAGACCAGTGCCTGC
NM_002980	SCTR	7192	ACGGCCTCTACCTTCACACAC
NM_002980	SCTR	7193	ACCTAGCCCTTGGCTCATTCC
NM_003301	TRHR	7194	ACCAGACAGTATCTACGGTTC
NM_003301	TRHR	7195	ACATCCCATTCTTCAGATCC
NM_003301	TRHR	7196	ACGGAGTCAGACCATTTCAGC
NM_003382	VIPR2	7197	ACACACAAAGCCTGCAGTGGC
NM_003382	VIPR2	7198	ACCTGTTCCTGTCTTCATC
NM_003468	FZD5	7199	ACGGAGTCACACCCGCTCTAC
NM_003468	FZD5	7200	ACGCTCATGATCCGCATCGGC

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NM_003485	GPR68	7201	ACCTGCCTGTCCCTCTACTTC
NM_003485	GPR68	7202	ACCATCTACATCAGCGTGGGC
NM_003485	GPR68	7203	ACCGCCTACCACTTCTCCCTC
NM_003505	FZD1	7204	ACGGTGTATGGGCTCATGTAC
NM_003505	FZD1	7205	ACGCTCATGGTGCGCATTGGC
NM_003506	FZD6	7206	ACAGCATTTGTACCAACCTGC
NM_003506	FZD6	7207	ACCTTGGTGACACTGTTGTCC
NM_003506	FZD6	7208	ACCCAGCACAGGAGCTACAGC
NM_003507	FZD7	7209	ACGACCATCACTATCCTGGCC
NM_003507	FZD7	7210	ACGTACCTGATGACCATGATC
NM_003508	FZD9	7211	ACGACCATCGTCATCCTGACC
NM_003508	FZD9	7212	ACGCTGGAGAAGCTCATGGTC
NM_003553	OR1E1	7213	ACGGGTATCTGCAAGGCCTTC
NM_003554	OR1E2	7213	ACGGGTATCTGCAAGGCCTTC
NM_003608	GPR65	7214	ACGACAACTGGACTTTCTCTC
NM_003608	GPR65	7215	ACGTCTACCAAGCTGTGCGGC
NM_003608	GPR65	7216	ACTTCTGGGAAGCGAACTTAC
NM_003614	GALR3	7217	ACTAAACCCTGCCGCCTGGAC
NM_003667	GPR49	7218	ACCCTCAGCGTCTTCACCTCC
NM_003667	GPR49	7219	ACGCTGGACCTATCGTCCAAC
NM_003667	GPR49	7220	ACACACATTGCCCTGTTGCTC
NM_003775	EDG6	7221	ACGCGCTACATCCTCTTCTGC
NM_003775	EDG6	7222	ACTGGGCTTCCCATGGTCACC
NM_003857	GALR2	7223	ACGGTGACACGCATGATCCTC
NM_003857	GALR2	7224	ACGCACTTCCGCAAAGGCTTC
NM_003950	F2RL3	7225	ACCAGCTGCGTGGATCCCTTC
NM_003965	CCRL2	7226	ACTGTGACAAGTATGACGCCC
NM_003965	CCRL2	7227	ACTCTCCTGGTTGTGCTTATC
NM_003965	CCRL2	7228	ACGTGTCCTGGCATGGGTAAC
NM_003965	CCRL2	7229	ACACACTAAGGTTCAAGGAGC
NM_003965	CCRL2	7230	ACATACCTCTGCCGCTGTTTC
NM_003967	PNR	7231	ACGATCTTTGTGGTTGCTACC
NM_003979	RAI3	7232	ACATGCTGCCTACTCAGTTTC
NM_003979	RAI3	7233	ACTAGGACCAACGTCAATGTC
NM_004054	C3AR1	7234	ACCATGTTTGCCAGTGCTTTC
NM_004054	C3AR1	7235	ACCCAGCCCACTGGATAACTC
NM_004054	C3AR1	7236	ACACTCTGATGTCTTGGGATC
NM_004072	CMKLR1	7237	ACCATGGTCTGGTTCCCTCAAC
NM_004072	CMKLR1	7238	ACCCTCCTAGAGCTCCACCAC
NM_004072	CMKLR1	7239	ACGTGAAGATACAGGCCACTC
NM_004101	F2RL2	7240	ACCAACTTGGCAAAGCCAACC
NM_004101	F2RL2	7241	ACCTGGGTATTTGGAGAGGTC
NM_004101	F2RL2	7242	ACCCAGAAATCACTCCACTGC
NM_004122	GHSR	7243	ACGCTGGTCATCTTCGTCATC
NM_004122	GHSR	7244	ACATGCTGGGTGGGTCTCAGC
NM_004154	P2RY6	7245	ACCTATGCCCAAGGTGATCAC

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NM_004224	GPR50	7246	ACCCGTTACTGCTACATCTGC
NM_004224	GPR50	7247	ACCTGGCTTTATCTTGCAGCC
NM_004224	GPR50	7248	ACGCCTGCCTCTGTCCATTTC
NM_004230	EDG5	7249	ACGTTCCACTCGGCAATGTAC
NM_004246	GLP2R	7250	ACGCAAGTTACAGGATCCCTC
NM_004246	GLP2R	7251	ACCCTTGCAGCTGATGTACAC
NM_004246	GLP2R	7252	ACTCAACACTGGTCCTCATTC
NM_004248	GPR10	7253	ACCGTGACGAACCTTCCTCATC
NM_004248	GPR10	7254	ACTATGACCGTCAGCGTGGTC
NM_004382	CRHR1	7255	ACCAATGGCTACCGGGAGTGC
NM_004382	CRHR1	7256	ACCATCATCCACTGGAACCTC
NM_004382	CRHR1	7257	ACTAGTGAGGTCCGTTCTGCC
NM_004624	VIPR1	7258	ACGATGTGGGACAACCTCACC
NM_004624	VIPR1	7259	ACCTACATCCACATGCACCTC
NM_004624	VIPR1	7260	ACGATGGTCTTTGAGCTCGTC
NM_004720	EDG4	7261	ACTCTGCTGGTCATAGCAGCC
NM_004720	EDG4	7262	ACAGTACTTCCTACTGTTGGC
NM_004720	EDG4	7263	ACGTACTTCCTACTGTTGGCC
NM_004720	EDG4	7264	ACTGCTGCTGTGTACTCTTGC
NM_004767	ET(B)R-LP-2	7265	ACCCTGTCCGGTCATGTGCATC
NM_004767	ET(B)R-LP-2	7266	ACCCAGTTCTCCACCTTCTTC
NM_004767	ET(B)R-LP-2	7267	ACTGGGTCCGGACAACAAGCTC
NM_004778	GPR44	7268	ACCATGTTCCGCCAGCGGCTTC
NM_004885	NPGR	7269	ACGCCTATGGAAGCTTATACC
NM_004951	EBI2	7270	ACCTTACTAGCCTTGGTCGTC
NM_004951	EBI2	7271	ACCACATATGCAGGTGTGAAC
NM_004951	EBI2	7272	ACTCTCTTCCCTGGATTCTGC
NM_005048	PTHR2	7273	ACGACAGAGTAGTCCATGCTC
NM_005048	PTHR2	7274	ACTCGACACTGGTCCTGGTCC
NM_005048	PTHR2	7275	ACCCAGACACTGAAGGATGC
NM_005201	CCR8	7276	ACATGGCAAGTTGCTCCTTGC
NM_005201	CCR8	7277	ACACCACAACAAGACCAAGGC
NM_005201	CCR8	7278	ACCAGCTGACTTATGCCACCC
NM_005226	EDG3	7279	ACGACGTTACGCCTGTCTCCC
NM_005226	EDG3	7280	ACCAAGAGGCACCGCGTCTTC
NM_005226	EDG3	7281	ACTCTCCCTGACTGCTCTACC
NM_005226	EDG3	7282	ACGGTGGCCAACCACAACAAC
NM_005242	F2RL1	7283	ACGGTTGATGGCACATCCCAC
NM_005242	F2RL1	7284	ACCATTGCCATTGGCATCTCC
NM_005242	F2RL1	7285	ACACACTCCAGGAAATCCAGC
NM_005279	GPR1	7286	ACGTGGAAGAAGACAGTCACC
NM_005279	GPR1	7287	ACGCGAACAGTCCTGATCTCC
NM_005279	GPR1	7288	ACGAAGTTCCAAGCTCGCTTC
NM_005281	GPR3	7289	ACATCTGCCGCATCGTCTGCC
NM_005282	GPR4	7290	ACTATCTACATCAGCATCGCC
NM_005282	GPR4	7291	ACCCTTTGTGCTCCCAGATCC

NM_005283	CCXCR1	7292	ACGTATGAGAGCCTGGAGTCC
NM_005283	CCXCR1	7293	ACACATGTTCTCCGGCAGTTC
NM_005284	GPR6	7294	ACTGGGTCTCTGGAGCTGTCC
NM_005284	GPR6	7295	ACCTCCATGATCAATCCCATC
NM_005285	GPR7	7296	ACCACCTTCTCCAGCCTCTAC
NM_005286	GPR8	7297	ACGATGAAGACGGTGACCAAC
NM_005286	GPR8	7298	ACCATCTTCTCCAGCATCTAC
NM_005286	GPR8	7299	ACCTTCCGGAAGAAGTCCGC
NM_005288	GPR12	7300	ACTAGGCAGCCTGGCTCTTGC
NM_005288	GPR12	7301	ACGATTGTGATGAGGCACGCC
NM_005288	GPR12	7302	ACTTCCATCATCAACCCTGTC
NM_005290	GPR15	7303	ACTCTGGCTGCCTCTGACTTC
NM_005290	GPR15	7304	ACTATGCACTGCAGTGTCCCTC
NM_005290	GPR15	7305	ACCTATGACTTTGGGAGTAGC
NM_005291	GPR17	7306	ACCATGCTGTTCCGCTCCTTC
AF261135	AF261135	7307	ACGAAGAGAACCACGGTAACC
NM_005292	GPR18	7307	ACGAAGAGAACCACGGTAACC
AF261135	AF261135	7308	ACAGCTGTGAACGTGCTGAAC
NM_005292	GPR18	7308	ACAGCTGTGAACGTGCTGAAC
AF261135	AF261135	7309	ACTTACCTTCGAAGCATGCGC
NM_005292	GPR18	7309	ACTTACCTTCGAAGCATGCGC
NM_005293	GPR20	7310	ACGACACCCTCAGTCATCTAC
NM_005294	GPR21	7311	ACGAGGACTAAAGCGCCTCTC
NM_005295	GPR22	7312	ACGTGTCTCTCACCGGATTTTC
NM_005295	GPR22	7313	ACTTCTGACAATGGGCAGAGC
NM_005295	GPR22	7314	ACCCACACAACATGAGGCTAC
NM_005296	GPR23	7315	ACCATCTATGGGAGCATGCTC
NM_005296	GPR23	7316	ACCAATGCAACCACCACCTGC
NM_005296	GPR23	7317	ACGTCCTTCTACATCAATGCC
NM_005297	GPR24	7318	ACCCTCTCGGTAGTAGATCTC
NM_005297	GPR24	7319	ACTAGTCAGTTCACCAGCACC
NM_005297	GPR24	7320	ACCCCAGACACTGACCTCTAC
NM_005298	GPR25	7321	ACCTCGCTGCGCATCATCTTC
NM_005298	GPR25	7322	ACGGATCAGCTCAGCCTCCTC
NM_005300	GPR34	7323	ACCCAATCATAGCGACCAACC
NM_005300	GPR34	7324	ACCGTAGCCATTGCAGACCTC
NM_005300	GPR34	7325	ACGTAGGAGTGAAAGCACTTC
NM_005301	GPR35	7326	ACCAGGTACATGAGCATCAGC
NM_005301	GPR35	7327	ACCCTCCTGGTGTTCGTGGTC
NM_005301	GPR35	7328	ACCCAGCAAGCTCTCAGATGC
NM_005302	GPR37	7329	ACGGGTGGACAATTGCACTCC
NM_005302	GPR37	7330	ACCTGTTTCCTCAACAAGTCC
NM_005302	GPR37	7331	ACGCAGAGAAAGCCTGTACCC
NM_005303	GPR40	7332	ACCACCTCCCTGGGCATCAAC
NM_005303	GPR40	7333	ACTCCGCTGGTGACCGGTTAC
NM_005304	GPR41	7334	ACGGACCAGCTAGCCATCCTC

NM_005305	GPR42	7334	ACGGACCAGCTAGCCATCCTC
NM_005304	GPR41	7335	ACGCCGACTTTCATGAGCTGC
NM_005305	GPR42	7335	ACGCCGACTTTCATGAGCTGC
NM_005306	GPR43	7336	ACTACTTGAACACGACTGAGC
NM_005306	GPR43	7337	ACTAGCCGTGGTGTTCAGTTC
NM_005314	GRPR	7338	ACCGTGTGCTCCAGTGGATGC
NM_005314	GRPR	7339	ACAGCCGCCTTTATCTGGATC
NM_005314	GRPR	7340	ACGGAGTACAACCTGCATGAC
NM_005458	GPR51	7341	ACGGCTGGAATCTGGTGCAGC
NM_005458	GPR51	7342	ACTGCCATGAACGAGACCAAC
NM_005458	GPR51	7343	ACGAGGTCACCATGCAGCTGC
NM_005508	CCR4	7344	ACTTCTGTGGTGGTCTGGTC
NM_005508	CCR4	7345	ACCAAGGCGGTGAAGATGATC
NM_005508	CCR4	7346	ACATTTACTCTGCTGACACCC
NM_005631	SMOH	7347	ACTGCGTGCTTCTTTGTGGGC
NM_005631	SMOH	7348	ACCTGGCATCGCCATGAGCAC
NM_005631	SMOH	7349	ACGAGGAAGAAGGAGGTGTGC
NM_005682	GPR56	7350	ACGACTTTCGCTTCTGCAGCC
NM_005682	GPR56	7351	ACCACCAAAGTAGCCAACCTC
NM_005682	GPR56	7352	ACACCTCGGGACTACACCATC
NM_005683	GPR55	7353	ACTCTGGGTCTTGGTGTGGAC
NM_005683	GPR55	7354	ACAGCCTGCATCTACAGCATC
NM_005684	GPR52	7355	ACACCTGGTTACCATGGTGAC
NM_005756	GPR64	7356	ACTGGCACCTTAAGTGGAGTC
NM_005756	GPR64	7357	ACGTAGTGGATGACATTGGCC
NM_005756	GPR64	7358	ACGAAGAAGCAACTGGGAGCC
NM_005767	P2Y5	7359	ACCAATGCCTCAGAAGCCTGC
NM_005795	CALCRL	7360	ACACTGGTTTACAGATCCAGC
NM_005795	CALCRL	7361	ACGTGTCCCAGTTCATTCATC
NM_005795	CALCRL	7362	ACTTTGTGCTGATTCCATGGC
NM_005912	MC4R	7363	ACCAAGAATCTGCATTACCCC
NM_005912	MC4R	7364	ACACAGTACAGATACGGATGC
NM_005912	MC4R	7365	ACGGGAGCGATTACCTTGACC
NM_005913	MC5R	7366	ACGCACCTAGTGATAGCAGAC
NM_005913	MC5R	7367	ACTTCCGTGATGGACCCCTC
NM_005958	MTNR1A	7368	ACGCTCAGGAACGCAGGAAAC
NM_005958	MTNR1A	7369	ACCCTGACCGCAAACCCAAAC
NM_005958	MTNR1A	7370	ACACCGTCTCCACTGATGACC
NM_005959	MTNR1B	7371	ACTGCCATTGTCTATGGGCTC
NM_005972	PPYR1	7372	ACCCTGGCCTTCTCTGACTTC
NM_005972	PPYR1	7373	ACCAGCATCCTGGAGAATGTC
NM_005972	PPYR1	7374	ACCCTCATCTTCTTAGTGTGC
NM_006018	HM74	7375	ACTTGGACAGCAGCCATCATC
NM_006018	HM74	7376	ACTGTGTGCATCAGCTTCAGC
NM_006018	HM74	7377	ACGATCAAGAGAGCCATCACC
XM_090326	LOC160484	7377	ACGATCAAGAGAGCCATCACC

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NM_006018	HM74	7378	ACCCAGCATCTCTGGAGAAAC
NM_006018	HM74	7379	ACACAGTTGGGCTGTTGCATC
NM_006056	GPR66	7380	ACCATGGTAGTGACAGACCACC
NM_006056	GPR66	7381	ACGATGCTGTTTGTCTGGTC
NM_006143	GPR19	7382	ACACAGACCTTCACTATGTGC
NM_006143	GPR19	7383	ACTATCTCACTCCAGGTGTCC
NM_006143	GPR19	7384	ACGCTTGCTTGGCCCATTAAC
NM_006174	NPY5R	7385	ACGACTACGGTAAACTTCCTC
NM_006174	NPY5R	7386	ACGAAGTCAGCTCTCTTCATC
NM_006564	TYMSTR	7387	ACCTTCTACACGTCCATGCTC
NM_006564	TYMSTR	7388	ACTTTCCACTGTGGTTCTTGC
NM_006564	TYMSTR	7389	ACGTTTCATCCGCAGCACACAC
NM_006583	RRH	7390	ACTTTGGATACGCAGGCTGTC
NM_006583	RRH	7391	ACACATCACACTACCAGTGAC
NM_006639	CYSLTR1	7392	ACTGGCTTTGTGCTCTATGTC
NM_006639	CYSLTR1	7393	ACTACCAAGTGCTTTGAGCCC
NM_006639	CYSLTR1	7394	ACCCTTGCTCTCTGGCTGCATC
NM_006641	CCR9	7395	ACTGTCAGGCAGTTTGCGAGC
NM_031200	CCR9	7395	ACTGTCAGGCAGTTTGCGAGC
NM_006641	CCR9	7396	ACGTTCCAGACCTTCATGTGC
NM_031200	CCR9	7396	ACGTTCCAGACCTTCATGTGC
NM_006641	CCR9	7397	ACGAACCTGGGTTCATCAGC
NM_031200	CCR9	7397	ACGAACCTGGGTTCATCAGC
NM_006794	GPR75	7398	ACCCTGTCTTCTGTGACCTC
NM_006794	GPR75	7399	ACGAGTCCCAACCACTGGTC
NM_006794	GPR75	7400	ACCACTCGGATTGAACCTTAC
NM_007197	FZD10	7401	ACCATGACTCGTATGCCCAAC
NM_007223	GPR	7402	ACCCGTGTTCAAATCTGTAC
NM_007223	GPR	7403	ACTGTGGCTGACATCTATGCC
NM_007223	GPR	7404	ACGTACATTGGCTCAGCTGAC
NM_007227	GPR45	7405	ACCACTGTGGTCTGCATCATC
NM_007227	GPR45	7406	ACGGTGATCATCGCGGTCTCC
NM_007227	GPR45	7407	ACGGAGAATCCAGCCAAGCAC
NM_007232	HRH3	7408	ACCCTCGCCATCTCCGACTTC
NM_007232	HRH3	7409	ACCCTCAGCATCTACCTGAAC
NM_007232	HRH3	7410	ACGCGCATGAAGATGGTGTCC
NM_007264	ADMR	7411	ACCTGGACCGAGCTGCTTGAC
NM_007264	ADMR	7412	ACCTTTCTCAGCCCACACTTC
NM_007369	RE2	7413	ACACCTGGTCATCGTGGTCAC
NM_007369	RE2	7414	ACCCAGTGCAAAGCCCTCATC
NM_007369	RE2	7415	ACCAGGATCACAGACCTGGGC
D13814	HUMAGRT1B	7416	ACCAGCTTGGTGGTGATAGTC
NM_000685	AGTR1	7416	ACCAGCTTGGTGGTGATAGTC
NM_004835	AGTR1	7416	ACCAGCTTGGTGGTGATAGTC
NM_009585	AGTR1	7416	ACCAGCTTGGTGGTGATAGTC
NM_031850	AGTR1	7416	ACCAGCTTGGTGGTGATAGTC

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NM_032049	AGTR1	7416	ACCAGCTTGGTGGTGATAGTC
D13814	HUMAGRT1B	7417	ACGATTGCTTCAGCCAGCGTC
NM_000685	AGTR1	7417	ACGATTGCTTCAGCCAGCGTC
NM_004835	AGTR1	7417	ACGATTGCTTCAGCCAGCGTC
NM_009585	AGTR1	7417	ACGATTGCTTCAGCCAGCGTC
NM_031850	AGTR1	7417	ACGATTGCTTCAGCCAGCGTC
NM_032049	AGTR1	7417	ACGATTGCTTCAGCCAGCGTC
D13814	HUMAGRT1B	7418	ACGCCAAATCCCACTCAAACC
NM_000685	AGTR1	7418	ACGCCAAATCCCACTCAAACC
NM_004835	AGTR1	7418	ACGCCAAATCCCACTCAAACC
NM_009585	AGTR1	7418	ACGCCAAATCCCACTCAAACC
NM_031850	AGTR1	7418	ACGCCAAATCCCACTCAAACC
NM_032049	AGTR1	7418	ACGCCAAATCCCACTCAAACC
NM_010935	Npy6r	7419	ACCCTGTCCCTCTCTGACATC
NM_010935	Npy6r	7420	ACTCTCTCTCTCCCTACTGAC
NM_010935	Npy6r	7421	ACGAGCCGTCTCAATGAGAAC
AF236117	AF236117	7422	ACTTTAGCTGCTGCCGATTTTC
NM_012152	EDG7	7422	ACTTTAGCTGCTGCCGATTTTC
AF236117	AF236117	7423	ACCATCTCTGCCTGCTCTTCC
NM_012152	EDG7	7423	ACCATCTCTGCCTGCTCTTCC
AF236117	AF236117	7424	ACACCAACGTCTTGTCTCCGC
NM_012152	EDG7	7424	ACACCAACGTCTTGTCTCCGC
NM_012152	EDG7	7425	ACGGACGAGGACATGTATGGC
NM_012193	FZD4	7426	ACCGTGACCAAGATGCCCAAC
NM_012193	FZD4	7427	ACCGACCACAACCACATGTGC
NM_012193	FZD4	7428	ACGGATGGGACAAAGACAGAC
NM_012302	LPHH1	7429	ACCTATGGTCGGACGGATGAC
NM_012302	LPHH1	7430	ACCAAGGGTCTCAATGCCAC
NM_012302	LPHH1	7431	ACTGCTTTCCAGGGAGTGTTTC
NM_012344	NTSR2	7432	ACGTGCCGTCCACTTCTACCC
NM_012344	NTSR2	7433	ACACTCTTCCCTGGAAGCCGTC
NM_012352	OR1A2	7434	ACTCTGCTCATCATCTTGGCC
NM_012352	OR1A2	7435	ACGTTGTCTCTGTCTGACGTC
NM_012352	OR1A2	7436	ACGGCAGCCCTACAGAACTC
NM_013308	H963	7437	ACTCACAGGTGTGTGAGCATC
NM_013308	H963	7438	ACTACAAGAACCCGATTTGC
NM_013308	H963	7439	ACAGCATTCCGCTCAAAGGTC
NM_013345	G2A	7440	ACCGTGTCCTTCGAAGAGAGC
NM_013345	G2A	7441	ACGCAGAGCATGGGCTTAAGC
NM_013345	G2A	7442	ACGACAGACGTCACCAGGCTC
NM_013447	EMR2	7443	ACCACGTGTCAAGATGTGGAC
NM_013447	EMR2	7444	ACCCTGAGAAGCAGATGCTTC
NM_013447	EMR2	7445	ACCCTGACGGTGGTCAACTAC
NM_014246	CELSR1	7446	ACCGTCACTGATGCCAACACC
NM_014246	CELSR1	7447	ACCTACATGAAGTGCGTGTCC
NM_014246	CELSR1	7448	ACTGAGAAGCACGACTTCATC

NM_014262	GRCB	7449	ACTGTCCTGAGTGTCTGCTC
NM_014262	GRCB	7450	ACGCTGCTTCTGGAGGTGAGC
NM_014262	GRCB	7451	ACGAAGTCTGTCAGGAGTCAC
NM_014322	OPN3	7452	ACCAACCTGCTGGTGCTCGTC
NM_014322	OPN3	7453	ACGGATGCCAACGATTCCCTCC
NM_014322	OPN3	7454	ACTGGTCATGGTCACCTGGTC
NM_014373	GPCR150	7455	ACGCCTGAAGGCACAGAATGC
NM_014373	GPCR150	7456	ACCCTGTTGGGAAGAAGTTAC
NM_014449	GRCA	7457	ACGGCACATGCTCTTCCCTCC
NM_019858	GRCA	7457	ACGGCACATGCTCTTCCCTCC
NM_014449	GRCA	7458	ACGTGGTCATCCTCTGATGAC
NM_019858	GRCA	7458	ACGTGGTCATCCTCTGATGAC
NM_014499	P2Y10	7459	ACGCGTAGGTACGATGTGGGC
NM_014499	P2Y10	7460	ACTCGCACTGTATTTCCACCC
NM_014565	OR1A1	7461	ACCCTGCTCATTTGTCCTAGCC
NM_014565	OR1A1	7462	ACCCAGGAAGTGGCCAACTTC
NM_014565	OR1A1	7463	ACTCGGGACATGAAGGCTGCC
NM_014566	OR1D5	7464	ACCCTTCTCTACCTGTGCCTC
NM_014626	GPR58	7465	ACCCAAGTTCCTCATCCTCTC
NM_014627	GPR57	7466	ACACAGCATGCTCGAGTCATC
NM_014879	GPR105	7467	ACTCCTACTCAATGGAGTGTC
NM_014879	GPR105	7468	ACGATCCTTGGTGACTCAGGC
NM_014879	GPR105	7469	ACAGCTCAGAATGACCTAGAC
NM_014921	KIAA0821	7470	ACAGTGAGCAGAAAGTCTTC
NM_014921	KIAA0821	7471	ACCAACTATTTTCGTGGTGCGC
NM_014921	KIAA0821	7472	ACCCTGTGCATCAACCTCTTC
NM_015236	LEC3	7473	ACGTGCCAACTATGGCAGGAC
NM_015236	LEC3	7474	ACTTGAACCCCTACACCCTAC
NM_015236	LEC3	7475	ACGAGAGCGCTCTTGACAGAGC
NM_015727	TACR1	7476	ACCTCAGCCTGGCTGATTATC
NM_016235	GPRC5B	7477	ACCACGCCCCAACTACTTCGAC
NM_016540	GPR72	7478	ACCAACTACACCTTCTCCGAC
NM_016540	GPR72	7479	ACTACAGTGAGGACATTGTGC
NM_016540	GPR72	7480	ACTGCCCTCTACTTTGCCTTC
NM_016557	CCRL1	7481	ACGGACACTCATGAAGATGCC
NM_016557	CCRL1	7482	ACTATGGGTCTTGAGAGAAGAC
NM_016568	SALPR	7483	ACGTCTCTATCAACCTCTTC
NM_016568	SALPR	7484	ACGGCGCTGTGTGTGTGGATC
NM_016568	SALPR	7485	ACTCAGTGACCATCGTTGTCC
NM_017412	FZD3	7486	ACTATGGACGTGTCAGACTTC
NM_017412	FZD3	7487	ACAGCATTGCTGTTTCACGCC
NM_017412	FZD3	7488	ACGAGATAGTGAATGAGAGCC
NM_017986	FLJ10060	7489	ACGAAGAGGCTTTGCCATTGC
NM_018485	GPR77	7490	ACGTGTGGACAGCAAGAAATC
NM_018485	GPR77	7491	ACGAAATCCACCAGCCATGAC
NM_018490	GPR48	7492	ACGGACTTGTTTCAGTTACGGC

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NM_018490	GPR48	7493	ACGATAACAGCCTCCAGGACC
NM_018490	GPR48	7494	ACGCATGTGCTTGGCTAATC
NM_018653	GPRC5C	7495	ACCTTCCTGGCCCCGGAAGAAC
NM_022036	GPRC5C	7495	ACCTTCCTGGCCCCGGAAGAAC
NM_018653	GPRC5C	7496	ACAGAGCAGAAGGGTCAGAGC
NM_022036	GPRC5C	7496	ACAGAGCAGAAGGGTCAGAGC
NM_018653	GPRC5C	7497	ACGGAGCTTACGACATCATCC
NM_022036	GPRC5C	7497	ACGGAGCTTACGACATCATCC
NM_018654	GPRC5D	7498	ACTATGACACCCTGCCAGCTC
NM_018654	GPRC5D	7499	ACGCAGCATGGAAGGCTCATC
NM_018949	GPR14	7500	ACCGCAACCCTCAACAGCTCC
NM_018949	GPR14	7501	ACCTACCTGACCACCTGCCTC
NM_018969	SREB3	7502	ACGATTGTGGCCTTTATGGCC
NM_018969	SREB3	7503	ACCTGGACATTCCATGGTCCC
NM_018969	SREB3	7504	ACCAAGGACCTCAAGAAGTGC
NM_018970	GPR85	7505	ACGATCAATGCACCTTCCAAC
NM_018970	GPR85	7506	ACTCCAGGTTACCAAGGGAAC
NM_018971	GPR27	7507	ACTTCAAGACGGAGAAGAGGC
NM_018971	GPR27	7508	ACGACGGAGAAGAGGCTGTGC
NM_018971	GPR27	7509	ACGAGGCTGTGCAAGATGTTT
NM_014430	CIDEB	7510	ACGGCGGTGTACTACGTGTGC
NM_019839	BLTR2	7510	ACGGCGGTGTACTACGTGTGC
NM_019888	MC3R	7511	ACCATCCTGGTTATCCTGGCC
NM_019888	MC3R	7512	ACCATCTTCGACTCCATGATC
NM_019888	MC3R	7513	ACCACCTACCTGGTCCTCATC
NM_020061	OPN1LW	7514	ACCCAGGTCTCTGGCTACTTC
NM_020167	NMU2R	7515	ACGACGCCCACCAACTACTAC
NM_020167	NMU2R	7516	ACCCTACTGTCTCGCCGCTTC
NM_020167	NMU2R	7517	ACCTCTCACCTCCCAACAGCC
NM_020370	GPR84	7518	ACGCTCCGTACCCGATTCAAC
NM_020370	GPR84	7519	ACTTCTGTCTCCATCCTGACC
NM_020370	GPR84	7520	ACCCCTGTGCTCTATGCAGCC
NM_020377	CYSLTR2	7521	ACGAAGTCCACATCTGTGAAC
NM_020377	CYSLTR2	7522	ACCGGCAGTGTACATCATGC
NM_020377	CYSLTR2	7523	ACGGCACTGACCACCATCATC
NM_020400	GPR92	7524	ACCATGTACGGCAGCTGCATC
NM_020960	GPR107	7525	ACCCCTGCTTCAGCAGGCAAC
NM_020960	GPR107	7526	ACGGATCCTGACAGCTACCTC
NM_021624	HRH4	7527	ACCTTGGCCATCTCTGACTTC
NM_021624	HRH4	7528	ACTGGGTTCTTCTCCCAATC
NM_021634	LGR7	7529	ACGCTTCCTCCTGATTGCTTC
NM_021634	LGR7	7530	ACCCCTCTGTCAACACATGC
NM_021634	LGR7	7531	ACTCTATGGACAGCAAAGGTC
NM_001470	GABBR1	7532	ACGACAGGGTCATCGACCAAC
NM_021903	GABBR1	7532	ACGACAGGGTCATCGACCAAC
NM_021904	GABBR1	7532	ACGACAGGGTCATCGACCAAC

NM_021905	GABBR1	7532	ACGACAGGGTCATCGACCAAC
NM_022049	GPR88	7533	ACGCTGCAGACCACCAGCAAC
NM_022049	GPR88	7534	ACCCGCTACCTGCTCATCACC
NM_022146	OT7T022	7535	ACCCTCACCTTCTCCTCCTAC
NM_022146	OT7T022	7536	ACAGGTTCCGCTGCATCGTGC
NM_022146	OT7T022	7537	ACCCGCTCCTACCCTCTCTAC
NM_022159	ETL	7538	ACCTCATGCACACTGTTGAAC
NM_022159	ETL	7539	ACTGAGCTCAAACCCACCCAC
NM_022159	ETL	7540	ACGGTCTTGTGCAAGAGGAGC
NM_022788	P2RY12	7541	ACATCAGAGTTCCGGTCTAGTC
NM_022788	P2RY12	7542	ACTGCATGCCTGGATCCGTTC
NM_023914	GPR86	7543	ACATCCTCTCTGACTCACACC
NM_023914	GPR86	7544	ACTCATAGCAGTCAGACAGAC
NM_023914	GPR86	7545	ACACGCCCCAACTCTTGAAGTC
NM_024012	HTR5A	7546	ACCGTCATGATCGCGCTCACC
NM_024012	HTR5A	7547	ACGGACTCTGCCAAACAGCCC
NM_024012	HTR5A	7548	ACCAAGAACTACAACAGCGCC
NM_030760	EDG8	7549	ACGGCCTACGTGCTCTTCTGC
NM_030784	GPR63	7550	ACCTTGCCCTCTTCAGATCACC
NM_030784	GPR63	7551	ACCCAATCCAGGCTACCAGGC
NM_030784	GPR63	7552	ACCTGGGTCTCATGAGTCTGC
NM_004367	CCR6	7553	ACGGCCAGGTCTATGACAGAC
NM_031409	CCR6	7553	ACGGCCAGGTCTATGACAGAC
NM_004367	CCR6	7554	ACATACAACACCCAAGGCAGC
NM_031409	CCR6	7554	ACATACAACACCCAAGGCAGC
NM_004367	CCR6	7555	ACGTACAAGTCCCTCAGGCTTC
NM_031409	CCR6	7555	ACGTACAAGTCCCTCAGGCTTC
NM_031866	FZD8	7556	ACGACAGGCCAGATCGCTAAC
NM_031866	FZD8	7557	ACGCTGGAGAAGCTGATGATC
NM_031936	GPR61	7558	ACTTTGTCTTCGTCTTCCACC
NM_031936	GPR61	7559	ACGCAGTTTGTCTGCTTCTTC
NM_031940	BLP1	7560	ACCCATGGCAGAAGTAGAATC
NM_031940	BLP1	7561	ACACAGCGATTTGCAAAGACC
NM_032027	BBP	7562	ACATGACGCTACGCAAGAACC
NM_032027	BBP	7563	ACTGCAGATTGTTGGACCTTC
NM_032119	VLGR1	7564	ACATGTGAAGCTTGGATGGCC
NM_032119	VLGR1	7565	ACCCAGAAGATTGAAAGCAGC
NM_032119	VLGR1	7566	ACGCAGCGTTCCACATATCAC
NM_032503	SLT	7567	ACCTGCCAGTGTGGTGGATAC
NM_032503	SLT	7568	ACCCAATTTGCCTGTAGTGCC
NM_032503	SLT	7569	ACATTTCCAGAAACGTCTGCC
NM_032551	GPR54	7570	ACCTCGCTGGTCATCTACGTC
NM_032553	FKSG79	7571	ACTGTCAACCTGGCCCAGTCC
NM_032553	FKSG79	7572	ACTATCCCATGGCCCAAGATC
NM_032553	FKSG79	7573	ACTTCATGTCTTGACCCAGTC
NM_032554	GPR81	7574	ACTTTGGCCGTGGCTGATTTTC

NM_032554	GPR81	7575	ACGAAGGCGACCCGGTTCATC
NM_032554	GPR81	7576	ACGAGATGCCAATTTCTGAACC
NM_032571	EMR3	7577	ACTAACACTCACTGCACCTGC
NM_032571	EMR3	7578	ACCTCAATGGACATCCGTTGC
NM_032571	EMR3	7579	ACCACAAGGATGCTGGCTTTC
NM_033050	GPR91	7580	ACGTATCCTTTCCGAGAACAC
NM_033050	GPR91	7581	ACGCCTCTCAACTTGGTCATC
NM_033050	GPR91	7582	ACCAGTGTCAATCAACCCTGTC
NM_033282	OPN4	7583	ACCCTGACGGTCACTCTATACC
NM_033282	OPN4	7584	ACGATCATGCTGCTGGTCATC
NM_033282	OPN4	7585	ACGTACAGGGTGGCCATTGCC
NM_033302	ADRA1A	7586	ACGCATCCATCTGACTAAGGC
NM_052967	MRG	7587	ACTGTTGTCTGCACCCCTCATC
NM_052967	MRG	7588	ACCAGCAGCGCCAACCCTATC
NM_052967	MRG	7589	ACTGGAGCAACCACACTCTAC
NM_053036	GPR74	7590	ACAGCCTATGGAAGCTTATGC
NM_053036	GPR74	7591	ACGCCTATGGAAGCTTATGCC
NM_053278	GPR102	7592	ACGCAGCTGCACTCTCCAACC
NM_054021	GPR101	7593	ACTGCTCTCTGCTCCATGATC
NM_054021	GPR101	7594	ACGGAGGGCAGAATGGAAGCC
NM_054021	GPR101	7595	ACGAAGATAGCCACCCAGACC
NM_001401	EDG2	7596	ACTGGCTAATCTGGCTGCTGC
NM_057159	EDG2	7596	ACTGGCTAATCTGGCTGCTGC
NM_057159	EDG2	7597	ACTACTCGGAGACTGACTGTC
NM_001401	EDG2	7598	ACTTGTTCCAACATGGCACCC
NM_057159	EDG2	7598	ACTTGTTCCAACATGGCACCC
NM_001401	EDG2	7599	ACATGAGCGCCACCTTTAGGC
NM_057159	EDG2	7599	ACATGAGCGCCACCTTTAGGC
NM_080817	GPR82	7600	ACCTTACTTGTGTGCAGTGCC
NM_080817	GPR82	7601	ACAGGATTCTCGCAAGAGAC
NM_080817	GPR82	7602	ACCTAGGAGCCATGATCTCTC
NM_080818	GPR80	7603	ACCATCCCCTCAAGATGCAC
NM_080818	GPR80	7604	ACGCACGAAGGCTAACCATTC
NM_080818	GPR80	7605	ACGTAAGCGGGAACCTTGAGC
NM_130806	GREAT	7606	ACCCACAACCTGCATCACAACC
NM_130806	GREAT	7607	ACCAACTTCAGTCTCTAGACC
NM_130806	GREAT	7608	ACCAGCTGCTGCACAAACATC
NM_138964	GPR73	7609	ACCCTGGCCATCTCTGACTTC
NM_138964	GPR73	7610	ACGATCTTCTGCGGCCAGATC
NM_138964	GPR73	7611	ACGACAATTGGGATGCCTGCC
NM_144773	GPR73L1	7612	ACGAAGTTGCGCAACCTCACC
NM_144773	GPR73L1	7613	ACGAGCCAGGAGAAGATCTTC
NM_144773	GPR73L1	7614	ACGTCCAGTGCTGACCTTGAC
NM_148962	TG1019	7615	ACCTTCATAACCTGAGCTCTC
NM_148962	TG1019	7616	ACCAGTTTGGCCCTCTTCATC
XM_092406	LOC165140	7616	ACCAGTTTGGCCCTCTTCATC

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NM_148963	GPRC6A	7617	ACGCAATGGCTCACCTGATTC
XM_167040	LOC222545	7617	ACGCAATGGCTCACCTGATTC
NM_148963	GPRC6A	7618	ACGAGGTTCTTCCAGCCTTTC
XM_167040	LOC222545	7618	ACGAGGTTCTTCCAGCCTTTC
NM_148963	GPRC6A	7619	ACTGTCTCCTTGCCCAGAGTC
XM_167040	LOC222545	7619	ACTGTCTCCTTGCCCAGAGTC
NM_152232	TAS1R2	7620	ACGGTGATAGGCTACAACCTC
NM_152232	TAS1R2	7621	ACCAACACGATCCCTATGTCC
NM_152232	TAS1R2	7622	ACCGAGGCCAAGTTCATCACC
NM_153840	GPR110	7623	ACCTATTATCAGCATGGCCTC
NM_153840	GPR110	7624	ACTGGATCACCTATGTGGGAC
NM_153840	GPR110	7625	ACGCTGCGACAACCTTCTGTTC
AF280399	AF280399	7626	ACGTTCTTCTTCTGGATCGGC
AF280400	AF280400	7626	ACGTTCTTCTTCTGGATCGGC
D13538	HUMA2CIIA	7626	ACGTTCTTCTTCTGGATCGGC
J03853	HUMADRA2C	7626	ACGTTCTTCTTCTGGATCGGC
NM_000682	ADRA2B	7626	ACGTTCTTCTTCTGGATCGGC
NM_000683	ADRA2C	7626	ACGTTCTTCTTCTGGATCGGC
U72648	HSU72648	7626	ACGTTCTTCTTCTGGATCGGC
XM_044591	GPR108	7627	ACCAGTAGCAGTTTCCTGGTC
XM_044591	GPR108	7628	ACCGTGGCCTACATCATCATC
XM_061555	LOC119586	7629	ACCTCCATGCTCAGCATGGCC
XM_061555	LOC119586	7630	ACGGAGATTCTGAACAGGCTC
XM_062863	LOC121928	7631	ACGATCAACTGCACAGGCATC
XM_062863	LOC121928	7632	ACGCTGGCCTGCATGGAGTAC
XM_062863	LOC121928	7633	ACCATGAACTGTGGCATTACC
XM_064220	LOC124601	7634	ACTCAATGGTGTCCCATGCAC
XM_064220	LOC124601	7635	ACCATCCTGGAGTTTGCTGCC
XM_064220	LOC124601	7636	ACTATGGTGGCCATGCTCCAC
XM_066873	GPCR2	7637	ACTGATGGTGTCACTCTCTGC
XM_066873	GPCR2	7638	ACGATTGCCTCCATGCACAGC
XM_066873	GPCR2	7639	ACGTTCCCTGTACATCGTCAC
XM_068829	LOC134391	7640	ACCCTGTGTGTGATTGGCATC
XM_068829	LOC134391	7641	ACTGTGCCCTCGTGGATGTACC
XM_068829	LOC134391	7642	ACGGTTCCATCTCCAGAATCC
XM_068013	LOC132745	7643	ACACTTGCCCTGTTCTGACAGC
XM_068167	LOC133061	7643	ACACTTGCCCTGTTCTGACAGC
XM_089954	LOC159954	7643	ACACTTGCCCTGTTCTGACAGC
XM_115784	LOC205316	7643	ACACTTGCCCTGTTCTGACAGC
XM_167303	LOC222972	7643	ACACTTGCCCTGTTCTGACAGC
XM_172665	LOC253261	7643	ACACTTGCCCTGTTCTGACAGC
XM_092364	LOC165082	7644	ACCTCTCCAGGACACTGACTC
XM_092364	LOC165082	7645	ACTCTCCTGATTGCCACAGAC
XM_092364	LOC165082	7646	ACGCCCTGCTCATTCTTACAC
NM_145242	LOC115131	7647	ACTCCTCACCTCTGTGTCTTC
XM_068013	LOC132745	7647	ACTCCTCACCTCTGTGTCTTC

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XM_068167	LOC133061	7647	ACTCCTCACCTCTGTGTCTTC
XM_115784	LOC205316	7647	ACTCCTCACCTCTGTGTCTTC
XM_116236	LOC205940	7647	ACTCCTCACCTCTGTGTCTTC
XM_166794	LOC220328	7647	ACTCCTCACCTCTGTGTCTTC
XM_172294	LOC253232	7647	ACTCCTCACCTCTGTGTCTTC
XM_172665	LOC253261	7647	ACTCCTCACCTCTGTGTCTTC
XM_167080	LOC222656	7648	ACACAGATCCAGGCCTCAGAC
XM_167080	LOC222656	7649	ACGTGCTTTGTGCTGCAGCTC
XM_167080	LOC222656	7650	ACAGTAGGCAACGACAGCAGC
XM_172703	LOC256774	7651	ACCGGTAACAGCATCATCCAC
XM_172703	LOC256774	7652	ACCAATGATGCGGACAGCGGC
XM_173965	LOC253201	7653	ACTGTGAACTGCGGCGTTGCC
XM_173965	LOC253201	7654	ACAGGAAACGGACAGTGAGCC
XM_173965	LOC253201	7655	ACGGAGCAAGGCTGTGGTTGC
NM_004834	MAP4K4	7656	ACTACGTTTCATAGGCACTCCC
NM_145686	MAP4K4	7656	ACTACGTTTCATAGGCACTCCC
NM_145687	MAP4K4	7656	ACTACGTTTCATAGGCACTCCC
SK437	ZC1/HGK	7656	ACTACGTTTCATAGGCACTCCC
XM_038748	MAP4K4	7656	ACTACGTTTCATAGGCACTCCC
NM_004834	MAP4K4	7657	ACGTTCCATTGTGAACGTGCC
NM_145686	MAP4K4	7657	ACGTTCCATTGTGAACGTGCC
NM_145687	MAP4K4	7657	ACGTTCCATTGTGAACGTGCC
SK437	ZC1/HGK	7657	ACGTTCCATTGTGAACGTGCC
XM_038748	MAP4K4	7657	ACGTTCCATTGTGAACGTGCC
NM_145686	MAP4K4	7658	ACGGCTTGGTCTAGATCAGAC
SK437	ZC1/HGK	7658	ACGGCTTGGTCTAGATCAGAC
NM_004834	MAP4K4	7659	ACCACTAGGCCACAGAGTGAC
NM_145686	MAP4K4	7659	ACCACTAGGCCACAGAGTGAC
NM_145687	MAP4K4	7659	ACCACTAGGCCACAGAGTGAC
SK437	ZC1/HGK	7659	ACCACTAGGCCACAGAGTGAC
XM_038748	MAP4K4	7659	ACCACTAGGCCACAGAGTGAC
NM_004834	MAP4K4	7660	ACGCCATTACTGGTGGATCTC
NM_145686	MAP4K4	7660	ACGCCATTACTGGTGGATCTC
NM_145687	MAP4K4	7660	ACGCCATTACTGGTGGATCTC
SK437	ZC1/HGK	7660	ACGCCATTACTGGTGGATCTC
XM_038748	MAP4K4	7660	ACGCCATTACTGGTGGATCTC
NM_002562	P2RX7	7663	ACCCAGAGGAGATACAGCTGC
NM_000204	IF	7664	ACGTCTTCTGCCAGCCATGGC
NM_000204	IF	7665	ACCTGTGTTGTAAAGCATGCC
NM_000204	IF	7666	ACGGATGCCAGTGGAATCACC
NM_000312	PROC	7667	ACATGTGGATGACACACTGGC
NM_000312	PROC	7668	ACGAAGACCAAGTAGATCCGC
NM_000312	PROC	7669	ACGAGAAACCGCACCTTCGTC
NM_000789	ACE	7670	ACGGAGCTGTATGAACCGATC
NM_000789	ACE	7671	ACCATCACCACAGAGACCAGC
NM_000789	ACE	7672	ACCGGCAAGGACTTCCGGATC

NM_000893	KNG	7673	ACCCAGTTTGTATTGTACCGC
NM_000893	KNG	7674	ACCATTCCCTCCCTCTTCATGC
NM_000893	KNG	7675	ACCCACTGGGAATGATCTCAC
NM_000895	LTA4H	7676	ACTCCTTCCTTGTTCAGGACAC
NM_000895	LTA4H	7677	ACCCTATACTGCAGAGGTGTC
NM_000895	LTA4H	7678	ACGAGCACAAAGCAAGCATGC
NM_000936	PNLIP	7679	ACCTGGCTGGCCAATGTGTGC
NM_000936	PNLIP	7680	ACCGTGCATGTCAATTGGCCAC
NM_000936	PNLIP	7681	ACACAAGTGTTTCCCTTGTCC
NM_001333	CTSL2	7682	ACACATGGCTTCACAATGGCC
NM_001333	CTSL2	7683	ACCTTGTCTCACTGAGCGAGC
NM_001333	CTSL2	7684	ACCAGCAAGTATTGGCTCGTC
NM_001335	CTSW	7685	ACACTGCAACTGCTGCTGGGC
NM_001335	CTSW	7686	ACGAAGTACCAGAAGGTGGCC
NM_001335	CTSW	7687	ACGGTGTGATCAAGGCCACAC
NM_001336	CTSZ	7688	ACCGTCATCGACTGCGGTAAC
NM_001336	CTSZ	7689	ACTGACCTGTCCGTGTGGGAC
NM_001336	CTSZ	7690	ACCAACTACCAGGCCAAGGAC
NM_001397	ECE1	7691	ACGCAATCATCAAGCACCTCC
NM_001397	ECE1	7692	ACGAAGACCTGTCTTCCTCGC
NM_001397	ECE1	7693	ACCTTTGGTGGCATAGGTGTC
NM_001553	IGFBP7	7694	ACGGTCCTTCCATAGTGACGC
NM_001633	AMBP	7695	ACGTGGTACAACCTGGCCATC
NM_001633	AMBP	7696	ACCCAGAGCCCATCTTAATCC
NM_001633	AMBP	7697	ACGGAGTGTCTGCAGACCTGC
NM_001733	C1R	7698	ACGATGCTGCTGACCTTCCAC
NM_001733	C1R	7699	ACGACCCTAGACGAGTTCACC
NM_001733	C1R	7700	ACCATGTTCTGTGCTGGACAC
NM_001086	AADAC	7701	ACGTGGTTATGACTTGCTGTC
NM_001086	AADAC	7702	ACGCCATGCTTTCAGACAAC
NM_001086	AADAC	7703	ACCCATGTTGAGGATGGATTG
NM_001097	ACR	7704	ACCCAGTAAAGGCGCCTGTGC
NM_001097	ACR	7705	ACAGACAGCAAGGAAAGCGCC
NM_001097	ACR	7706	ACCCATTATGACATGGAGACC
NM_000666	ACY1	7707	ACCCCTACACTCTCCTCCATC
NM_000666	ACY1	7708	ACGGATTCTGAGGGCTACATC
NM_000666	ACY1	7709	ACGGCATGGAGCTGTTTCGTGC
NM_001109	ADAM8	7710	ACCCAGGACCACAGCAAGAAC
NM_001109	ADAM8	7711	ACGAAGGACATGTGTGACCTC
NM_001109	ADAM8	7712	ACAGCAGGTCATCAAGCCAAC
NM_001622	AHSG	7713	ACGTAAAGGTGTGGCCTCAGC
NM_001622	AHSG	7714	ACGGTGCCAATGAAGCAGTCC
NM_001622	AHSG	7715	ACACACGCACAGTGGTGCAGC
NM_014767	KIAA0275	7716	ACTGGCTGTGCTCCATCTCGC
NM_014767	KIAA0275	7717	ACGAAGCTGGAGCACAGGATC
NM_014767	KIAA0275	7718	ACGAAGCCAGGCATCTTCATC

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NM_014871	KIAA0710	7719	ACGGTTTCCCTGAGAGACCTC
NM_014871	KIAA0710	7720	ACAGTTGGAGAGACCTACCAC
NM_014871	KIAA0710	7721	ACGGACTTCCGGGTCATCAAC
NM_016352	LOC51200	7722	ACTCTCCCTCCTCCTTCAATC
NM_016352	LOC51200	7723	ACCCCTTGCTCCGAAGTGTAC
NM_016352	LOC51200	7724	ACTTTCAAGGGCTTCATCGAC
NM_007058	CAPN11	7725	ACCTGCTATACCGCGTGGTGC
NM_007058	CAPN11	7726	ACTGTTGTGGTCTGCACCTGC
NM_007058	CAPN11	7727	ACAGCAGGCATCAAGCTGAAC
NM_012122	CES3	7728	ACGCAAGAGTTTGGCTGGATC
NM_012122	CES3	7729	ACGAAAGACCTGTTCCAGGAC
NM_005932	MIPEP	7730	ACCTTGTGGATTCCCTTGATC
NM_005932	MIPEP	7731	ACTCACCAGATGACTTGGTGC
NM_005932	MIPEP	7732	ACTCTACCATGGGAAGCATCC
NM_006846	SPINK5	7733	ACTGTGCCATGAATTTTCAGGC
NM_006846	SPINK5	7734	ACGGAAGGCGAATCAAGAAAC
NM_006846	SPINK5	7735	ACAGAGGATGAAGACAGGAGC
NM_019609	CPX-1	7736	ACCAAGAAACAGGCTGTCTC
NM_019609	CPX-1	7737	ACGGTCCAGTTCAGCAATGAC
NM_019609	CPX-1	7738	ACCCAGAGCATCGATCTTAAC
NM_019844	SLC21A8	7739	ACCCATTCTTACGGTTGCAAC
NM_019844	SLC21A8	7740	ACCATGTATGAAGTGGTCCAC
NM_019844	SLC21A8	7741	ACAGATACCAAGGCATCGGAC
NM_020426	LOC57151	7742	ACTGCAGATGGAAGCTTTGAC
NM_020426	LOC57151	7743	ACGATCTGCTGAATCCCAACC
NM_020426	LOC57151	7744	ACCCCTTCTTGCCAGGCATCCAC
NM_005143	HP	7745	ACGCCCCAAGAATCCGGCAAAC
NM_020995	HPR	7745	ACGCCCCAAGAATCCGGCAAAC
NM_020995	HPR	7746	ACCGCATTATGAAGGCAGCAC
NM_020995	HPR	7747	ACGTACCAGGAAGACACCTGC
NM_003291	TPP2	7748	ACGAGTGCTTAAGATTCTGCTC
NM_003291	TPP2	7749	ACGTGCTGGAAATAATGGTCC
NM_003291	TPP2	7750	ACTAACCGTGGCATCTACCTC
NM_003235	TG	7751	ACCGGCCTTTCTGAAGCAAGC
NM_003235	TG	7752	ACACCACCCTGTACCGGATAC
NM_003235	TG	7753	ACGGAAGCTATGAGGATGTCC
NM_000444	PHEX	7754	ACGCTAAACAGGAGTACTGCC
NM_000444	PHEX	7755	ACATCCGACGACTGTCAATGC
NM_000444	PHEX	7756	ACCAAGTCCAAATTGGTGCTC
NM_002639	SERPINB5	7757	ACTGTCCTCTTCTCTCCAATC
NM_002639	SERPINB5	7758	ACTCCTTGTTGGTTAATGCTGC
NM_002639	SERPINB5	7759	ACAGATGATTGATCCCAAGGC
NM_000613	HPX	7760	ACGGTCACAACAGTGTCTTTC
NM_000613	HPX	7761	ACCCAATTCTGCGCTTCGAC
NM_000613	HPX	7762	ACTGGGACTGGCCATGGGAAC
NM_021111	RECK	7763	ACACATCTGTTGCAGCGAGCC

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NM_021111	RECK	7764	ACGGGACACTAATCCAGGTGC
NM_021111	RECK	7765	ACGCAGAGAAGATTGAGTCCC
NM_001748	CAPN2	7766	ACCTATGCAGGGATCTTTCAC
NM_001748	CAPN2	7767	ACAGCGCCAAGATATCAAGTC
NM_001748	CAPN2	7768	ACTAGAGCTCGACCTTATCTC
NM_005186	CAPN1	7769	ACTGCCATCAAGTACCTGGGC
NM_005186	CAPN1	7770	ACGGCTCCCAGTGACCTCTAC
NM_005186	CAPN1	7771	ACCACCACACTCTACGAAGGC
AJ012755	HSA012755	7772	ACGAAGAAGTGGATGCCAGC
NM_004505	USP6	7772	ACGAAGAAGTGGATGCCAGC
NM_145809	LOC220594	7772	ACGAAGAAGTGGATGCCAGC
X63546	HSTRE210	7772	ACGAAGAAGTGGATGCCAGC
X63547	HSTRE213	7772	ACGAAGAAGTGGATGCCAGC
XM_165948	USP6	7772	ACGAAGAAGTGGATGCCAGC
NM_016192	TMEFF2	7773	ACGTGACTGCCAAACGCCCAC
NM_016192	TMEFF2	7774	ACTATGCAGGAGCCATCTTGC
NM_016192	TMEFF2	7775	ACATACAGGGCACTACAGTTC
NM_021804	ACE2	7776	ACGCCGAAGACCTGTTCTATC
NM_021804	ACE2	7777	ACTGGACGACTTCCTGACAGC
NM_021804	ACE2	7778	ACTGTAAGGCCACTGCTCAAC
NM_000055	BCHE	7779	ACTTCCCTATGCACAGCCACC
NM_000055	BCHE	7780	ACATGTATGGATTCCAGCACC
NM_000055	BCHE	7781	ACCACCGATCCTCCAAACTTC
NM_000665	ACHE	7782	ACTGACACAGAGCTGGTAGCC
NM_015831	ACHE	7782	ACTGACACAGAGCTGGTAGCC
NM_000665	ACHE	7783	ACATTGCTCAGCGCCACCGAC
NM_000902	MME	7784	ACAGATGTCCTTCAAGAACCC
NM_007287	MME	7784	ACAGATGTCCTTCAAGAACCC
NM_007288	MME	7784	ACAGATGTCCTTCAAGAACCC
NM_007289	MME	7784	ACAGATGTCCTTCAAGAACCC
NM_000902	MME	7785	ACGGAGTCCAGAAATGCTTTC
NM_007287	MME	7785	ACGGAGTCCAGAAATGCTTTC
NM_007288	MME	7785	ACGGAGTCCAGAAATGCTTTC
NM_007289	MME	7785	ACGGAGTCCAGAAATGCTTTC
NM_000902	MME	7786	ACAGATGGAGACCTCGTTGAC
NM_007287	MME	7786	ACAGATGGAGACCTCGTTGAC
NM_007288	MME	7786	ACAGATGGAGACCTCGTTGAC
NM_007289	MME	7786	ACAGATGGAGACCTCGTTGAC
NM_003812	ADAM23	7787	ACGGGTGGAGAGCACTGTTAC
NM_003812	ADAM23	7788	ACGAGAAGCAGTCTGAGTTAC
NM_003812	ADAM23	7789	ACGCAAGACGGATATGCATGC
NM_002056	GFPT1	7790	ACTAGCTCATACCCGTTGGGC
NM_002056	GFPT1	7791	ACCACAATGAGAGGAAGAGTC
NM_002056	GFPT1	7792	ACAGACGCAAAGAGATCATGC
NM_005265	GGT1	7793	ACGCTGAGGTCATCAACGCC
NM_013421	GGT1	7793	ACGCTGAGGTCATCAACGCC

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NM_013430	GGT1	7793	ACGCTGAGGTCATCAACGCCC
NM_005265	GGT1	7794	ACCATCCTCAAAGGGTACAAC
NM_013421	GGT1	7794	ACCATCCTCAAAGGGTACAAC
NM_013430	GGT1	7794	ACCATCCTCAAAGGGTACAAC
NM_005265	GGT1	7795	ACTGGACGACTTCAGCTCTCC
NM_013421	GGT1	7795	ACTGGACGACTTCAGCTCTCC
NM_013430	GGT1	7795	ACTGGACGACTTCAGCTCTCC
NM_080839	GGTL4	7795	ACTGGACGACTTCAGCTCTCC
XM_086868	LOC257456	7795	ACTGGACGACTTCAGCTCTCC
NM_007038	ADAMTS5	7796	ACGGTGGGCTACCTCGTCTAC
NM_007038	ADAMTS5	7797	ACATGGCTATCAGTCTGATGC
NM_007038	ADAMTS5	7798	ACCTATAGCGGTTGGAGCCAC
NM_014244	ADAMTS2	7799	ACCGAGCAATGCCGCTTTGAC
NM_021599	ADAMTS2	7799	ACCGAGCAATGCCGCTTTGAC
NM_014244	ADAMTS2	7800	ACGATGGTACACCGTGGCTTC
NM_014244	ADAMTS2	7801	ACTGCCGTAGATGAACCCTAC
NM_014272	ADAMTS7	7802	ACGCGGGATGTATCTGTGCGC
NM_014272	ADAMTS7	7803	ACGATCACGCACCATGCAGAC
NM_014272	ADAMTS7	7804	ACGAACGTGGGCTGTGACTTC
NM_004562	PARK2	7805	ACTGCAACTGGAGGCGACGAC
NM_013987	PARK2	7805	ACTGCAACTGGAGGCGACGAC
NM_004562	PARK2	7806	ACACACCAGTAGCTTTGCACC
NM_013987	PARK2	7806	ACACACCAGTAGCTTTGCACC
NM_013988	PARK2	7806	ACACACCAGTAGCTTTGCACC
NM_004562	PARK2	7807	ACGAGCAGTACAACCGGTACC
NM_013987	PARK2	7807	ACGAGCAGTACAACCGGTACC
NM_013988	PARK2	7807	ACGAGCAGTACAACCGGTACC
NM_004562	PARK2	7808	ACGCCTCAGGAACAACACTACTC
NM_013987	PARK2	7808	ACGCCTCAGGAACAACACTACTC
NM_013988	PARK2	7808	ACGCCTCAGGAACAACACTACTC
NM_015831	ACHE	7809	ACCCCGCCCCAATGTCCGATC
NM_001640	APEH	7810	ACCTGCTGAGCAGAGAGTCTC
NM_001640	APEH	7811	ACCTTCTCTGGGATCTACTGC
NM_001640	APEH	7812	ACCAGGTGCTCCAGGAGG AAC
NM_003183	ADAM17	7813	ACACGAAAGCGAGTACACTGC
NM_003183	ADAM17	7814	ACCCACCTGAAGAGCTTGTTT
NM_021832	ADAM17	7814	ACCCACCTGAAGAGCTTGTTT
NM_003183	ADAM17	7815	ACGCTGACCTGGTTACAACCTC
NM_021832	ADAM17	7815	ACGCTGACCTGGTTACAACCTC
NM_003183	ADAM17	7816	ACCTGTCAAGTTTGAGACTGCC
NM_021832	ADAM17	7816	ACCTGTCAAGTTTGAGACTGCC
NM_014269	ADAM29	7817	ACGCAAAGTTCTTATGTGGGC
NM_021779	ADAM29	7817	ACGCAAAGTTCTTATGTGGGC
NM_021780	ADAM29	7817	ACGCAAAGTTCTTATGTGGGC
NM_014269	ADAM29	7818	ACGTCGGAGAACATTACGCCC
NM_021779	ADAM29	7818	ACGTCGGAGAACATTACGCCC

NM_021780	ADAM29	7818	ACGTCGGAGAACATTACGCCC
NM_014269	ADAM29	7819	ACAGTGTGTAGAAAGGAGGTC
NM_021779	ADAM29	7819	ACAGTGTGTAGAAAGGAGGTC
NM_021780	ADAM29	7819	ACAGTGTGTAGAAAGGAGGTC
NM_014269	ADAM29	7820	ACCCTCCTGTGATGCCCTTCCC
NM_020334	ADAM30	7821	ACGTCACCATTTCCTGAGAAGC
NM_021794	ADAM30	7821	ACGTCACCATTTCCTGAGAAGC
NM_020334	ADAM30	7822	ACGTTGCAACCAGGTGCCAAC
NM_021794	ADAM30	7822	ACGTTGCAACCAGGTGCCAAC
NM_020334	ADAM30	7823	ACCCCATGGGAATACCTGACC
NM_021794	ADAM30	7823	ACCCCATGGGAATACCTGACC
NM_006988	ADAMTS1	7824	ACCTGGCAGAAGCAGCACAAC
NM_006988	ADAMTS1	7825	ACCCAAACACTTCCCCTGGGC
NM_006988	ADAMTS1	7826	ACTTGGGTTGGCAGAGAAGAC
NM_003474	ADAM12	7827	ACGTTGTGTCAGTGCCCTCTGTTC
NM_021641	ADAM12	7827	ACGTTGTGTCAGTGCCCTCTGTTC
NM_003474	ADAM12	7828	ACAGGAGGCTGCATCATGAAC
NM_021641	ADAM12	7828	ACAGGAGGCTGCATCATGAAC
NM_021641	ADAM12	7829	ACGGCAGGAAGCTGCAGAGTC
NM_003815	ADAM15	7830	ACGTTGGAGCTGGACGGTGAC
NM_003815	ADAM15	7831	ACTCCAAGATCTCCACCTGCC
NM_003815	ADAM15	7832	ACCTCCATCTGTCTCCTGAC
NM_001464	ADAM2	7833	ACATCTGTGGTGATGGTTAGC
NM_001464	ADAM2	7834	ACCTGTGCTGAAGGACCATGC
NM_001464	ADAM2	7835	ACGTGGACATCTCTGCATTGC
NM_002425	MMP10	7836	ACGGATCTTGCCCAGCAATAC
NM_002425	MMP10	7837	ACCTCATTACAGAGCTCGCC
NM_002425	MMP10	7838	ACGTGTGATCCTGCTTTGTCC
NM_002429	MMP19	7839	ACCTTCCAGTCTCAGGTCAGC
NM_002429	MMP19	7840	ACTTTCAAGATGTCTCCTGGC
NM_022790	MMP19	7840	ACTTTCAAGATGTCTCCTGGC
NM_022791	MMP19	7840	ACTTTCAAGATGTCTCCTGGC
NM_022792	MMP19	7840	ACTTTCAAGATGTCTCCTGGC
NM_002429	MMP19	7841	ACCTGGATGCACTGTCGTCCC
NM_022790	MMP19	7841	ACCTGGATGCACTGTCGTCCC
NM_022791	MMP19	7841	ACCTGGATGCACTGTCGTCCC
NM_022792	MMP19	7841	ACCTGGATGCACTGTCGTCCC
NM_002426	MMP12	7842	ACATGCAGCACTTCTTGGGTC
NM_002426	MMP12	7843	ACGGAGACAGATGATGGACCC
NM_002428	MMP15	7844	ACCTACACGGAGAAGTTGGGC
NM_002428	MMP15	7845	ACTGCCATCATGGCGCCGTTTC
NM_002428	MMP15	7846	ACTTCGACAATGAGCGCCTGC
NM_005940	MMP11	7847	ACGAGGTTTCGTGCTTTCTGGC
NM_005940	MMP11	7848	ACGATCTACTTCTCCGAGGC
NM_002427	MMP13	7849	ACGGAGCATGGCGACTTCTAC
NM_002427	MMP13	7850	ACGACAGATTCTTCTGGCGCC

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NM_002427	MMP13	7851	ACTACAGCATCTGGAGTAACC
NM_004995	MMP14	7852	ACCATTGGAGGAGACACCCAC
NM_004995	MMP14	7853	ACATGACATCTTCCTGGTGGC
NM_004995	MMP14	7854	ACGCTGAAGGTAGAACCGGGC
NM_004142	MMPL1	7855	ACGGGATGTAAGGGATATGGC
NM_002421	MMP1	7856	ACGAGCAGATGTGGACCATGC
NM_002421	MMP1	7857	ACGCCATATATGGACGTTCCT
NM_002421	MMP1	7858	ACTGGGCTTGAAGCTGCTTAC
NM_005941	MMP16	7859	ACTTGACTGGATGAAGAAGCC
NM_022564	MMP16	7859	ACTTGACTGGATGAAGAAGCC
NM_005941	MMP16	7860	ACGATATATGGTCCACCTGAC
NM_022564	MMP16	7860	ACGATATATGGTCCACCTGAC
NM_022564	MMP16	7861	ACAGGCAGTCAGTGCCTGTGC
NM_002424	MMP8	7862	ACGCAACCAGTATCAGTCTAC
NM_002424	MMP8	7863	ACGGTATTGGAGGAGATGCTC
NM_002424	MMP8	7864	ACGCATATCAGGTGCCTTTCC
NM_004771	MMP20	7865	ACGTCACCGGGAAGTTAGACC
NM_004771	MMP20	7866	ACGATGATGTGAAAGGGATCC
NM_004771	MMP20	7867	ACATAGATGCTGCTGTCTACC
NM_021251	CAPN10	7868	ACCCAGGATTGACAGGCCATC
NM_023083	CAPN10	7868	ACCCAGGATTGACAGGCCATC
NM_023084	CAPN10	7868	ACCCAGGATTGACAGGCCATC
NM_023085	CAPN10	7868	ACCCAGGATTGACAGGCCATC
NM_023086	CAPN10	7868	ACCCAGGATTGACAGGCCATC
NM_023087	CAPN10	7868	ACCCAGGATTGACAGGCCATC
NM_023088	CAPN10	7868	ACCCAGGATTGACAGGCCATC
NM_023089	CAPN10	7869	ACGACCTGAAACTCTACCAAC
NM_014289	CAPN6	7870	ACGACAGGAATGGAGTGGCCC
NM_014289	CAPN6	7871	ACCTATGTGCTTGTCCCAACC
NM_014289	CAPN6	7872	ACTGTGGAAAGGAGGAAGTCC
NM_006178	NSF	7873	ACTCCATGGATCCTAGCATCC
NM_006178	NSF	7874	ACGGCCGACTACAGATTCTTC
NM_006178	NSF	7875	ACCGCTTTCAGCACCACCATC
NM_021102	SPINT2	7876	ACTGCAGCGGATTCTCTGTC
NM_021102	SPINT2	7877	ACCTTCATCTATGGAGGCTGC
NM_020998	MST1	7878	ACGAAAGACTACGTACGGACC
NM_020998	MST1	7879	ACTACGCGTGCAAAGACCTTC
NM_020998	MST1	7880	ACTCGGCAGGGCCAGCATTTTC
NM_025054	FLJ23132	7881	ACGAATCAGAGTCTCAGCTCC
NM_025054	FLJ23132	7882	ACGGAGAAGAAGATCCGAATC
NM_025054	FLJ23132	7883	ACGAGGCTGTAAGTCAGGTTC
NM_003791	MBTPS1	7884	ACGGAGAGAACCAACTGGACC
NM_003791	MBTPS1	7885	ACTGTCACCATCTCAACGGC
NM_003791	MBTPS1	7886	ACGTTTCCAGAAGATGGCGTC
NM_000412	HRG	7887	ACGAATCGGACTGTTCCGGTCC
NM_000412	HRG	7888	ACGTCTTCGACCCTCAGGAAC

NM_000412	HRG	7889	ACTTCCAGTGACCTCCATCCC
NM_017493	HSHIN1	7890	ACGAAAGCTCTGCTATGTGTC
NM_017493	HSHIN1	7891	ACGCTCTGCTATGTGTCAGTC
NM_001642	APLP2	7892	ACGTGATGTCCTGCTAGTTCC
NM_001642	APLP2	7893	ACGATCGCTTACATACCATCC
NM_001642	APLP2	7894	ACCAAGATGCAGAACCATGGC
AJ242586	HSA242586	7895	ACTGGAGAACCCTTGTCTGAC
NM_020216	RNPEP	7895	ACTGGAGAACCCTTGTCTGAC
AJ242586	HSA242586	7896	ACGGCCTATGTGCATGAATTC
NM_020216	RNPEP	7896	ACGGCCTATGTGCATGAATTC
AJ242586	HSA242586	7897	ACTGCCCGGAATGCAGAGCTC
NM_020216	RNPEP	7897	ACTGCCCGGAATGCAGAGCTC
NM_006313	USP15	7898	ACGATGGTGATGCCCAGTCAC
NM_006313	USP15	7899	ACTGGCATACATGAAGAAGGC
NM_006313	USP15	7900	ACCTAAAGGTGCTTCAGCTGC
NM_000091	COL4A3	7901	ACTGTGGAGATCCTGGTCTTC
NM_031362	COL4A3	7901	ACTGTGGAGATCCTGGTCTTC
NM_031363	COL4A3	7901	ACTGTGGAGATCCTGGTCTTC
NM_031364	COL4A3	7901	ACTGTGGAGATCCTGGTCTTC
NM_031365	COL4A3	7901	ACTGTGGAGATCCTGGTCTTC
NM_031366	COL4A3	7901	ACTGTGGAGATCCTGGTCTTC
NM_000091	COL4A3	7902	ACAGGGAGACCCAGGAATTCC
NM_031362	COL4A3	7902	ACAGGGAGACCCAGGAATTCC
NM_031363	COL4A3	7902	ACAGGGAGACCCAGGAATTCC
NM_031364	COL4A3	7902	ACAGGGAGACCCAGGAATTCC
NM_031365	COL4A3	7902	ACAGGGAGACCCAGGAATTCC
NM_031366	COL4A3	7902	ACAGGGAGACCCAGGAATTCC
NM_032549	IMMP2L	7903	ACTCTGTTCTTCCTCCAGAGC
NM_001710	BF	7904	ACGGCAGAGTGCAGAGCAATC
NM_020249	ADAMTS9	7905	ACGACAGGATATCTGCAGAGC
NM_020249	ADAMTS9	7906	ACTATTGATGTGCGGCAGCAC
NM_015571	SUSP1	7907	ACGAATACCCACCTCATGTCC
NM_015571	SUSP1	7908	ACGCATATCTCCTCAGCCTGC
AJ312398	HSA312398	7909	ACGGTCTGAAAGTTTGGGTCC
AJ312399	HSA312399	7909	ACGGTCTGAAAGTTTGGGTCC
NM_033029	LMLN	7909	ACGGTCTGAAAGTTTGGGTCC
NM_004346	CASP3	7910	ACGGATGGCTCCTGGTTCATC
NM_032991	CASP3	7910	ACGGATGGCTCCTGGTTCATC
NM_001224	CASP2	7911	ACTGAGGGAGCTCATCCAGGC
NM_032982	CASP2	7911	ACTGAGGGAGCTCATCCAGGC
NM_032983	CASP2	7911	ACTGAGGGAGCTCATCCAGGC
NM_032984	CASP2	7911	ACTGAGGGAGCTCATCCAGGC
NM_001224	CASP2	7912	ACGATGGTCTGTCTGCCTTC
NM_001226	CASP6	7913	ACAGCAGAAGAACTACTGCTC
NM_001230	CASP10	7914	ACCATCTCTTGGCAGAGGATC
NM_032976	CASP10	7914	ACCATCTCTTGGCAGAGGATC

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NM_032977	CASP10	7914	ACCATCTCTTGGCAGAGGATC
NM_001230	CASP10	7915	ACGAGTGGACAAACAGGGAAC
NM_032976	CASP10	7915	ACGAGTGGACAAACAGGGAAC
NM_032977	CASP10	7915	ACGAGTGGACAAACAGGGAAC
NM_014629	ARHGEF10	7916	ACGAATGGGATTCCCAGGTCC
NM_014629	ARHGEF10	7917	ACGAGAGATGCTGATCAACGC
NM_014629	ARHGEF10	7918	ACGACCAGAAGGACGCACTTC
NM_015984	UCH37	7919	ACTGCTTGTGCTACTCAAGCC
NM_015984	UCH37	7920	ACCACCAGCAGTTAATACCAC
NM_004826	ECEL1	7921	ACCTCCTCGCGCTACGTCATC
NM_004826	ECEL1	7922	ACCATCTTGAACAGCATCCGC
NM_004826	ECEL1	7923	ACGTACACACATGACCAGCTC
NM_006102	PGCP	7924	ACGATGGGCTGGAGAAAGTTC
NM_016134	PGCP	7924	ACGATGGGCTGGAGAAAGTTC
NM_006102	PGCP	7925	ACGGTGGAGTTGGTGCCTTCC
NM_016134	PGCP	7925	ACGGTGGAGTTGGTGCCTTCC
NM_001223	CASP1	7926	ACTGGACAAGTCAAGCCGCAC
NM_033292	CASP1	7926	ACTGGACAAGTCAAGCCGCAC
NM_033293	CASP1	7926	ACTGGACAAGTCAAGCCGCAC
NM_033294	CASP1	7926	ACTGGACAAGTCAAGCCGCAC
NM_001223	CASP1	7927	ACCCGAAGGTGATCATCATCC
NM_033292	CASP1	7927	ACCCGAAGGTGATCATCATCC
NM_033293	CASP1	7927	ACCCGAAGGTGATCATCATCC
NM_033294	CASP1	7927	ACCCGAAGGTGATCATCATCC
NM_001223	CASP1	7928	ACGATGTTTCTACCTCTTCCC
NM_033292	CASP1	7928	ACGATGTTTCTACCTCTTCCC
NM_033293	CASP1	7928	ACGATGTTTCTACCTCTTCCC
NM_033294	CASP1	7928	ACGATGTTTCTACCTCTTCCC
NM_033295	CASP1	7928	ACGATGTTTCTACCTCTTCCC
NM_013379	DPP7	7929	ACCTTCGAGCGCTTCGGCAAC
NM_013379	DPP7	7930	ACGGACCTGACCCAGCTCTTC
NM_030955	ADAMTS12	7931	ACGATGATGGCTTCCTCTGCC
NM_030955	ADAMTS12	7932	ACTGGGAGACAGAAGAAGTGC
NM_005467	NAALAD2	7933	ACCTATGCTCGCACTGAAGAC
NM_004598	SPOCK	7934	ACACTGGAATCCCAACAAGCC
NM_004598	SPOCK	7935	ACAGAGGATGAGGTCGGGTAC
NM_001971	ELA1	7936	ACCAACAGTCCCTGCTACATC
NM_001971	ELA1	7937	ACTAATGTCACTCGCCTCCAAC
NM_001228	CASP8	7938	ACTGACAATCTCGGACTCTCC
NM_033355	CASP8	7938	ACTGACAATCTCGGACTCTCC
NM_033356	CASP8	7938	ACTGACAATCTCGGACTCTCC
NM_033357	CASP8	7938	ACTGACAATCTCGGACTCTCC
NM_003814	ADAM20	7939	ACGCTGTTGTTTGCTGCACAC
NM_003814	ADAM20	7940	ACCAACACTGTCACTGCAACC
NM_033467	MMEL2	7941	ACCCGTGTGACGACTTCTACC
NM_033467	MMEL2	7942	ACGAGCATGGTCAGAGAACTC

NM_033467	MMEL2	7943	ACTCCATCAAGACAGACGTCC
NM_032857	MRPL56	7944	ACCAGAGCAGGAGAATGAAGC
NM_004347	CASP5	7945	ACGATGTTGGAATACCTGGGC
NM_004347	CASP5	7946	ACTATTCTTGCTGCTGCCACC
NM_020886	USP28	7947	ACAGGGAGCATTCGGATCATC
NM_020886	USP28	7948	ACTGGAGTCCTCCACCAACTC
NM_014296	CAPN7	7949	ACCAGTTGGCTCGACAGGCAC
NM_014296	CAPN7	7950	ACAGTGGAGTGGTCAGAGTGC
NM_006615	CAPN9	7951	ACAGTGGAGATCTGCAACCTC
NM_002581	PAPPA	7952	ACGTGACCACCATCAATGCCC
NM_002581	PAPPA	7953	ACTCCTGGTGCAGTATGCTTC
NM_002581	PAPPA	7954	ACGTATAAGGTGGTCCGGGAC
NM_053284	WFIKKN	7955	ACCGTGTGTGGACTGCACAGC
NM_001872	CPB2	7956	ACTGTGAGCGGAATTCATGC
NM_016413	CPB2	7956	ACTGTGAGCGGAATTCATGC
NM_001872	CPB2	7957	ACCCTACTGTGGACTTTATCC
NM_016413	CPB2	7957	ACCCTACTGTGGACTTTATCC
NM_001872	CPB2	7958	ACGACCATGAGGAAGTGTCTC
NM_016413	CPB2	7958	ACGACCATGAGGAAGTGTCTC
NM_033423	CTLA1	7959	ACGAAGACACAGACCGGTTTC
NM_025090	KIAA1453	7960	ACCACCTGCTTTCTCAATGCC
NM_025090	KIAA1453	7961	ACCGTCAAGGTGGTTCGAAC
NM_025090	KIAA1453	7962	ACAGAAGGTGAAGAAGCCAGC
NM_006590	SAD1	7963	ACTGTTCTCTCTCTCCGGAAC
NM_006590	SAD1	7964	ACGGAGCAGCTCATCATTCCC
NM_021627	SENP2	7965	ACCAGTCTCTACAATGCTGCC
NM_021627	SENP2	7966	ACCCACACGAGATTCTCAAC
NM_021626	RISC	7967	ACATGGCAGCTGGCATTGGTC
NM_021626	RISC	7968	ACCTGAAGTGGCCAGAAGTGC
NM_032859	FLJ14906	7969	ACTCTCTCAGTGTAGAATGCC
NM_018235	FLJ10830	7970	ACGGATGTGGACTATGTCTGC
NM_024778	FLJ22612	7971	ACGTTGGCTCCAAATGACCAC
NM_024778	FLJ22612	7972	ACCCTGCTCTCAGTTTACCAC
NM_024778	FLJ22612	7973	ACCACAGCCGACATTGAATAC
NM_023112	FLJ21916	7974	ACACATCCCACTACAACATCC
NM_000094	COL7A1	7975	ACATGGCAGCCCTGGATCATC
NM_006660	CLPX	7976	ACTGTGGCGACTTGTGCACAC
NM_002402	MEST	7977	ACGGGACTGCGTATCTTCTAC
NM_002402	MEST	7978	ACGATTTGGAAGGGTCTGACC
NM_005632	SOLH	7979	ACGCCCCGACCTCAACCACATC
NM_005632	SOLH	7980	ACGAAGTTCGTCAGCTGCGAC
NM_012072	C1QR1	7981	ACCCTGGCCACTGTGAAGAGC
NM_012072	C1QR1	7982	ACGGTGACAAGGACGAGACTC
NM_012072	C1QR1	7983	ACTGCGGCAGACAGTTACTCC
NM_003652	CPZ	7984	ACGTGGATGCAGACCATACCC
NM_003878	GGH	7985	ACGTGTTGACCTCAGACGCTC

NM_003878	GGH	7986	ACCCTCTGACTGCCAATTTC
NM_031907	USP26	7987	ACAGGAAGTGGGACAGGTGTC
NM_031907	USP26	7988	ACAGATATCCTGGCTCCACAC
NM_031907	USP26	7989	ACAGAGAAGAGAATGCCCAGC
NM_006012	CLPP	7990	ACCTCCCGTATCATGATCCAC
NM_006796	AFG3L2	7991	ACGGGTGACATTCCATGGGAC
NM_006796	AFG3L2	7992	ACGTTCAAAGATGTGGCTGGC
NM_006796	AFG3L2	7993	ACGAACAGTAGCTCTTCTCAC
NM_012291	ESPL1	7994	ACTCTACCGTTGTCTGGATGC
NM_012291	ESPL1	7995	ACCCAGCCATCAAACGAGAGC
NM_012291	ESPL1	7996	ACGTACATCATGGCTGGTTGC
NM_000537	REN	7997	ACCCCATGAAGAGGCTGACAC
NM_002792	PSMA7	7998	ACGGATAGTCATCAACAGGGC
NM_002792	PSMA7	7999	ACGCAGCGTTATACGCAGAGC
NM_000638	VTN	8000	ACGTGCCAGTGTGACGAGCTC
NM_000638	VTN	8001	ACGGGTAGTCAGTACTGGCGC
NM_025220	ADAM33	8002	ACCCACACGGATCATTGCCAC
NM_004654	USP9Y	8003	ACAGGTTGGCTAGTGGATCTC
NM_001641	APEX	8004	ACTGTGGATGGGCTTCGAGCC
NM_080648	APEX	8004	ACTGTGGATGGGCTTCGAGCC
NM_080649	APEX	8004	ACTGTGGATGGGCTTCGAGCC
NM_022122	MMP27	8005	ACATGTGCAACTGGCTCAGGC
NM_022122	MMP27	8006	ACCCTGCTAAGCCAAAGGAAC
NM_022122	MMP27	8007	ACCCATGGACAAAGGGTTCCC
NM_005857	ZMPSTE24	8008	ACGCACTTTTCAGCTTCTGGTC
NM_016155	MMP17	8009	ACGCAGGTTGCGTTACCTGCC
NM_004659	MMP23A	8010	ACGTGTACTGGTACAAGGACC
NM_006983	MMP23B	8010	ACGTGTACTGGTACAAGGACC
NM_004659	MMP23A	8011	ACTGAGGGCACCTACACCTGC
NM_006983	MMP23B	8011	ACTGAGGGCACCTACACCTGC
NM_032557	HP43.8KD	8012	ACCCAGGAGGTGAAACCACAC
NM_007352	ELA3B	8013	ACGCGGAAGCTTCTACCACAC
NM_007352	ELA3B	8014	ACCGAGACACCCTGCTACATC
NM_001266	CES1	8015	ACGAGAACATTCTCTCAAGC
NM_016280	LOC51716	8015	ACGAGAACATTCTCTCAAGC
NM_130901	LOC161725	8016	ACCAAGCTGGGCAGCTTCAGC
NM_001225	CASP4	8017	ACCGTATGGCAGGACAAATGC
NM_033306	CASP4	8017	ACCGTATGGCAGGACAAATGC
NM_033307	CASP4	8017	ACCGTATGGCAGGACAAATGC
NM_001225	CASP4	8018	ACTGGGCTCTATCTTCATCAC
NM_033306	CASP4	8018	ACTGGGCTCTATCTTCATCAC
NM_033307	CASP4	8018	ACTGGGCTCTATCTTCATCAC
NM_001225	CASP4	8019	ACTATTCTTGGTGCTGCCACC
NM_033306	CASP4	8019	ACTATTCTTGGTGCTGCCACC
NM_033307	CASP4	8019	ACTATTCTTGGTGCTGCCACC
NM_032236	FLJ23277	8020	ACGTCTCAGACACGTAAACCC

NM_020398	SPINLW1	8021	ACGGACAGACAATGCCAGGAC
NM_020398	SPINLW1	8022	ACGTGTTGTGTCTTCAGCTGC
NM_014375	FETUB	8023	ACCAACCCAAGTAGAGTTCTC
NM_014375	FETUB	8024	ACGGTTCTCTGACTCGAACAC
NM_020241	SEMA6B	8025	ACCTGCTCTGTACCCGGAGAC
NM_032108	SEMA6B	8025	ACCTGCTCTGTACCCGGAGAC
NM_133327	SEMA6B	8025	ACCTGCTCTGTACCCGGAGAC
NM_052955	TGM7	8026	ACTTCAACTGGACCTCTACCC
NM_080830	CST11	8027	ACGGACAGCTTGCACTGGATC
NM_130794	CST11	8027	ACGGACAGCTTGCACTGGATC
NM_080830	CST11	8028	ACAGTCCAGAGGCAGCAAGTC
NG_000839	NG_000839	8029	ACGGCCACTGAAGATGAGTAC
NM_001322	CST2	8029	ACGGCCACTGAAGATGAGTAC
NG_000839	NG_000839	8030	ACTTCCAGGTGTCAAGAAGCC
NM_001322	CST2	8030	ACTTCCAGGTGTCAAGAAGCC
NM_001899	CST4	8030	ACTTCCAGGTGTCAAGAAGCC
NG_000839	NG_000839	8031	ACGAAGCCTAGGGATCTGTGC
NM_001322	CST2	8031	ACGAAGCCTAGGGATCTGTGC
NM_000099	CST3	8032	ACAGCCAGCAACGACATGTAC
NM_000099	CST3	8033	ACGACCCAGCCCAACTTGGAC
NG_000839	NG_000839	8034	ACTAGGATAATCCCAGGTGGC
NM_001899	CST4	8034	ACTAGGATAATCCCAGGTGGC
NG_000839	NG_000839	8035	ACGGCCACCGAAGATGAGTAC
NM_001899	CST4	8035	ACGGCCACCGAAGATGAGTAC
NG_000839	NG_000839	8036	ACGGATGAGTACTACAGCCGC
NM_001900	CST5	8036	ACGGATGAGTACTACAGCCGC
NM_005492	CST8	8037	ACGCAGTGTCTGTGGTTTGCC
NM_005492	CST8	8038	ACGTATGTCTTCTGGTGGTC
NM_080610	CST9L	8039	ACGACCTGCTTGGAGGGATTC
NM_006310	NPEPPS	8040	ACTGCTGCCACAGAGGATCTC
NM_005075	SLC21A3	8041	ACCAGGAGCTATTATTGGTCC
NM_021094	SLC21A3	8041	ACCAGGAGCTATTATTGGTCC
NM_134431	SLC21A3	8041	ACCAGGAGCTATTATTGGTCC
NM_021094	SLC21A3	8042	ACGAGTATTTGCTGGCATTCC
NM_022148	CRLF2	8042	ACGAGTATTTGCTGGCATTCC
NM_134431	SLC21A3	8042	ACGAGTATTTGCTGGCATTCC
NM_004917	KLK4	8043	ACCGAATTGTTCTGCTCGGGC
NM_004917	KLK4	8044	ACGTTGGACGAATCCGTGTCC
NM_004917	KLK4	8045	ACACCGTCCAGGCCAGTTAAC
NM_000628	IL10RB	8046	ACGACAAAGTACGCCTTCTCC
NM_002800	PSMB9	8047	ACCCCTGGGAGGAATGCTGAC
NM_002703	PPAT	8048	ACTCACACAAGGGAATGGGTC
NM_002703	PPAT	8049	ACCAGAAGGATGGGTGGTGTG
NM_002703	PPAT	8050	ACCCGGTATGTAGGGAGAACC
NM_004155	SERPINB9	8051	ACGTGAACAAGGCTGGCACAC
NM_004155	SERPINB9	8052	ACCTCACAGCCTGGACCAAGC

NM_004155	SERPINB9	8053	ACCAGCATTCTGTTCTGTGGC
NM_012397	SERPINB13	8054	ACCTGAACATAACCAACAGGC
NM_012397	SERPINB13	8055	ACAGGTGAATCTGCACTTGCC
NM_012397	SERPINB13	8056	ACGGTGAATCTGCACTTGCCC
AF134213	AF134213	8057	ACACAGGGCATTGAGGAGAC
NM_013396	USP25	8057	ACACAGGGCATTGAGGAGAC
AF134213	AF134213	8058	ACGGCCAAGCTAATGCTGGGC
NM_013396	USP25	8058	ACGGCCAAGCTAATGCTGGGC
AF134213	AF134213	8059	ACTGAGCAAGCCGCAGAACTC
NM_013396	USP25	8059	ACTGAGCAAGCCGCAGAACTC
NM_007192	FACTP140	8060	ACTGAGAATGCTAATGGAGCC
NM_007192	FACTP140	8061	ACGAGAAGCGAAGAGCACATC
NM_007192	FACTP140	8062	ACTGGTTGAATTCTGCGACC
NM_012465	TLL2	8063	ACGCACACCTGTGTGACCTTC
NM_012465	TLL2	8064	ACCATCTTGGGCAAGGGCTTC
NM_012465	TLL2	8065	ACTAAAGCGGGCTTTGCAGCC
NM_004079	CTSS	8066	ACGCCATGGATCAGAAATGTC
NM_004079	CTSS	8067	ACGCTGTGGCCAATAAAGGCC
NM_004079	CTSS	8068	ACTCATTGTGGGATTGCTAGC
NM_018226	RNPEPL1	8069	ACGGCTGAAGCAGACACAGAC
NM_024663	NPEPL1	8070	ACTGAGATGAACACCGACACC
NM_015884	MBTPS2	8071	ACCAACGGACTGAGCATCTCC
NM_015884	MBTPS2	8072	ACTGATGGCTGACTCTCCCTC
NM_015884	MBTPS2	8073	ACCTCTTTCTTGGATGCCACC
NM_002726	PREP	8074	ACCATACTGTCTGACGATGGC
NM_002726	PREP	8075	ACGGATGTGATCCAGTAAACC
NM_002726	PREP	8076	ACGGAAGGTTACACATCTCCC
NM_005551	KLK2	8077	ACCCTGTTTGAGCCTGAAGAC
NM_005551	KLK2	8078	ACCCAGAGGAGTTCTTGCGCC
NM_006002	UCHL3	8079	ACTCAGCAATGCCTGTGGAAC
NM_006002	UCHL3	8080	ACTGAGCCCTGAAGAACGAGC
NM_006002	UCHL3	8081	ACGAAGTTTATGGAGCGCGAC
NM_007282	RNF13	8082	ACCCAGAGAATGCCTGTGAAC
NM_007262	DJ-1	8083	ACACCGGAAGGGCCTGATAGC
NM_007262	DJ-1	8084	ACTGGAGGTCATTACACCTAC
NM_007262	DJ-1	8085	ACGACTAGAGCAGCGAACTGC
NM_080385	CPA5	8086	ACGATGAGAAGCAGCTTTTCAC
NM_080385	CPA5	8087	ACGTCCATCAGACCTGGAATC
NM_080385	CPA5	8088	ACGGTCCATGGGATCGAGTAC
NM_015907	LAP3	8089	ACGCTGAGAGAGACTTTGAAC
NM_015907	LAP3	8090	ACAGAAGATGGCTGTGTCGGC
NM_015907	LAP3	8091	ACCAGGTGCCATGGATGTAGC
NM_017509	KLK15	8092	ACAGCCGCTTCATGAGAGTGC
NM_023006	KLK15	8092	ACAGCCGCTTCATGAGAGTGC
NM_138563	KLK15	8092	ACAGCCGCTTCATGAGAGTGC
NM_138564	KLK15	8092	ACAGCCGCTTCATGAGAGTGC

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NM_002569	PACE	8093	ACGTACAGTGGCTGGAACAGC
NM_002569	PACE	8094	ACCACTATCTACACGCTGTCC
NM_002569	PACE	8095	ACCAACTATGGGACGCTGACC
NM_000439	PCSK1	8096	ACTGAATGGGCAGCGGAGATC
NM_000439	PCSK1	8097	ACGTTGGAGGCATAAGAATGC
NM_000439	PCSK1	8098	ACGAGGAGACCTTCATGTCAC
NM_002594	PCSK2	8099	ACGCGAGGTTACAGAGACATC
NM_002594	PCSK2	8100	ACCTCCAAGGTTGCAGGCATC
NM_002594	PCSK2	8101	ACGAGGAGCTGGAGGAAGAGC
NM_004716	PCSK7	8102	ACTGGCACCTGAATAACCGAC
NM_004716	PCSK7	8103	ACTGACATCTACAGCTGCAGC
NM_004716	PCSK7	8104	ACCAAGGCGATTCCGCACTCC
NM_005213	CSTA	8105	ACCTCAAGTTGTTGCTGGAAC
NM_005213	CSTA	8106	ACACAAGGATGACGAGCTGAC
NM_003184	TAF2	8107	ACGTATGGCAGAGAGAGGTGC
NM_003184	TAF2	8108	ACTCCGGCTTCCCCTCTACAC
NM_003184	TAF2	8109	ACATATCGGCCAGCTAGCTCC
NM_020903	USP29	8110	ACTGCATGTTGGTAGTGCTGC
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NM_020903	USP29	8112	ACGCAGAGAACTCTCGGCTAC
NM_021114	SPINK2	8113	ACCCCTGTGTGTGGCAGTGAC
NM_020726	NLN	8114	ACTGTCTTCTTATACTGTGGC
NM_020726	NLN	8115	ACCCCTCAATGAGGATGATACC
NM_020726	NLN	8116	ACATACAATCATGCGGCCTGC
NM_015247	CYLD	8117	ACTGCAGGTCTGAACCTTCCCTCC
NM_015247	CYLD	8118	ACGTGCTCGCTGGACTGGAAC
NM_015247	CYLD	8119	ACGACACTCCCAGACAGTGCC
NM_022060	FLJ12816	8120	ACGAATGTGGAAGCCAGGATC
NM_022060	FLJ12816	8121	ACCATGGACTCACTGAGTGCC
NM_022060	FLJ12816	8122	ACTGCTGTGGTGGAGGAGATC
NM_022164	LIECG3	8123	ACGAACCATGCCTGGTGGATC
NM_022164	LIECG3	8124	ACCCCTGCTGTCTTGTGACACC
NM_022164	LIECG3	8125	ACTGAGTGCGACATCGAGAGC
NM_022353	LOC64172	8126	ACACAGGTGGGATTGTTCCCTC
NM_022353	LOC64172	8127	ACCCAGGACTTGCTTTAAGCC
NM_022353	LOC64172	8128	ACATGTCCCTCTTGGAGTAGAC
NM_022357	LOC64180	8129	ACTTTCAGCCATGGTCAGACC
NM_022357	LOC64180	8130	ACCCCTGCTTGCTAACGTGTCC
NM_022357	LOC64180	8131	ACGCAGCCAACCAATCGGGTC
NM_022832	FLJ12552	8132	ACGAAGAAGGTTGGCGTCATC
NM_022832	FLJ12552	8133	ACCCAGAACTCACCTGGGTCC
NM_022832	FLJ12552	8134	ACCCCTGGACCGCATGTATGAC
NM_024922	FLJ21736	8135	ACGCAACTCGGACGCACAAGC
NM_024922	FLJ21736	8136	ACGCAGAAGAACAGGAAGGCC
NM_032147	DKFZP434D0127	8137	ACTGATAACGCAACTGGAGAC
NM_032147	DKFZP434D0127	8138	ACGGAGCCAACCTTCACAGTAC

NM_032147	DKFZP434D0127	8139	ACCATGGAGCCCTATTGCTGC
NM_032324	MGC13186	8140	ACCGTGAATGCCGAGTTGGGC
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NM_032566	ECG2	8142	ACAGTGGACTGCAGCATTTAC
NM_032566	ECG2	8143	ACGAAGTATCCAGTGGTGGCC
NM_032566	ECG2	8144	ACGTATCCAGTGGTGGCCATC
NM_032582	NY-REN-60	8145	ACCGAACTCCACAGCTGATTC
NM_032582	NY-REN-60	8146	ACCAGGACTCCCAAGAACTTC
NM_032582	NY-REN-60	8147	ACTTCCTGTCCCTGTGTCTCC
NM_032663	MGC10702	8148	ACTTGCTGCTGCTCTTGACAGC
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NM_032929	MGC14793	8151	ACGAGTTCAGAACAGAGCCC
NM_032929	MGC14793	8152	ACCTTTCAAGGCCTGGACCAC
NM_080920	GGTLA4	8153	ACTGGATGACTTCAGCTCTAC
NM_080920	GGTLA4	8154	ACACATTGACCAGGAAGTGAC
NM_013325	Apg4B	8155	ACGTCCATAGGCCAGTGGTAC
NM_013325	Apg4B	8156	ACTCAGAAGGTTGTGCAGGAC
NM_002789	PSMA4	8157	ACGCACTATGGCTTTCAGCTC
NM_016442	ARTS-1	8158	ACCCTTACCACGCTGACCTTC
NM_016442	ARTS-1	8159	ACGATAACCAAGAGTGGAGTC
NM_016442	ARTS-1	8160	ACCAGATGTGCTCATCCTCCC
NM_002787	PSMA2	8161	ACGAACCCATTCTACAGCTC
NM_002787	PSMA2	8162	ACCCCATTCCTACAGCTCAGC
NM_005154	USP8	8163	ACGAGTTATGTGCACAGTGCC
NM_005154	USP8	8164	ACGTCAACAGGAGATGTGCCC
NM_005154	USP8	8165	ACACTGAAGCGCTCCTACTCC
NM_005396	PNLIPRP2	8166	ACCTAATCACTGGCACGGAAC
NM_005396	PNLIPRP2	8167	ACGGTGGGCCATCTGGATTTC
NM_005396	PNLIPRP2	8168	ACCACAGGAGAGAGTGGTAAC
NM_005575	LNPEP	8169	ACGCTGCTGGGCATGTCCTTC
NM_005575	LNPEP	8170	ACGGGATGAGCAATACACCGC
NM_005575	LNPEP	8171	ACCATGCTGTTGTCTCTTACC
NM_006229	PNLIPRP1	8172	ACAGTTCACCTCATTGGCCAC
NM_006229	PNLIPRP1	8173	ACGAATGCCCTGTCTCAGATC
NM_006229	PNLIPRP1	8174	ACGGATGCCCACAGATGGGTC
NM_006676	USP20	8175	ACGCACAACCTTGACCGTGAAC
NM_006676	USP20	8176	ACGGGTGACAACATGTACAGC
NM_006676	USP20	8177	ACCAGCAGGATTGCACAGGTC
NM_006838	METAP2	8178	ACACAGACCCCTCCCTCAGTTC
NM_006838	METAP2	8179	ACGCTGCAGAAGCACATCGAC
NM_006838	METAP2	8180	ACGTTGGAAGACTGTTACGCG
NM_014300	SPC18	8181	ACAGTCCGATTGTAGTGGTGC
NM_014300	SPC18	8182	ACGAAGCCTGCCTTGCTGTTT
NM_014932	NLGN1	8183	ACTTGGATGATGTGGACCCAC
NM_014932	NLGN1	8184	ACTGTGATCGTCATCACAGTC

NM_014932	NLGN1	8185	ACGAGGAAATCATGTCCCTCC
NM_016950	HSAJ1454	8186	ACGGAAGTCGGACAGTGGAAAC
NM_016950	HSAJ1454	8187	ACCTATGACCTGCTATTGGAC
NM_016950	HSAJ1454	8188	ACATGGTGTTCAGATTGTGC
NM_016302	LOC51185	8189	ACTTTCATGGCAGGACTTTGC
NM_016302	LOC51185	8190	ACGGGAAGCACAGTTTGGAAAC
NM_016302	LOC51185	8191	ACTCTAACTTCATGGCCTCGC
NM_016546	LOC51279	8192	ACCCCTGCCAAGGTCCAGAAC
NM_016546	LOC51279	8193	ACCCAGAGTGTGAATGTGTTC
NM_016546	LOC51279	8194	ACGGTGCTCAGCTATGTGGAC
NM_016023	LOC51633	8195	ACCATAGAGAGGAAGTGGAGC
NM_016023	LOC51633	8196	ACCAGATTCCATCTGATGGCC
NM_016023	LOC51633	8197	ACTACAGGCAGATTCTCCTCC
NM_017659	FLJ20084	8198	ACTGTGGTGGCCACACTGGAC
NM_017676	FLJ20125	8199	ACGTGGCATAAGAAGAGCAGC
NM_017676	FLJ20125	8200	ACCAAGTGGGTATATGCTTGTC
NM_017676	FLJ20125	8201	ACTAAGACAACCTTCACTGGGC
NM_017944	FLJ20727	8202	ACGGTCTTTTCGAGTGTATGCC
NM_017944	FLJ20727	8203	ACCATGGAAGAATCCTGGCAC
NM_017944	FLJ20727	8204	ACGCAGTCGACTCCAGAAGAC
NG_000013	NG_000013	8205	ACCGTGAATATCTCGGGTGGC
NM_000063	C2	8205	ACCGTGAATATCTCGGGTGGC
NM_000063	C2	8206	ACGACAAAGGAAAGCCTGGGC
NM_000063	C2	8207	ACGAGGAATGACTATCTGGAC
NM_017670	FLJ20113	8208	ACGAGATTGCTGTGCAGAAC
NM_017670	FLJ20113	8209	ACGTTCTTCGAGCACTTCATC
NM_017670	FLJ20113	8210	ACGGAGAGCGACCACATCCAC
NM_018186	FLJ10706	8211	ACTTAGACCTGCCATGTGAAC
NM_018186	FLJ10706	8212	ACCTGTCCATGAGGTCCACCAC
NM_018186	FLJ10706	8213	ACGAAGAGTACAGGTCCAGCGC
NM_020205	CEZANNE	8214	ACTTGGGATGTGAATGCCGCC
NM_020205	CEZANNE	8215	ACTGAAGACTTCCGCAGCTTC
NM_020205	CEZANNE	8216	ACCAAAGTGGGCAGCTTTGGC
NM_032489	ACRBP	8217	ACCCTGGAAGGCAGAGACTAC
NM_032489	ACRBP	8218	ACGCTTCAGCTGAAGTCTCAC
NM_032489	ACRBP	8219	ACGTACATGGAGGAGGAGATC
NM_014237	ADAM18	8220	ACGGATATGCTGCCGAATTTTC
NM_014237	ADAM18	8221	ACTCATGAAGCAGTGAGTGCC
NM_014237	ADAM18	8222	ACGTTGGGAAGTGCCTATTGC
NM_014479	ADAMDEC1	8223	ACGAATTCTGTTGCCAGCATC
NM_014479	ADAMDEC1	8224	ACGATAAAGGTGGTGCCGAGC
NM_014479	ADAMDEC1	8225	ACGGAGTGTACCAATCTCTGC
NM_001873	CPE	8226	ACCCCAATTGCGAATGCCACC
NM_001308	CPN1	8227	ACTCCACGAGCCCTTGGAAACC
NM_001308	CPN1	8228	ACGCTGGCCAAGGTCTACTCC
NM_001308	CPN1	8229	ACCTGAGTTGCGACAAGTTTC

NM_004132	HABP2	8230	ACGAGAACACCAGTAGCACAC
NM_004132	HABP2	8231	ACGTGGTTCCTGTATGCAGGC
NM_004132	HABP2	8232	ACCTCCCGCCAACTCTATGAC
NM_000239	LYZ	8233	ACATGGGAGAGTGGTTACAAC
NM_000239	LYZ	8234	ACAGAGGGTGTCCGTGATCC
NM_000239	LYZ	8235	ACGGTTGTGGAGTGTA ACTCC
NM_013381	TRHDE	8236	ACGATGGATGGGTTACGGATC
NM_013381	TRHDE	8237	ACGCCATGTGTCTTCAGAAGC
NM_013381	TRHDE	8238	ACATACCAGGTATGGAGAAGC
NM_139159	DPP9	8239	ACGTACTCGGGCCTCATTGTC
NM_139159	DPP9	8240	ACATACGCCTGGGCCATGTTT
NM_139159	DPP9	8241	ACCGAGAGACACAGTATTTCGC
NM_012105	BACE2	8242	ACTGATGAGTCCTCTCTGGTC
NM_138991	BACE2	8242	ACTGATGAGTCCTCTCTGGTC
NM_138992	BACE2	8242	ACTGATGAGTCCTCTCTGGTC
NM_002769	PRSS1	8243	ACTCAAGCTCTCCTCACGTGC
NM_002769	PRSS1	8244	ACCAAGCCTGGAGTCTACACC
NM_002770	PRSS2	8245	ACTTCTGGCTACCACTTCTGC
NM_002770	PRSS2	8246	ACCACTCTGAGTTCTGGTGCC
NM_139000	TRY6	8247	ACTGCCCATGTGTCCACGATC
NM_139000	TRY6	8248	ACGATGTTCTGTGTGGGCTTC
NM_020361	CPA6	8249	ACCTTAAGGTGGACCTGTGGC
NM_020361	CPA6	8250	ACGGGAAGCAGCTTGACACC
NM_020361	CPA6	8251	ACATATGAGTCCAGAGGACTC
NM_001879	MASP1	8252	ACTGAGGAGCGTTTCACAGGC
NM_139125	MASP1	8252	ACTGAGGAGCGTTTCACAGGC
NM_001879	MASP1	8253	ACGCTGATGGCCAGGATCTTC
NM_001879	MASP1	8254	ACGGACCGCTACGGAGTATAC
NM_139125	MASP1	8255	ACGGAGCATGTACCGTCTAC
NM_139125	MASP1	8256	ACGGTCTCCAATTACGTGGAC
NM_006610	MASP2	8257	ACGCAACACGGTGACCATCAC
NM_006610	MASP2	8258	ACAGCTGTGATTAGTACAGC
NM_006610	MASP2	8259	ACGGACAGCTGCAGAGGTGAC
NM_030957	ADAMTS10	8260	ACGATGAGTTCCTGTCCAGTC
NM_030957	ADAMTS10	8261	ACGCCTACGATGCAGATGAGC
NM_030957	ADAMTS10	8262	ACGGATGTGAACAAGGTCGCC
NM_014243	ADAMTS3	8263	ACTGAAACAATGAGACGCCGC
NM_014243	ADAMTS3	8264	ACCTGGTGCATGATGGAACGC
NM_014243	ADAMTS3	8265	ACTACTGCATGGGTGACCGTC
NM_139055	ADAMTS15	8266	ACCATTATCTGCTGACGCTGC
NM_139055	ADAMTS15	8267	ACGAAGGTGACTGGACTCTTC
NM_139055	ADAMTS15	8268	ACGTCTCTCATCCCAAGGAC
NM_139056	ADAMTS16	8269	ACGGGCGAATATGACCTGGTC
NM_139056	ADAMTS16	8270	ACGGCTTGTCAGGCATGATAC
NM_139056	ADAMTS16	8271	ACGCTATCTGCCTTGCTGATC
NM_139057	ADAMTS17	8272	ACGTGACCAAGCTTGTCTCTGC

NM_139057	ADAMTS17	8273	ACGCCATGTGAACTCTACTGC
NM_139057	ADAMTS17	8274	ACCGACAGGATCAACGCCAAC
NM_139054	ADAMTS18	8275	ACGATGGTGCTTCAGAGACTC
NM_139054	ADAMTS18	8276	ACACCTTTCCGTGGATGGTTC
NM_139054	ADAMTS18	8277	ACTACCAGCGCTCTTTCAACC
NM_012475	USP21	8278	ACCGGCTCAAGAACTGGAGC
NM_016572	USP21	8278	ACCGGCTCAAGAACTGGAGC
NM_012475	USP21	8279	ACGATGGCTCATCACACTC
NM_016572	USP21	8279	ACGATGGCTCATCACACTC
NM_012475	USP21	8280	ACGTTGTCTCAAGTGCCAGGC
NM_016572	USP21	8280	ACGTTGTCTCAAGTGCCAGGC
NM_012475	USP21	8281	ACGCCGGAAGTCCTGTATACC
NM_014554	SENP1	8282	ACCTAACCAGGAACAGCTGTC
NM_014554	SENP1	8283	ACCAGAAGGCATTGGCCTTAC
NM_014554	SENP1	8284	ACGTGACTGTGGGATGTTTGC
NM_020654	SENP7	8285	ACTCTAAACCCTCACAAGAGC
NM_020654	SENP7	8286	ACTCACTGATCTCAGCTGAAC
NM_020654	SENP7	8287	ACACTGTATCCCAGCAGTCCC
NM_005860	FSTL3	8288	ACCATTGACACCGCCTGGTCC
NM_005860	FSTL3	8289	ACGATCAACCTCCTCGGCTTC
NM_032802	SPPL2A	8290	ACTTGCACAGAAAGGAGGTGC
NM_032802	SPPL2A	8291	ACTTGCAGGTGTTCACTGTGGC
NM_032802	SPPL2A	8292	ACCAGCTATCAGATGATGGAC
NM_007085	FSTL1	8293	ACTGCAAACCTCACAAGAGGC
NM_007085	FSTL1	8294	ACTGGTGATTCTCGCCTGGAC
NM_007085	FSTL1	8295	ACGACCAAGAGAGTGAGCACC
NM_133638	ADAMTS19	8296	ACTGGCCATAACAGGTCAACC
NM_133638	ADAMTS19	8297	ACTTCTGTGATGGTTCCTCC
NM_133638	ADAMTS19	8298	ACTGCAGAGCAGACAAGTGGC
NM_002775	PRSS11	8299	ACCACCTACGCCAACCTGTGC
NM_002775	PRSS11	8300	ACCGGTGCCACTTACGAAGCC
NM_002775	PRSS11	8301	ACCTCAGACATGGACTACATC
NM_003619	PRSS12	8302	ACTGATTCCCTCCACCACAGC
NM_003619	PRSS12	8303	ACAGAAGATGCTGGAGTGTCC
NM_003619	PRSS12	8304	ACCTCCATGAACACAAACGC
NM_002774	KLK6	8305	ACCCGAATCTTCAGGTCTTCC
NM_002774	KLK6	8306	ACGACAGCAGATGGTGATTTC
NM_018297	NGLY1	8307	ACCATTCAAGCATGTGCTGGTC
NM_018297	NGLY1	8308	ACACATGAAGAGGTGATTGCC
NM_018297	NGLY1	8309	ACCTGACAGGCGATAACAGTC
NM_004684	SPARCL1	8310	ACCGGTAGCACCTGACAACAC
NM_004684	SPARCL1	8311	ACCAGGAGCAGTAAACATAGC
NM_004684	SPARCL1	8312	ACTCAGACCTATGCTAGTTCC
NM_016354	SLC21A12	8313	ACACCATCAGAGACCTGCCTC
NM_016354	SLC21A12	8314	ACGGTGTACCGAGACTGTAGC
NM_016354	SLC21A12	8315	ACCTTGCTGCCAGCCAGTC

NM_022450	FLJ22357	8316	ACTGGCAGCGCAAGAGCATCC
NM_022450	FLJ22357	8317	ACGTACGTGCAGCAGGAGAAC
NM_022450	FLJ22357	8318	ACCCTGGCCAGTGCCATCTTC
NM_004181	UCHL1	8319	ACGCAGACCATTGGGAATTCC
NM_004181	UCHL1	8320	ACTGAGGCCATACAGGCAGCC
NM_004181	UCHL1	8321	ACGGTCTGCAGAGAATTCACC
NM_003368	USP1	8322	ACCACACTGAGGGAACCTCAAC
NM_003368	USP1	8323	ACGTCTGCAACTAAGCAACCC
NM_003368	USP1	8324	ACTGAAGACCCTGAGATGGGC
NM_005747	ELA3A	8325	ACCCTTGCTGTGAAGGAGGGC
NM_001948	DUT	8326	ACTACCACCTATGGAGAAAAGC
NM_014122	PRO0245	8326	ACTACCACCTATGGAGAAAAGC
NM_012464	TLL1	8327	ACTTGACCTTACGCAGAACCC
NM_012464	TLL1	8328	ACAGAGGAAGATGAGTGTGCC
NM_012464	TLL1	8329	ACCTACCCAGGACAGGTTGAC
NM_015670	SENP3	8330	ACAGCACCTCGCTGACATTCC
NM_015670	SENP3	8331	ACGTCTCCTCTGGACCCTGAC
NM_015670	SENP3	8332	ACGACCGACTGGATTTCACC
NM_017435	SLC21A14	8333	ACGCATTGGCAGAAGGCTATC
NM_017435	SLC21A14	8334	ACCTGTCTCCTACCAAGGAAC
NM_017435	SLC21A14	8335	ACGAGTTCTTGACAGGAATCCC
NM_018561	DKFZP586D2223	8336	ACCCTGGGCAACACCTGCTAC
NM_018561	DKFZP586D2223	8337	ACTTCACAGAGACAGAGGCCCC
NM_003879	CFLAR	8338	ACCCCTCACCTTGTTTCGGAC
NM_003879	CFLAR	8339	ACTTTGCCTGTATGCCCCGAGC
NM_003879	CFLAR	8340	ACCTATGTGGTGTCTAGAGGGC
NM_032823	FLJ14675	8341	ACCTATGCCAATGCCAGCCTC
NM_032823	FLJ14675	8342	ACCTGGCCACACAAGTGACTC
NM_032823	FLJ14675	8343	ACTGCTACTGGAGAACATTCC
NM_024539	FLJ23516	8344	ACCATGGCCCTTGGGTGAATC
NM_024539	FLJ23516	8345	ACGGAGACAAGGAAATTGGCC
NM_144575	CAPN13	8346	ACGATCCTGATGGTCCAAAGC
NM_144575	CAPN13	8347	ACGCTGCTCGGATCCTATTCC
NM_144575	CAPN13	8348	ACGTGATTCTGGCTGGCTCAC
NM_144691	MGC20576	8349	ACCAAGTTCGATGAGGACACC
NM_144691	MGC20576	8350	ACCAACCAGCTGACCCAGACC
NM_004793	PRSS15	8351	ACGCAGACCCACCGTAAGTAC
NM_004793	PRSS15	8352	ACGAAACGCATCCTGGAGTTC
NM_004793	PRSS15	8353	ACGGAGAAGACCATTTGCGGCC
NM_005865	PRSS16	8354	ACTGACCAACATTGGGTTGGC
NM_005865	PRSS16	8355	ACTGACGTGGTATCCCGAAGC
NM_005865	PRSS16	8356	ACCACAGGCTTTAGGATCCTC
NM_144981	FLJ25059	8357	ACTCCTCACCAGTAGTCCATC
NM_144981	FLJ25059	8358	ACTTCTACAGATTCCAGGTGC
NM_017414	USP18	8359	ACCATGAAGAGAGAGCAGCCC
NM_017414	USP18	8360	ACCCTGATTAAGGACCAGATC

NM_017414	USP18	8361	ACACAGGTCTTGAAGCTGACC
NM_003869	CES2	8362	ACTTCCATTTGCCAAGCCACC
NM_003869	CES2	8363	ACTATCGCCCACTTTGGAGGC
NM_003869	CES2	8364	ACGATGATGAAGTACTGGGCC
NM_014273	ADAMTS6	8365	ACCTTTCAGCCTATGGCAAGC
NM_014273	ADAMTS6	8366	ACCCACCATGCAGACAAGTCC
NM_014273	ADAMTS6	8367	ACGACACTGTGACAGTCCAGC
NG_001337	NG_001337	8368	ACTTCTGGCTCCCCTTCTGC
NM_002771	PRSS3	8368	ACTTCTGGCTCCCCTTCTGC
NM_002771	PRSS3	8369	ACGGATTCTTCCAGCGTGAC
NM_003816	ADAM9	8370	ACGGGACTTTAATCACTGACC
NM_003816	ADAM9	8371	ACGAAGAAGAGCTGTCTTGCC
NM_003816	ADAM9	8372	ACTCACTGTGGAGACATTTGC
NM_003816	ADAM9	8373	ACCCAGTGAGTGTGATGTTCC
NM_006799	PRSS21	8374	ACTATCTATCTGAGCCCTCGC
NM_144956	PRSS21	8374	ACTATCTATCTGAGCCCTCGC
NM_144957	PRSS21	8374	ACTATCTATCTGAGCCCTCGC
NM_022119	PRSS22	8375	ACCCATACCTGTTCTCTGTGC
NM_022119	PRSS22	8376	ACGGAAGGTGCCTGTGCAGAC
NM_022119	PRSS22	8377	ACGCTGAAGGTTCTTATCATC
NM_013247	PRSS25	8378	ACTCTCCTTTGCCATCCCTTC
NM_145074	PRSS25	8378	ACTCTCCTTTGCCATCCCTTC
NM_013247	PRSS25	8379	ACCCAAGCTTTCCCGATGTTC
NM_007173	SPUVE	8380	ACGGACTTCCTGCTCAACTAC
NM_007173	SPUVE	8381	ACGCATGTCCCTCACAGCTGCC
NM_006853	KLK11	8382	ACGATGGCATCGCCAGTCTCC
NM_144947	KLK11	8382	ACGATGGCATCGCCAGTCTCC
NM_006853	KLK11	8383	ACTCCTGCTTGCTCTGGCAAC
NM_144947	KLK11	8383	ACTCCTGCTTGCTCTGGCAAC
NM_012413	QPCT	8384	ACGAATTACCACCAGCCAGCC
NM_012413	QPCT	8385	ACACGACATTTGGTCCTCGCC
NM_012413	QPCT	8386	ACGATTCTCTCTATGGGTCTC
NM_032319	C2orf7	8387	ACCGGTTTCTTCATCCAGGAC
NM_017807	OSGEP	8388	ACCAGAGTCTGGATTAACCTC
NM_017807	OSGEP	8389	ACTACGCAGGTGATTGCATAC
NM_001836	CMA1	8390	ACGAAGACACATGGCAGAAGC
NM_001836	CMA1	8391	ACGAACAGGTGTGTTGAAGCC
NM_001836	CMA1	8392	ACTCTTCAGCTGTGTGTGGGC
NM_022137	SMOC1	8393	ACCTCCTGTATGTTTCAGGTTT
NM_022137	SMOC1	8394	ACGACTACAGAGGCGGATGAC
NM_022350	LOC64167	8395	ACGATCGAAGTCTTGGTGAGC
NM_022350	LOC64167	8396	ACCAAGACGGGTGTTCACTCC
NM_022350	LOC64167	8397	ACGGATGATCATCTCTGGCAC
NM_017829	CECR5	8398	ACCACAGCAAAGCCCAGGAGC
NM_033070	CECR5	8398	ACCACAGCAAAGCCCAGGAGC
NM_017829	CECR5	8399	ACCCCTATGTCTGACGTATAC

NM_033070	CECR5	8399	ACCCCTATGTCTGACGTATAC
NM_017829	CECR5	8400	ACTCCCAGGAACCCACAGTCC
NM_033070	CECR5	8400	ACTCCCAGGAACCCACAGTCC
NM_005606	LGMN	8401	ACTTATAGGCACCAGGCAGAC
NM_016441	CRIM1	8402	ACGCCAGATTGCTCCAAGGCC
NM_016441	CRIM1	8403	ACTGATACAAAGCCAGCCTGC
NM_016441	CRIM1	8404	ACCGCGATCACAAATGGTTGTC
NM_000391	CLN2	8405	ACAGACTCTCGGAGCTGGTGC
NM_000391	CLN2	8406	ACTAACAGCCAAGCCTGTGCC
NM_000391	CLN2	8407	ACGACACCAGTTCCGCCCTAC
NM_014464	TINAG	8408	ACTTCTGATTGCTGTCTCTGAC
NM_014464	TINAG	8409	ACTGGATGTGCCATGGCAAGC
NM_014464	TINAG	8410	ACGCTTCAGACACATGCAGTC
NM_001734	C1S	8411	ACGTCCCAATTATCCCAAACC
NM_025191	C1orf22	8412	ACTGAGGTATATTAGCCAGCC
NM_025191	C1orf22	8413	ACCATCCAGAATGCTGGAGCC
NM_005700	DPP3	8414	ACCAGTGATCAACCCAGAGAC
NM_017743	DPP8	8415	ACGGCAGAGACTCATTGAGTC
NM_130434	DPP8	8415	ACGGCAGAGACTCATTGAGTC
NM_000131	F7	8416	ACGGAGGAGCAGTGCTCCTTC
NM_019616	F7	8416	ACGGAGGAGCAGTGCTCCTTC
NM_000131	F7	8417	ACGAACTGGAGGAACCTGATC
NM_019616	F7	8417	ACGAACTGGAGGAACCTGATC
NM_022468	MMP25	8418	ACCGCAGGTGACACCTACTTC
NM_022718	MMP25	8418	ACCGCAGGTGACACCTACTTC
NM_004341	CAD	8419	ACCTGTGTGGGCTTTGATCAC
NM_014481	APEX2	8420	ACCTCCTATTTTCAGCTTCAGC
NM_014481	APEX2	8421	ACGTGGATGGACAGCTTGCTC
NM_014481	APEX2	8422	ACGGAGTTACGGACCTCATTC
NM_014265	ADAM28	8423	ACGGTTTCTGACGCTAGCATC
NM_021777	ADAM28	8423	ACGGTTTCTGACGCTAGCATC
NM_021778	ADAM28	8423	ACGGTTTCTGACGCTAGCATC
NM_003813	ADAM21	8424	ACTTGAACCCATCAGGCACTC
NM_003813	ADAM21	8425	ACTGGTGCAATGGAACATCTC
NM_003813	ADAM21	8426	ACGTGTGTCACTCTGTCTGTC
NM_014893	KIAA0951	8427	ACCTACGACATCATGCTGGGC
NM_014893	KIAA0951	8428	ACTCACTCCTGCCAACAAATCC
NM_001304	CPD	8429	ACAGTCCCAGGAAGGAGATTC
NM_001304	CPD	8430	ACTATCGTCACATTTGGTCCC
NM_001304	CPD	8431	ACCATTCACAGGTCTTTGTGC
NM_001912	CTSL	8432	ACGTGGAAGGCGATGCACAAC
NM_145918	CTSL	8432	ACGTGGAAGGCGATGCACAAC
NM_001912	CTSL	8433	ACACTGGGAGGCTTATCTCAC
NM_145918	CTSL	8433	ACACTGGGAGGCTTATCTCAC
NM_001912	CTSL	8434	ACGACATGGATCATGGTGTGC
NM_145918	CTSL	8434	ACGACATGGATCATGGTGTGC

NM_019598	KLK12	8435	ACTGACTGTGCAACCGCTGGC
NM_145894	KLK12	8435	ACTGACTGTGCAACCGCTGGC
NM_019598	KLK12	8436	ACCCACCCACGGAACCCATTC
NM_145894	KLK12	8436	ACCCACCCACGGAACCCATTC
NM_019598	KLK12	8437	ACCCCATTCCTCCGGATCTGCTC
NM_145894	KLK12	8437	ACCCCATTCCTCCGGATCTGCTC
NM_145895	KLK12	8437	ACCCCATTCCTCCGGATCTGCTC
NM_015596	KLK13	8438	ACTGTGCCAACATCCAACCTTC
NM_001648	KLK3	8439	ACCCTTGGAATGACCAGGCC
NM_012427	KLK5	8440	ACTCTGGGCAGCAGATGTTCC
NM_012427	KLK5	8441	ACAGCAGGTAGAGACTCCTGC
NM_022046	KLK14	8442	ACCTACAACCTCCCGGACCCAC
NM_022046	KLK14	8443	ACGGCCTATCCTAGAACCATC
NM_022046	KLK14	8444	ACCCTGTGCAAGTACAGAAGC
NM_006523	XPNPEP1	8445	ACATGGACAGCAACTGGACAC
NM_020383	XPNPEP1	8445	ACATGGACAGCAACTGGACAC
NM_006523	XPNPEP1	8446	ACGACTGGCTGGTGAGTGTGC
NM_020383	XPNPEP1	8446	ACGACTGGCTGGTGAGTGTGC
AJ012755	HSA012755	8447	ACCTGCAAGTGGTACTGCTAC
NM_145809	LOC220594	8447	ACCTGCAAGTGGTACTGCTAC
AJ012755	HSA012755	8448	ACGTGTCACTGAGAGGCAAGC
NM_145809	LOC220594	8448	ACGTGTCACTGAGAGGCAAGC
AF311940	AF311940	8449	ACCGAACCCAAACCAGAGACC
AJ278348	HSA278348	8449	ACCGAACCCAAACCAGAGACC
U47927	HSU47927	8450	ACCGAAGACGAAGACTCCTTC
AF483215	AF483215	8451	ACGCACTGGATTGCCAACAAC
AJ420895	HSA420895	8451	ACGCACTGGATTGCCAACAAC
AF483215	AF483215	8452	ACTGGAGTAGAGCTCCTGCAC
AJ420895	HSA420895	8452	ACTGGAGTAGAGCTCCTGCAC
AJ417564	HSA417564	8453	ACAGGCACCGTGTGCTTCTAC
AJ417564	HSA417564	8454	ACGAATACCGGAATAGCAGCC
AJ417564	HSA417564	8455	ACATGTTCCAGGAGATCGTCC
X59417	HSPROS27	8456	ACGTGTGATCCTGCAGGTTAC
XM_034809	LOC90906	8457	ACACAAGCTTTCTGCTTGCCC
XM_034809	LOC90906	8458	ACGTTACCCGGAACAGGAGTC
XM_034809	LOC90906	8459	ACGGGAACAGATGCTCTACTC
XM_065537	LOC130028	8460	ACCCTTCAGGAATTTGGCTTC
XM_065537	LOC130028	8461	ACGGTGGAGAAACCTTCAGCC
XM_068321	LOC133384	8462	ACGATTCCAGCCACTGATGTC
XM_067618	LOC131934	8463	ACTGTGTTGTCCAGTCGGATC
XM_067618	LOC131934	8464	ACGACCCAGACATTGAAGCAC
XM_067618	LOC131934	8465	ACGTGGGAGTATGATGAGCGC
XM_068227	LOC133179	8466	ACGGAGTACTATCATGGCTCC
XM_068227	LOC133179	8467	ACGCCTCTGCATCCTTCCAAC
XM_068227	LOC133179	8468	ACACCTGGAATGTTCTGTGCC
XM_065827	LOC130677	8469	ACACCGCCAAGGAGTCATTCC

XM_065827	LOC130677	8470	ACGGAGTCATTCCAGGACAGC
XM_065827	LOC130677	8471	ACGGCTGCCTTTCATGCTTAC
XM_070459	LOC137491	8472	ACTAGCAGCAGTGTTAGCGCC
XM_070459	LOC137491	8473	ACTGTGCCGAAGGATGTAAGC
XM_070459	LOC137491	8474	ACCTGCTGGAGTACTGACTAC
XM_063011	LOC122217	8475	ACGCAGCAGGTGGTGACATGC
XM_063011	LOC122217	8476	ACGAAGCCAACTATAGCTCCC
XM_063011	LOC122217	8477	ACCATCTCCATTATGCCTGTC
XM_061993	LOC120320	8478	ACCAAGATGCAGAGATAGTCC
XM_061993	LOC120320	8479	ACTCTCCATGACAATTCTCCC
XM_061993	LOC120320	8480	ACATATGCAGTCCGTGGATGC
XM_062003	LOC120332	8481	ACGACCTCTGACAGCACCTTC
XM_062003	LOC120332	8482	ACGGTGATCATCTTCGAGGCC
XM_066484	LOC139116	8483	ACTGAGCGTGATGGGCTGTAC
XM_066484	LOC139116	8484	ACGGATGTTTCAGATAGGGCCC
XM_070928	LOC138482	8485	ACGGCACTGAAGCTTGGGACC
XM_070928	LOC138482	8486	ACTGAAGTTGCAGGCAAGCAC
XM_061692	LOC119795	8487	ACGAGCAGTGGAGATGGCCTC
XM_062536	LOC121244	8488	ACTACCTATGCACTGGACAGC
XM_062536	LOC121244	8489	ACACAGTAACAGCAGAGCAGC
XM_062536	LOC121244	8490	ACACACAGCAGCAGTCGGCAC
XM_062734	LOC121656	8491	ACTCCTGGAAAGTACCAGGGC
XM_062849	LOC121906	8492	ACCTCCTTTGTGGAGCCTCTC
XM_062849	LOC121906	8493	ACGTGTGATGCTGCAGGTTAC
XM_062849	LOC121906	8494	ACCCGCAATTACATGCCTTTC
XM_063398	LOC122985	8495	ACTCAAACACCTGGAGGCTTC
XM_063398	LOC122985	8496	ACCAGTGAGTGTTATGCCAGC
XM_064936	LOC126071	8497	ACCATCCATCTTATCCTAGCC
XM_064936	LOC126071	8498	ACGGACTCAGTGTGGAGAAAC
XM_064936	LOC126071	8499	ACGCAATGTGGGAGAGCTTTC
XM_066005	C2orf137	8500	ACCTATCCTCTGAAGAAGGGC
XM_066005	C2orf137	8501	ACGTGCTGTCAATTCCCTACC
XM_066031	LOC128559	8502	ACGAGAGGAGACAGCTCAGCC
XM_066031	LOC128559	8503	ACCTCCTGCCCTGTATCAGCC
XM_066181	TGM3L	8504	ACCTGCACCACAAAGCCCATC
XM_066181	TGM3L	8505	ACGATTGGGAGATGCATCAGC
XM_066181	TGM3L	8506	ACGCTTCTGGTGGAGAAGGAC
XM_066924	LOC139853	8507	ACTTCTGCCTGGTGGTGTGAC
XM_066924	LOC139853	8508	ACTCGCCATATTCTGGATGAC
XM_033922	USP10	8509	ACAGAAGCAAGCTATGGCTCC
XM_033922	USP10	8510	ACGCATAGACTTGGACCCAAC
XM_033922	USP10	8511	ACGAATCTGCCACTTTGCAGC
XM_058785	LOC124221	8512	ACAGACTCCTGCCAGGGTGAC
XM_058785	LOC124221	8513	ACTGATACGTGGATCCAGGCC
XM_060167	LOC126767	8514	ACGCCTGGCATCGTGTACTAC
XM_060167	LOC126767	8515	ACCTTGTGGACAGGCCAGATC

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XM_060167	LOC126767	8516	ACGGGACTGTGACCATCTTTC
XM_087076	LOC151005	8517	ACGAAGAGGACTGCTCTATAC
XM_086756	LOC149992	8518	ACGTGAAGAACAAGGCTGGCC
XM_087076	LOC151005	8518	ACGTGAAGAACAAGGCTGGCC
XM_086756	LOC149992	8519	ACGCTTGGTGGAAAGAACACC
XM_087076	LOC151005	8519	ACGCTTGGTGGAAAGAACACC
XM_087229	LOC151516	8520	ACTGACCTCAACCATTGGGAC
XM_087229	LOC151516	8521	ACCAGCATGGGTAAGGGCTAC
XM_087229	LOC151516	8522	ACGATGAGTTTGACCTGGAGC
XM_087628	LOC153218	8523	ACCGTGACTTCACTAGGTGGC
XM_087628	LOC153218	8524	ACTGGGTACCAGAGTAACTAC
XM_051452	SMOC2	8525	ACGTATACCCAGGAGCAAGCC
XM_051452	SMOC2	8526	ACGCATGAGTTTCTGACCAGC
XM_051452	SMOC2	8527	ACCCCTTCAAGAGGTTCTCTC
NM_001807	CEL	8528	ACTGCCAAGAGTGCCAAGACC
NM_001808	CELL	8528	ACTGCCAAGAGTGCCAAGACC
XM_070951	LOC138529	8528	ACTGCCAAGAGTGCCAAGACC
XM_070951	LOC138529	8529	ACTACTGACAGGCTGGAGGCC
XM_070951	LOC138529	8530	ACCCGGGACATAACTAAATCC
XM_089437	LOC159195	8531	ACGTGCTTCCATCTGACACTC
XM_089437	LOC159195	8532	ACGGAAGCACTGTGGCTATAC
XM_089437	LOC159195	8533	ACGAAGGAAGAGGCATTGCTC
XM_058378	LOC119180	8534	ACATATTCTCGAGGGCTGGCC
XM_166129	LOC84569	8534	ACATATTCTCGAGGGCTGGCC
XM_058378	LOC119180	8535	ACGCTGAAGGAGAACAACCAC
XM_166129	LOC84569	8535	ACGCTGAAGGAGAACAACCAC
XM_058378	LOC119180	8536	ACGGAGAACAACCACTGCCAC
XM_037557	KIAA0984	8537	ACAGGTTTGGTTGACCTTGGC
XM_037557	KIAA0984	8538	ACTGCACTGAAGCGGCAGTAC
XM_037557	KIAA0984	8539	ACATCTGCTACTGCCAGGAAC
XM_086031	LOC148066	8540	ACGCCTTGCTGGTCTTGTGCG
XM_086138	LOC148293	8541	ACCAATGGAACCTCACAGAAGC
XM_030162	DKFZp566D234	8542	ACGCAAATGGCAGTGAGGTTT
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XM_068179	LOC133083	8545	ACGTGACACCACCACGTATGC
XM_068179	LOC133083	8546	ACTCGGGAAGTGCTGCATTCC
XM_068179	LOC133083	8547	ACGGGCATATTCTCCAGGCTC
XM_070851	LOC138319	8548	ACCGCCTTTGGAGAAATGACC
XM_070851	LOC138319	8549	ACAGCCTGTAGGTACAATCCC
XM_070851	LOC138319	8550	ACTCATCTGGCTGGAGAGGCC
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XM_070231	LOC137098	8552	ACTCTGGCTCTTGGTGTGTCC
XM_070231	LOC137098	8553	ACATGACAGGATGTCTGCGTC
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XM_030312	DKFZP586H2123	8557	ACCATCTGCATACCCAGCTCC
XM_030312	DKFZP586H2123	8558	ACCATGCAGCCACAGGCTCTC
XM_049476	MGC4840	8559	ACGAGGGTTATAGCAATACGC
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XM_049476	MGC4840	8561	ACCACAGACATCCATCTGCAC
XM_064073	LOC124294	8562	ACTAACAGCAAGTGTGAGGGC
XM_064073	LOC124294	8563	ACGACGTGGAAATGTGTCTCC
XM_060074	KIAA0951	8564	ACGTTCCACCTCATTTGACAGC
XM_035312	KIAA1492	8565	ACTCCTCCAGAAGTAGAGGAC
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XM_035312	KIAA1492	8567	ACTGTGGATCCGTGGTTGCAC
XM_068226	LOC133178	8568	ACTTGCTGATGGTCGGATTGC
XM_068226	LOC133178	8569	ACCTATGCTGCCCATAAACAC
XM_068226	LOC133178	8570	ACATTAGATGGTCCCTTTCCC
XM_068225	LOC133177	8571	ACACATGCCATTACCAGCATC
XM_068225	LOC133177	8572	ACCATGCCATTACCAGCATCC
XM_068000	LOC132722	8573	ACTTCTGGCTGATGTGGGAAC
XM_068002	LOC132724	8574	ACGATTTGTCTTCTCTGAAGCC
XM_087526	LOC152805	8575	ACGAACTCAGCCATCAAGGGC
XM_010822	KIAA0436	8576	ACGTGTGGTTGATAGATGGCC
XM_010822	KIAA0436	8577	ACTTCTGACCCAAAGAACTGC
XM_010822	KIAA0436	8578	ACCCCTGACTGCTTTTCAGTGC
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XM_052334	METAP1	8582	ACCTCAGACCACATTATCCAC
XM_052334	METAP1	8583	ACGCCATTGATGCAGTGAAGC
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XM_067726	LOC132194	8586	ACGGTCAAGATCTGGTTGAGC
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XM_086914	LOC150426	8588	ACTGGCTCTTACGTGATTAC
XM_086914	LOC150426	8589	ACGTAACAGGCTCTGCAATGC
XM_071013	LOC138652	8590	ACACCTCCTCATCCTTCATCC
XM_071013	LOC138652	8591	ACGATGTCTGTGCACCGGATC
XM_071013	LOC138652	8592	ACGAACTGGCAAAGGCGAGAC
XM_070195	LOC137042	8593	ACTCCAGCGGACTTCTCTCTC
XM_070195	LOC137042	8594	ACTCACTCTAAGGACACCACC
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XM_172434	LOC253804	8594	ACTCACTCTAAGGACACCACC
XM_172437	LOC255606	8594	ACTCACTCTAAGGACACCACC
XM_172440	LOC255609	8594	ACTCACTCTAAGGACACCACC
XM_070736	LOC138051	8595	ACTACTGGCAGTGTGGACACC
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XM_070736	LOC138051	8597	ACAGGTGTGGTACCCGGGATC

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XM_059830	LOC136242	8599	ACAGACAAGCTCCAGGGAATC
XM_048786	KIAA1061	8600	ACGAATGTCCTTCTGGCACTC
XM_048786	KIAA1061	8601	ACTTACACCTGCCATGCTTCC
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XM_027341	LOC89932	8603	ACCATCAGGTGGTCCAGGAAC
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XM_050285	KIAA1466	8606	ACGCCCAAGAAGTAACCAGAC
XM_050285	KIAA1466	8607	ACCTGCACATAGTCTACCACC
XM_058409	LOC119587	8608	ACCCATGACATCCGAACAGCC
XM_058409	LOC119587	8609	ACCCCTGGAGAGTATGTGGTC
XM_058409	LOC119587	8610	ACACCAACATGGCCAGGATCC
XM_068765	LOC134269	8611	ACTTCCAAGAGGAGTTGGAGC
XM_068765	LOC134269	8612	ACGCTGTTGCATCTACGCTTC
XM_068765	LOC134269	8613	ACGTATGCCGAGTCGTAAAGC
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XM_054098	DKFZp761A052	8615	ACCCACATTGAGATGCAGGCC
XM_066522	LOC139171	8616	ACGGGAGGTGGGTGAGACAAC
XM_069410	LOC135525	8617	ACGTTTGCTCCAGTTTACTGC
XM_069410	LOC135525	8618	ACGCCAGAGTCCCTATCTATC
XM_069410	LOC135525	8619	ACCTTCTGTAGAGGCTCCTC
XM_066860	LOC139736	8620	ACAGGGAGAAGAAGAGGTGGC
XM_066860	LOC139736	8621	ACGATACCAACTTGTCCGCGC
XM_064616	LOC125439	8622	ACGCCTGGAACAAAGTTGGTC
XM_064616	LOC125439	8623	ACGAAGGCTCCAGGATCAATC
XM_064616	LOC125439	8624	ACCATTGAGAGAGTGCCACC
XM_029885	C20orf170	8625	ACGGAATACCAGAAGTGCTGC
XM_029885	C20orf170	8626	ACTTACCGCTGCACACCCTTC
XM_029885	C20orf170	8627	ACGGTTTCTGCCCACGCAAGC
XM_058864	LOC124912	8628	ACCAACGGGATCTTCCAGATC
XM_058864	LOC124912	8629	ACCGTGTGCCGGATGTACTGC
XM_058864	LOC124912	8630	ACGGATACCGTTATCTGTGCC
XM_042698	USP22	8631	ACGGCCAAGTCCTGTATCTGC
XM_042698	USP22	8632	ACGATCACCACGTATGTGTCC
XM_027825	PSMB6	8633	ACCCACTGGGTCTTACATCGC
XM_027825	PSMB6	8634	ACTGAGCCTCCACTGGTCCAC
XM_027825	PSMB6	8635	ACGGAAGAGTGTCTGCAATTC
XM_064383	LOC124975	8636	ACCCCTGGTGGCCAAGTCTACC
XM_086756	LOC149992	8637	ACCACCTGACGAATAGGATAC
XM_049683	KIAA1203	8638	ACATCTTGTGGACCAGGTGGC
XM_049683	KIAA1203	8639	ACCCAAGCGACAGTCATAGTC
XM_049683	KIAA1203	8640	ACGCTTGGGTTCTGACAGAGC
XM_099028	LOC159121	8641	ACGATGGACACTCGGCTCCTC
XM_099028	LOC159121	8642	ACCTATTGTTCCAGTGGAGGC
XM_099028	LOC159121	8643	ACGTGATAGCTCTGTGCACCC

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XM_092572	LOC165417	8645	ACGGCTGGGATGTTCCACTGC
XM_108675	LOC157788	8646	ACATTAGCTGCTGATGACCAC
XM_108793	LOC157917	8647	ACTGCTGGGCTCTGAGACTGC
XM_108793	LOC157917	8648	ACACAACACCCGACGCCCAAC
XM_108793	LOC157917	8649	ACAGCTAACTGACAAGGCGGC
XM_090479	LOC160768	8650	ACTATGGGCCAGGCCCTTTCTC
XM_090479	LOC160768	8651	ACCAGGCATAAGCAAGATGGC
XM_090479	LOC160768	8652	ACCAAAGTCTGCCTGAATTCC
XM_091358	LOC162106	8653	ACTTACCTGTTTGAACAGCCC
XM_092901	LOC164646	8654	ACCAGCTGGTCCTCATGTTTC
XM_091960	LOC163051	8655	ACCAGAACACCAGGACATCCC
XM_091960	LOC163051	8656	ACCGTTTCAGTCATCCCAGTTC
XM_091960	LOC163051	8657	ACACAATGTGGTAAGGCCCTTC
XM_166631	LOC219343	8658	ACCGCCTGCTTCCTGAGATCC
XM_166631	LOC219343	8659	ACTGAGGGCTGCAATGGTGGC
XM_166129	LOC84569	8660	ACCATTGTGAGGGCAGAGACC
XM_166244	KIAA1372	8661	ACGTACATGCTCCTGACCTTC
XM_166244	KIAA1372	8662	ACGATAGTGACTCGGATCTGC
XM_166244	KIAA1372	8663	ACGATCCTGGATGACGTCTCC
XM_092342	LOC165057	8664	ACGACCTCAAAGAAGCCATCC
XM_092342	LOC165057	8665	ACTAGGAAGGCAGATCTCAGC
XM_092342	LOC165057	8666	ACCAACAGAGAAGCAGAGGCC
XM_094142	LOC166867	8667	ACGACTCAGCAGGCAGTCCAC
XM_094142	LOC166867	8668	ACGTCCGGCTTTGCGTTTCAC
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XM_093541	LOC165927	8670	ACCAGACAATGTGGCTCACAC
XM_165973	USP24	8671	ACAGGTGAGCTTACAGCTTGC
XM_165973	USP24	8672	ACGCAACGACCACCCATTAGC
XM_165973	USP24	8673	ACCCATTTTCAGCTCAGGACAC
XM_093373	LOC165693	8674	ACGTGATGAAGAAGGCTGCAC
XM_093373	LOC165693	8675	ACACAGGCTGTCTAGATCCCAC
XM_116029	LOC205564	8676	ACCGTGGATCAAGGATGAACC
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XM_116029	LOC205564	8678	ACACACATGCTGGATATGGAC
XM_114627	LOC203100	8679	ACGCTACATACCCAGCCCTCC
XM_114627	LOC203100	8680	ACTGCCCATGTTGTCAGGAAC
XM_114627	LOC203100	8681	ACGCTCTTGACAGTGATTCCC
XM_168542	HGF	8682	ACAGGACTTCCATTCACTTGC
XM_168542	HGF	8683	ACCATCCGAGTTGGCTACTGC
XM_168542	HGF	8684	ACTGAAGCTTGCCAGGCCTGC
XM_090919	LOC161464	8685	ACCTGACCTTACAGAGCTACC
XM_090919	LOC161464	8686	ACGAGCTATGCTCAGGCTGCC
XM_090919	LOC161464	8687	ACTCAGAGCCCTCTGAGCTTC
XM_106407	LOC166977	8688	ACCTACGACTGCGAAGAGACC
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XM_092016	LOC163126	8691	ACCCTTTACGATAGCTCTGAC
XM_094257	LOC153217	8692	ACAGGCTTAAAGACTGCATGC
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XM_093148	LOC170172	8695	ACGATACTGGCAGACCTCTTC
XM_093148	LOC170172	8696	ACGTCAGTCTATACTGTAGGC
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XM_096824	LOC145624	8698	ACCACAAGCTTGGTTTCTCAC
XM_090422	LOC160662	8699	ACGAGGTGTGTGAAGGAATC
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XM_089945	LOC159938	8701	ACGTCTTGCAGGAAGTGAATC
XM_089945	LOC159938	8702	ACCTACAGTGACAAGGCTAAC
XM_102809	LOC147221	8703	ACATAATACCTTGTGGCTGGC
XM_102809	LOC147221	8704	ACCTATGTTTCAGCCCCAAGCGC
XM_102809	LOC147221	8705	ACTCCTCCTGGTAGACAAGGC
XM_090074	LOC160130	8706	ACGTGCTGTCTAATCTGAGAC
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XM_090078	LOC160131	8709	ACGAAATCTCACTGCTTCGAC
XM_090078	LOC160131	8710	ACGGTGCCATGAGGGTTAATC
XM_040082	LOC91694	8711	ACGAAACTGCTGAACCTCTCAC
XM_040082	LOC91694	8712	ACCGTGCATTTCTTACCGGAC
XM_040082	LOC91694	8713	ACCGGTTGACCAAGATACAGC
XM_050754	KIAA1594	8714	ACTAGCTCGGACGATTCTTTC
XM_050754	KIAA1594	8715	ACGATACCTGACCCTGTCTATC
XM_050754	KIAA1594	8716	ACGAGCAAGAGGCTTGGGAAC
XM_058840	LOC124739	8717	ACGGGAAGACAGAGCTGTTTC
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XM_058840	LOC124739	8719	ACGCATTAGCATGAAGGCACC
XM_061219	LOC118945	8720	ACCGCCTGCTTCTTGAGATCC
XM_061219	LOC118945	8721	ACTGAGGGCTGCAATGGTGAC
XM_064335	LOC124857	8722	ACCGACATGAATCCCAACCTC
XM_064335	LOC124857	8723	ACCCTGCCGCTATCACTTCAC
XM_064335	LOC124857	8724	ACCCTCAACCACTTTGAGACC
XM_064505	LOC125242	8725	ACTACCGTGGACAATGCCTGC
XM_064505	LOC125242	8726	ACGAACCGAAAGGAGCTGGAC
XM_064505	LOC125242	8727	ACGGCTGCATTCTGTGGCAC
XM_066765	LOC139562	8728	ACGTCCAAGACGACAGTAGC
XM_066765	LOC139562	8729	ACGCCGATCATCCTGGTCTAC
XM_088514	LOC158219	8730	ACTTGCCGGGAAATCTATCCC
XM_088514	LOC158219	8731	ACAGATTACTCCCTGGAGTCC
XM_092184	LOC164832	8732	ACCGTTTCTTGATGGAAGTTC
XM_092184	LOC164832	8733	ACAGAGCGGCTCCTTGCCATC
XM_093962	LOC152697	8734	ACACCGCCACTTGCCAACTAC
XM_114040	LOC199858	8735	ACTAGGAACTACAGCAGCCC

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XM_114040	LOC199858	8736	ACTGACGGTTTGGGTCCTCC
XM_114622	LOC203074	8737	ACCTCGGTATTCCAGAATCAC
XM_114622	LOC203074	8738	ACCGACTTAAGTAGCCCATCC
XM_114622	LOC203074	8739	ACCAGAAACCTATGGGCTCCC
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XM_115028	LOC203870	8742	ACATGGGAGAGAGTTTCCCAC
XM_115028	LOC203870	8743	ACAGGAGGAGTCCAGGCATC
XM_115028	LOC203870	8744	ACCAAGGATTGCAGGAGACTC
XM_115473	LOC201211	8745	ACGTCACCCAGTTCAAGGACC
XM_115473	LOC201211	8746	ACTGTTGGAAGAGGCTGAGAC
XM_115473	LOC201211	8747	ACTCAGGAGTGGTGGAACTTC
XM_115647	LOC199783	8748	ACGGGCCACCTGACACTTACC
XM_116020	LOC205548	8749	ACCTTCTGTAGCTCCAGGGTC
XM_116020	LOC205548	8750	ACTGACCAAGGGAAGGATGCC
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XM_116185	LOC201784	8752	ACCTGGTGCTGACAGAGGCAC
XM_116185	LOC201784	8753	ACCAACGATCTGCATGCATGC
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XM_116274	LOC206008	8755	ACCCACTTCACAGCTGACACC
XM_116274	LOC206008	8756	ACCGCTCAGGAAGTTATTCCC
XM_116274	LOC206008	8757	ACGAAGTGGATAGCCCTCATC
XM_120320	LOC205678	8758	ACGGCACCAGATCCTCATATC
XM_120320	LOC205678	8759	ACCAGAGCACAGGAGAGTCTC
XM_120320	LOC205678	8760	ACGCTGTGGGAGAACTATCCC
XM_120869	LOC206100	8761	ACGAGGATGACTTCTTGATTC
XM_166375	KIAA1925	8762	ACGAAGACCACACTTGGGATC
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XM_166659	LOC220213	8767	ACCTGCCTCTACCGAGCTGTC
XM_166937	LOC220056	8768	ACTGGGAAAGAACTGTGTGAC
XM_166942	LOC220369	8769	ACCTGCTGAGCGAACAGCACC
XM_166942	LOC220369	8770	ACTACTTGGCACTTCCAGAGC
XM_167030	LOC222530	8771	ACCCGTTATCCAGAATCCCAC
XM_167030	LOC222530	8772	ACTTTGAGTGGATGGAAAGGC
XM_167111	LOC222678	8773	ACGTGGGAAAGTAAGACTGTC
XM_167111	LOC222678	8774	ACATCATGAGCAACAGTCTCC
XM_167111	LOC222678	8775	ACAGTCACCATTGGGAAGATC
XM_167616	LOC219743	8776	ACCCCTCCTTGGCATAATCACC
XM_167616	LOC219743	8777	ACGCTCTGAGGCTGTGTTACC
XM_170927	LOC253152	8778	ACCCACTTATGCTGCTGCTTC
XM_171147	LOC255779	8779	ACGAACAGTGCAGGGCAATGC
XM_171300	LOC254639	8780	ACGGTGAGACCTCAGACGAGC
XM_171463	LOC254524	8781	ACCCTCGATGACCAGAGTGGC

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XM_171586	LOC256652	8782	ACGCTGGCAACTTCTATGTTT
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XM_171629	LOC257238	8784	ACAGAAGAAGGTATAGCAGGC
XM_171629	LOC257238	8785	ACGTGGCTGACAGAGCATTTC
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XM_171993	LOC255449	8789	ACAGATGCATCTTCCCTCCAC
XM_171993	LOC255449	8790	ACCCCATCTGATTACCGGATC
XM_171993	LOC255449	8791	ACGGCCATTTGCCGACGAGAC
XM_172159	LOC256251	8792	ACTGCTATGGGAGTGGTAGGC
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XM_172637	LOC254737	8799	ACTAACAAATGGGAGGGTGAC
XM_172713	LOC254580	8800	ACCTTGAAGGTACCCTGCCTC
XM_172789	LOC254989	8801	ACATCATGAGGCTCACTCCTC
XM_172791	LOC254584	8802	ACCACTTTATAAGCCTGCGGC
XM_173599	LOC254442	8803	ACCACCTGGAAGAATTTGGAC
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XM_174353	LOC257260	8807	ACCATCACTTCCCTGCTGGCC
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ENSG00000175194	ENSG00000175194	8813	ACAGGTCTTCAGGTCCAAACC
ENSG00000175194	ENSG00000175194	8814	ACCTCTCTGGACGTCAGTGGC
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NM_000045	ARG1	8817	ACGAAGAACGGAAGAATCAGC
NM_000045	ARG1	8818	ACGGAAAGATTCCCGATGTGC
NM_000045	ARG1	8819	ACGGTGATGGAAGAAACACTC
NM_000045	ARG1	8820	ACCAGTGAACACAGCAGTTGC
NM_000270	NP	8821	ACGGTTTGGAGATCGTTTCCC
NM_000270	NP	8822	ACGGCCAACCATGAAGAAGTC
NM_000305	PON2	8823	ACGTGTGAATGACATCACAGC
NM_000305	PON2	8824	ACCTGCCAGAACATGGATTCC
NM_000361	THBD	8825	ACTGCCAGTCAGATCTGCGAC
NM_000361	THBD	8826	ACGTGAAGGCCGATGGCTTCC
NM_000361	THBD	8827	ACCGACCTCTGCGAGCACTTC

NM_000361	THBD	8828	ACGGAGGTAGTGCTGCAGCAC
NM_000362	TIMP3	8829	ACGCTGGAGGTCAACAAGTAC
NM_000362	TIMP3	8830	ACGATCAAGTCCTGCTACTAC
NM_000852	GSTP1	8831	ACGTTCCAGGACGGAGACCTC
NM_000852	GSTP1	8832	ACGACCTTCATTGTGGGAGAC
NM_001152	SLC25A5	8833	ACGGAGCAGGGAGTTCTGTCC
NM_001152	SLC25A5	8834	ACTCTGATGGGATTAAGGGCC
NM_001676	ATP12A	8835	ACACGGATGGCCAAGAAGAAC
NM_001681	ATP2A2	8836	ACACATTGCTGCTGGGAAAGC
NM_001681	ATP2A2	8837	ACCAGAACAGGAGAGAACACC
NM_001681	ATP2A2	8838	ACTGCCATTGTTCTGAAGCCTC
NM_001681	ATP2A2	8839	ACACAGTTCATCCGCTACCTC
NM_002010	FGF9	8840	ACGTGACCACCTGGGTCAGTC
NM_002010	FGF9	8841	ACAGACCACAGCCGATTTGGC
NM_002010	FGF9	8842	ACGGGACTAGGACTAAACGGC
NM_002010	FGF9	8843	ACCGGCACCAGAAATTCACAC
NM_002068	GNA15	8844	ACCGTGATCGCCCTCATCTAC
NM_002079	GOT1	8845	ACAGACATTCGGTCCTATCGC
NM_002079	GOT1	8846	ACTGGCTGACCGGATTCTGAC
NM_002079	GOT1	8847	ACCGTGAGTGGCTTAACCACC
NM_002080	GOT2	8848	ACGTGAAAGGCATGGCTGACC
NM_002455	MTX1	8849	ACGTTCTTCTTTGGAGATGCC
NM_002462	MX1	8850	ACTCACCTGGAGATCAGCTC
NM_002462	MX1	8851	ACTCAGGACATCACTGCTCTC
NM_002462	MX1	8852	ACTCAAGGCACTGGAAGAGCC
NM_002629	PGAM1	8853	ACACGTGTACTGATTGCAGCC
NM_002701	POU5F1	8854	ACCTCGAGCAATTTGCCAAGC
NM_002701	POU5F1	8855	ACGGTATTTCAGCCAAACGACC
NM_002701	POU5F1	8856	ACCATGTGTAAGCTGCGGCC
NM_002701	POU5F1	8857	ACGCGAACCAGTATCGAGAAC
NM_002715	PPP2CA	8858	ACCAGTTACACTGCTTGTAGC
NM_002715	PPP2CA	8859	ACTCATGAGAGCAGACAGATC
NM_002715	PPP2CA	8860	ACTGTGTGACTTGCTGTGGTC
NM_002801	PSMB10	8861	ACTGTGGACGCATGTGTGATC
NM_002818	PSME2	8862	ACTGTGGCTGACTTGACTTCC
NM_002818	PSME2	8863	ACAGTCCTGTCCCTGCTTGCC
NM_002818	PSME2	8864	ACGCCAGAAGTCTGGACTCTC
NM_002818	PSME2	8865	ACGCCATCTATGTACTGAACC
NM_002961	S100A4	8866	ACCTAAAGGAGCTGCTGACCC
NM_019554	S100A4	8866	ACCTAAAGGAGCTGCTGACCC
NM_002961	S100A4	8867	ACGCTGATGAGCAACTTGGAC
NM_019554	S100A4	8867	ACGCTGATGAGCAACTTGGAC
NM_002961	S100A4	8868	ACCTTGGACAGCAACAGGGAC
NM_019554	S100A4	8868	ACCTTGGACAGCAACAGGGAC
NM_002961	S100A4	8869	ACGGCTTCCCAGATAAGCAGC
NM_019554	S100A4	8869	ACGGCTTCCCAGATAAGCAGC

NM_002962	S100A5	8870	ACGGAAGCTCAAGGAGCTGATC
NM_002962	S100A5	8871	ACGGAGAGCAGCATCGATGAC
NM_002962	S100A5	8872	ACGAACAGCGACCAGGAGATC
NM_002966	S100A10	8873	ACGGAGGACCTGAGAGTACTC
NM_002966	S100A10	8874	ACAGACCCTCTGGCTGTGGAC
NM_002966	S100A10	8875	ACAGTGGGCTTCCAGAGCTTC
NM_002966	S100A10	8876	ACGAGTTGTCCAAAGGGTCGC
NM_003129	SQLE	8877	ACAGCAGCTATGGCAGAGCCC
NM_003132	SRM	8878	ACGGCCCTGAATGATGTGAGC
NM_003246	THBS1	8879	ACAGGCTGCTCCAGCTCTACC
NM_003246	THBS1	8880	ACGGATCCGGCTCTGCAACTC
NM_003246	THBS1	8881	ACAGCCTGCAAGAAAGACGCC
NM_003345	UBE2I	8882	ACTCCCGATGGCAGCATGAAC
NM_003345	UBE2I	8883	ACGCAGCGACCTTGTGGCATC
NM_003348	UBE2N	8884	ACCCAGATGAGAGCAACGCCC
NM_003348	UBE2N	8885	ACGAATACCCAATGGCAGCCC
NM_003348	UBE2N	8886	ACGACCAACGAAGCCCCAAGCC
NM_003348	UBE2N	8887	ACAGCCCAGACATCTTCAGTC
NM_003364	UP	8888	ACCAGAGCAGGCAGTGGATAC
NM_003364	UP	8889	ACACGGACCTTAACAAGAAGC
NM_003364	UP	8890	ACCACCATGTGCACCTTGGAC
NM_003463	PTP4A1	8891	ACGTGGAAGTTGAGATAGGGC
NM_003463	PTP4A1	8892	ACGCTAGACAGATTTGGCAAC
NM_003463	PTP4A1	8893	ACCATTGAAAGTAGGGCCTAC
NM_003463	PTP4A1	8894	ACTGTTGCCTTTGTCTTGTGC
NM_004000	CHI3L2	8895	ACGAGTGAAGTGATGCTCTAC
NM_004000	CHI3L2	8896	ACTTTAAACCTGGGAGGAGCC
NM_004358	CDC25B	8897	ACGATGGAAGTGGAGGAGCTC
NM_021872	CDC25B	8897	ACGATGGAAGTGGAGGAGCTC
NM_021873	CDC25B	8897	ACGATGGAAGTGGAGGAGCTC
NM_021874	CDC25B	8897	ACGATGGAAGTGGAGGAGCTC
NG_001028	NG_001028	8898	ACAGGCTTTGGAAATGGGAGC
NM_004730	ETF1	8898	ACAGGCTTTGGAAATGGGAGC
NM_005116	SLC23A1	8899	ACCAGCAGAGCTGTTGCACAC
NM_005116	SLC23A1	8900	ACGTTACCTCAGACAGAACCC
NM_005389	PCMT1	8901	ACGTGATGCTGGCTACAGACC
NM_005389	PCMT1	8902	ACGCAACAATCAGTGCTCCAC
NM_005389	PCMT1	8903	ACTGGGATATGCTGAAGAAGC
NM_005389	PCMT1	8904	ACGCTACAAGATGGCAGCATC
NM_005729	PPIF	8905	ACTGCTGGTCCTAACACCAAC
NM_006198	PCP4	8906	ACGAAGGCTGGGTCTCAGTCC
NM_012319	LIV-1	8907	ACGATGTAAGCAGCTCCACTC
NM_012319	LIV-1	8908	ACTCCCTCCAAGACCTATTC
NM_002467	MYC	8913	ACGAAATTCGAGCTGCTGCC
NM_002467	MYC	8914	ACCCAGAGTTTCATCTGCGAC
NM_002467	MYC	8915	ACAGGTCAGAGTCTGGATCAC

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NM_002467	MYC	8916	ACTGTCAAGAGGCGAACACAC
NM_000799	EPO	8917	ACTATCACTGTCCCAGACACC
NM_000799	EPO	8918	ACACTCTTCCGAGTCTACTCC
NM_004573	PLCB2	8919	ACAGTGCCTTTAAGACCTCCC
NM_000125	ESR1	8920	ACCCGTCCGCAGCTCAAGATC
NM_000125	ESR1	8921	ACGTATGGCTATGGAATCTGC
NM_000125	ESR1	8922	ACCGACTATATGTGTCCAGCC
NM_000125	ESR1	8923	ACCGCTCTAAGAAGAAGAGCC
AF258451	AF258451	8924	ACGTCTCTGGAAGAGAAGGAC
NM_000125	ESR1	8924	ACGTCTCTGGAAGAGAAGGAC
NM_001437	ESR2	8925	ACATGTGTTGTGGCCAACACC
NM_001437	ESR2	8926	ACGGTTAGTGGGAACCGTTGC
NM_001437	ESR2	8927	ACGAGGGATGCTCACTTCTGC
NM_001437	ESR2	8928	ACTCTTTGACATGCTCCTGGC
NM_018417	SAC	8929	ACGATAGGACTGGCTGCTGGC
NM_018417	SAC	8930	ACAGGTACCTGACGAGCTCAC
NM_001438	ESRRG	8931	ACACTGTATGATGACTGCTCC
NM_001438	ESRRG	8932	ACGGCCGTGCAGCATTCTAC
NM_000719	CACNA1C	8933	ACTATGGGAAACCCAAGAAGC
NM_000719	CACNA1C	8934	ACCGTGGCTGGAGGTGACATC
NM_000719	CACNA1C	8935	ACGATCAACATGGATGACCTC
NM_000719	CACNA1C	8936	ACTGACACGATCTTCACCAAC
NM_000582	SPP1	8937	ACGTTTCGCAGACCTGACATC
NM_000582	SPP1	8938	ACTGGTGCATACAAGGCCATC
NM_000582	SPP1	8939	ACAGTCAGCCGTGAATTCCAC
NM_000582	SPP1	8940	ACGATATGCTGGTTGTAGACC
NM_017442	TLR9	8941	ACTCCCTCATATCCCTGTCCC
NM_138688	TLR9	8941	ACTCCCTCATATCCCTGTCCC
NM_017442	TLR9	8942	ACACCAGCTGAAGGCCCTGAC
NM_138688	TLR9	8942	ACACCAGCTGAAGGCCCTGAC
NM_017442	TLR9	8943	ACGACGCTGTTTGTGCTGGCC
NM_138688	TLR9	8943	ACGACGCTGTTTGTGCTGGCC
NM_002210	ITGAV	8944	ACTGTGACTGGTCTTCTACCC
NM_002210	ITGAV	8945	ACTTAGCAACTCGGACTGCAC
NM_002210	ITGAV	8946	ACCTGGGAGCACAAGGAGAAC
NM_016584	IL23A	8947	ACGGACTCAGGGACAACAGTC
NM_000965	RARB	8948	ACAGCTCTCAAAGCATGCTTC
NM_000965	RARB	8949	ACGCAAGAATGCACAGAGAGC
NM_016152	RARB	8949	ACGCAAGAATGCACAGAGAGC
NM_000965	RARB	8950	ACATTCAGTGAAGTGGCCACC
NM_016152	RARB	8950	ACATTCAGTGAAGTGGCCACC
NM_001489	NR6A1	8951	ACCCATGGTGATAGTGACCAC
NM_033334	NR6A1	8951	ACCCATGGTGATAGTGACCAC
NM_033335	NR6A1	8951	ACCCATGGTGATAGTGACCAC
NM_021724	NR1D1	8952	ACTGTCGCTTCAAGAAGTGTC
NM_021724	NR1D1	8953	ACCATGTACCCGCATGGACGC

NM_021005	NR2F2	8954	ACCTGCCACTCGTACCTGTCC
NM_003889	NR1I2	8955	ACGGAGATGATCATGTCCGAC
NM_022002	NR1I2	8955	ACGGAGATGATCATGTCCGAC
NM_033013	NR1I2	8955	ACGGAGATGATCATGTCCGAC
NM_003889	NR1I2	8956	ACAGGCATCATCAGCTTTGCC
NM_022002	NR1I2	8956	ACAGGCATCATCAGCTTTGCC
NM_033013	NR1I2	8956	ACAGGCATCATCAGCTTTGCC
NM_003889	NR1I2	8957	ACGATCATGGCTATGCTCACC
NM_022002	NR1I2	8957	ACGATCATGGCTATGCTCACC
NM_033013	NR1I2	8957	ACGATCATGGCTATGCTCACC
NM_000475	NR0B1	8958	ACCACACCAGGATGACGCACC
NM_014249	NR2E3	8959	ACGCACTATGGCATCTATGCC
NM_016346	NR2E3	8959	ACGCACTATGGCATCTATGCC
NM_014249	NR2E3	8960	ACGAACCTGCCTGTGTTCTCC
NM_016346	NR2E3	8960	ACGAACCTGCCTGTGTTCTCC
NM_014249	NR2E3	8961	ACTACTCCAATGGAGAAGCTC
NM_021969	NR0B2	8962	ACGATTCTGCTGGAGGAGCCC
NM_021969	NR0B2	8963	ACGGGACCATCCTCTTCAACC
XM_051522	RDC1	8964	ACGAAGATGGTACGCCGTGTC
XM_051522	RDC1	8965	ACGCACAGCAGCCGGAAGATC
NM_002198	IRF1	8966	ACGAGATGATCTTCCAGATCC
NM_000176	NR3C1	8974	ACGGTTTCTGCGTCTTCACCC
NM_000376	VDR	8975	ACTGCTATGACCTGTGAAGGC
NM_000376	VDR	8976	ACGTCAAGTGCCATTGAGGTC
NM_000376	VDR	8977	ACGATGATCCAGAAGCTAGCC
NM_000901	NR3C2	8978	ACCAGTACTCAAGGAAGCAGC
NM_000926	PGR	8979	ACGGAGTTGTGTGCGAGCTCAC
NM_000964	RARA	8980	ACGATTACTGACCTGCGAAGC
L27586	HUMTR4OR	8981	ACGAGAAGATTGTCCACAGACC
NM_003298	NR2C2	8981	ACGAGAAGATTGTCCACAGACC
L27586	HUMTR4OR	8982	ACTAAACATCACCGGAACCGC
NM_003298	NR2C2	8982	ACTAAACATCACCGGAACCGC
U10990	HSU10990	8982	ACTAAACATCACCGGAACCGC
NM_005036	PPARA	8983	ACGCTGGTGTATGACAAAGTGC
NM_005036	PPARA	8984	ACTGCCAAGATCTGAGAAAGC
NM_005036	PPARA	8985	ACATACGGAGTTTATGAGGCC
NM_005036	PPARA	8986	ACTGCACTGGAAGTGGATGAC
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NM_006186	NR4A2	8988	ACCCCAAGAGAGTGGAAGAAC
NM_017532	HSAJ2425	8989	ACGCCAACACTTGGTTAAGGC
NM_017532	HSAJ2425	8990	ACGAGGTGGATATGACCGGTC
NM_007121	NR1H2	8991	ACGAGGAACCAGAGCGCAAGC
NM_007121	NR1H2	8992	ACCAGCAGCAGCAGGAGTCAC
NM_007121	NR1H2	8993	ACTGATCCAGCAGTTGGTGCC
NM_001489	NR6A1	8994	ACCTGCCTTTCTTCTGCGAGC
NM_033334	NR6A1	8994	ACCTGCCTTTCTTCTGCGAGC

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NM_033335	NR6A1	8994	ACCTGCCTTTCTTCTGCGAGC
NM_001489	NR6A1	8995	ACCGATACTGGTACATTTGCC
NM_033334	NR6A1	8995	ACCGATACTGGTACATTTGCC
NM_033335	NR6A1	8995	ACCGATACTGGTACATTTGCC
NM_000461	THRB	8996	ACGAGCCATTTCAGAGAGGCGC
NM_000461	THRB	8997	ACGGTTGACTTGGAAGCCTTC
NM_005123	NR1H4	8998	ACCTGAGGTAGCAGAGATGCC
NM_005123	NR1H4	8999	ACAGCTACCAGGATTTTCAGAC
NM_005123	NR1H4	9000	ACTGACTCAAGAGGAGTATGC
ENSG00000172441	ENSG00000172441	9001	ACAGCCTTCTTCAAGAGGACC
NG_001009	NG_001009	9001	ACAGCCTTCTTCAAGAGGACC
NM_004451	ESRRA	9001	ACAGCCTTCTTCAAGAGGACC
NM_004451	ESRRA	9002	ACGCTCTATGCCATGCCGTGAC
NM_002943	RORA	9003	ACGCTCTTCAACCTGTAGCTC
NM_002943	RORA	9004	ACTATGTGACTACACACCAGC
NM_134260	RORA	9004	ACTATGTGACTACACACCAGC
NM_134261	RORA	9004	ACTATGTGACTACACACCAGC
NM_134262	RORA	9004	ACTATGTGACTACACACCAGC
NM_002943	RORA	9005	ACTGTGCCGTGCCTTTGACTC
NM_134260	RORA	9005	ACTGTGCCGTGCCTTTGACTC
NM_134261	RORA	9005	ACTGTGCCGTGCCTTTGACTC
NM_134262	RORA	9005	ACTGTGCCGTGCCTTTGACTC
NM_006914	RORB	9006	ACGGGATTCTTTAGGAGGAGC
NM_005060	RORC	9007	ACGTCGTCTGGGATCCACTAC
AF124247	AF124247	9008	ACGCCATGTCTCAGGTGATCC
AF146343	AF146343	9008	ACGCCATGTCTCAGGTGATCC
NM_003822	NR5A2	9008	ACGCCATGTCTCAGGTGATCC
U80251	HSU80251	9008	ACGCCATGTCTCAGGTGATCC
U93553	HSU93553	9008	ACGCCATGTCTCAGGTGATCC
AF124247	AF124247	9009	ACTACCTCTACTACAAGCACC
AF146343	AF146343	9009	ACTACCTCTACTACAAGCACC
NM_003822	NR5A2	9009	ACTACCTCTACTACAAGCACC
U80251	HSU80251	9009	ACTACCTCTACTACAAGCACC
U93553	HSU93553	9009	ACTACCTCTACTACAAGCACC
NM_004959	NR5A1	9010	ACTGCTGCAAGCCAAGCAGAC
NM_005234	NR2F6	9011	ACGTCGAGCGGCAAGCATTAC
NM_005234	NR2F6	9012	ACGCATTACGGTGTCTTCACC
NM_003250	THRA	9013	ACCCTCCATCCCACCTATTCC
NM_005654	NR2F1	9014	ACGCACTACGGCCAATTACACC
NM_005654	NR2F1	9015	ACCATTATGGGCATCGAGAAC
NM_005654	NR2F1	9016	ACGCTCAAGGCGCTACACGTC
NM_004133	HNF4G	9017	ACGCTGAAGTTCGGTCTCGCC
NM_004133	HNF4G	9018	ACTGATCGGCAGTATGACTCC
NM_004133	HNF4G	9019	ACGCATCAGTCATTTTCACACC
NM_005122	NR1I3	9020	ACGTCAGCAAGACTCAGAGGC
NM_005122	NR1I3	9021	ACGGGAGCAGCTGTGGAAATC

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NM_005693	NR1H3	9022	ACCCACACAGAGATCCGTCCAC
U22662	HSU22662	9022	ACCCACACAGAGATCCGTCCAC
NM_005693	NR1H3	9023	ACCAGATCCGCCTGAAGAAAC
U22662	HSU22662	9023	ACCAGATCCGCCTGAAGAAAC
NM_005693	NR1H3	9024	ACGACTTTGCCAAAGCAGGGC
U22662	HSU22662	9024	ACGACTTTGCCAAAGCAGGGC
NM_005693	NR1H3	9025	ACGTGTTTTGCACTGCGTCTGC
U22662	HSU22662	9025	ACGTGTTTTGCACTGCGTCTGC
M24857	HUMHRARC	9026	ACGCCCATCAGGAGACTTTCC
NM_000966	RARG	9026	ACGCCCATCAGGAGACTTTCC
M24857	HUMHRARC	9027	ACGTGGACAAGCTGCAGGAGC
NM_000966	RARG	9027	ACGTGGACAAGCTGCAGGAGC
M24857	HUMHRARC	9028	ACTGTTTGAGGATGACTCCTC
NM_000966	RARG	9028	ACTGTTTGAGGATGACTCCTC
NM_003269	NR2E1	9029	ACATCTGGAAACCAGGGAGGC
NM_003269	NR2E1	9030	ACGAGTGTGCCAGCCTTCTCC
NM_000457	HNF4A	9031	ACGAACCACATGTACTCCTGC
X76930	HSHNF4	9031	ACGAACCACATGTACTCCTGC
X87870	HSHNF4AGN	9031	ACGAACCACATGTACTCCTGC
X87871	HSHNP4BGN	9031	ACGAACCACATGTACTCCTGC
X87872	HSHNF4CGN	9031	ACGAACCACATGTACTCCTGC
Z49825	HSHNF4A	9031	ACGAACCACATGTACTCCTGC
NM_002135	NR4A1	9032	ACGGAAGTTGTCCGAACAGAC
NM_006917	RXRG	9033	ACGAGGACGATAAGGAAGGAC
NM_006917	RXRG	9034	ACATGCCTGGAGCACCTCTTC
NM_002957	RXRA	9035	ACGCACTATGGAGTGTACAGC
NM_002957	RXRA	9036	ACTGAGCTGCTCATCGCCTCC
NM_021976	RXRB	9037	ACACGGCTATGTGCAATCTGC
NM_021976	RXRB	9038	ACTGAACTCCTCATTCGCTCC
NM_021976	RXRB	9039	ACCAGAAGTACCCTGAGCAGC
NM_004452	ESRRB	9040	ACGAGGACTATCCAAGGGAAC
X87870	HSHNF4AGN	9041	ACGGACAAGAGGAACCAAGTGC
X87871	HSHNP4BGN	9041	ACGGACAAGAGGAACCAAGTGC
X87872	HSHNF4CGN	9042	ACTGGGAACAAGGCAATGGTC
D16815	D16815	9043	ACCAGCCAGTTTCAGTGGTCAC
D16815	D16815	9044	ACACCATCCAAATGAGGCCTC
M73069	HUMANRE	9045	ACGCTGGAGAACCTGCTGGAC
AF014402	AF014402	9046	ACGGAAGGCAGGTTGTCCTTC
AF014403	AF014403	9046	ACGGAAGGCAGGTTGTCCTTC
NM_003711	PPAP2A	9046	ACGGAAGGCAGGTTGTCCTTC
AF017999	AF017999	9047	ACGACCATAACCCACCACAGC
BC038293	BC038293	9047	ACGACCATAACCCACCACAGC
NG_001312	NG_001312	9047	ACGACCATAACCCACCACAGC
NG_001337	NG_001337	9047	ACGACCATAACCCACCACAGC
NM_000314	PTEN	9047	ACGACCATAACCCACCACAGC
AF024579	AF024579	9048	ACGACATATACCTGGATACCC

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NM_002711	PPP1R3A	9048	ACGACATATACCTGGATACCC
AF024579	AF024579	9049	ACGAACCAGAAAGTACTGCTTC
NM_002711	PPP1R3A	9049	ACGAACCAGAAAGTACTGCTTC
AF084944	AF084944	9050	ACGACTCGCTACGAGGATGTC
NM_004897	MINPP1	9050	ACGACTCGCTACGAGGATGTC
AF084944	AF084944	9051	ACCAGATCCGCAAGCTGAGGC
NM_004897	MINPP1	9051	ACCAGATCCGCAAGCTGAGGC
AF084944	AF084944	9052	ACGCACCGCTGCATGGATAGC
NM_004897	MINPP1	9052	ACGCACCGCTGCATGGATAGC
AF086924	AF086924	9053	ACTGGCCACACCTACCACATC
BC032954	BC032954	9053	ACTGGCCACACCTACCACATC
AF150732	AF150732	9054	ACGGACTGGTGTTATTTGTGC
NM_012411	PTPN22	9054	ACGGACTGGTGTTATTTGTGC
NM_015967	PTPN22	9054	ACGGACTGGTGTTATTTGTGC
AF150732	AF150732	9055	ACAGCACCATGACTCTAGTGC
NM_012411	PTPN22	9055	ACAGCACCATGACTCTAGTGC
NM_015967	PTPN22	9055	ACAGCACCATGACTCTAGTGC
AF150732	AF150732	9056	ACTATGGGCTGCAAGTACACC
NM_015967	PTPN22	9056	ACTATGGGCTGCAAGTACACC
AF213044	AF213044	9057	ACTCGCAGATGGAGGGACTCC
AF213045	AF213045	9057	ACTCGCAGATGGAGGGACTCC
AF213048	AF213048	9057	ACTCGCAGATGGAGGGACTCC
AF213050	AF213050	9057	ACTCGCAGATGGAGGGACTCC
NM_005192	CDKN3	9057	ACTCGCAGATGGAGGGACTCC
AF233436	AF233436	9058	ACTCAGCGCTTCTGGTAGTGC
AF233437	AF233437	9058	ACTCAGCGCTTCTGGTAGTGC
NM_021090	MTMR3	9058	ACTCAGCGCTTCTGGTAGTGC
AF290614	AF290614	9059	ACCTGAAGAAGCTGGAGTTGC
AF290614	AF290614	9060	ACGGTGTACCTGGAGCAGAAC
AF290614	AF290614	9061	ACGAACCGGCACCAGGATGTC
BC004881	BC004881	9061	ACGAACCGGCACCAGGATGTC
AF290614	AF290614	9062	ACCTTTCTGCAGGCCCATAC
BC004881	BC004881	9062	ACCTTTCTGCAGGCCCATAC
AF318616	AF318616	9063	ACAGGACAGTATGGCAAGCTC
AF318616	AF318616	9064	ACTCCGGTGTCTCCTGGAAGC
AF331843	AF331843	9065	ACGAGTATCCCTGTGGAGGAC
NM_004418	DUSP2	9065	ACGAGTATCCCTGTGGAGGAC
AF331843	AF331843	9066	ACATCAGCTAGACGCTATACC
NM_004418	DUSP2	9066	ACATCAGCTAGACGCTATACC
AF368319	AF368319	9067	ACGCATGCACAGACGGAGATC
NM_001566	INPP4A	9067	ACGCATGCACAGACGGAGATC
NM_004027	INPP4A	9067	ACGCATGCACAGACGGAGATC
AF416902	AF416902	9068	ACTCCTCCATGGTCCACAGCC
NM_052939	FCRH3	9068	ACTCCTCCATGGTCCACAGCC
AF416902	AF416902	9069	ACGAAGCCTGGGTAGAAAGAC
NM_052939	FCRH3	9069	ACGAAGCCTGGGTAGAAAGAC

AF416902	AF416902	9070	ACCTACTCATGTGAGGCTGAC
NM_052939	FCRH3	9070	ACCTACTCATGTGAGGCTGAC
AF458589	AF458589	9071	ACCGGGACAAGAAATCTCCAC
NM_002480	PPP1R12A	9071	ACCGGGACAAGAAATCTCCAC
AF508727	AF508727	9072	ACTGTCACACCCAACCTACCC
AY038927	AY038927	9073	ACGCGAAGGTTGCAACAGGAC
XM_039106	MKP-7	9073	ACGCGAAGGTTGCAACAGGAC
AY038927	AY038927	9074	ACGCTCCCAAGATGTTGCCTC
XM_039106	MKP-7	9074	ACGCTCCCAAGATGTTGCCTC
AY038927	AY038927	9075	ACGAGCTTCAACTCTGTTTCAC
XM_039106	MKP-7	9075	ACGAGCTTCAACTCTGTTTCAC
AY040091	AY040091	9076	ACCTGCCCCGTCAGAGAAGTGC
NM_016364	LOC51207	9076	ACCTGCCCCGTCAGAGAAGTGC
AY040091	AY040091	9077	ACTATCTGCCCTAACTCAGGC
NM_016364	LOC51207	9077	ACTATCTGCCCTAACTCAGGC
BC001175	BC001175	9078	ACGTCCCTGAGTGTCTACCAC
NM_006245	PPP2R5D	9078	ACGTCCCTGAGTGTCTACCAC
BC008216	BC008216	9079	ACCAATGGCCGCAAGAAGTGC
BC008216	BC008216	9080	ACTCAACACCCTGAAGCGGGC
BC017943	BC017943	9081	ACGAAGACCTACACCAGCATC
BC017943	BC017943	9082	ACGGAAGCAGAGTGTGTACAC
BC021714	BC021714	9083	ACGATGCAGAAATTGAGCGTC
BC021714	BC021714	9084	ACTCGACGGACTACATTTGCC
BC031614	BC031614	9085	ACTGGAAGGTCCACGGAAGGC
BC031614	BC031614	9086	ACGGGATGAATCAACATTGGC
BC033103	BC033103	9087	ACGCTAGAAAGAGACATGTCC
BC036539	BC036539	9088	ACGAATCTGCCTGGTGAGTTC
XM_045128	DKFZP566K0524	9088	ACGAATCTGCCTGGTGAGTTC
BC036539	BC036539	9089	ACTCTGCCTGGTGAGTTCAAC
XM_045128	DKFZP566K0524	9089	ACTCTGCCTGGTGAGTTCAAC
ENSG00000139304	ENSG00000139304	9090	ACACCAGTCTTGACTCGAGTC
ENSG00000139304	ENSG00000139304	9091	ACTTTACCCTTCCTGTAGTGC
NM_000151	G6PC	9092	ACTGCCTTCTACGTCTCTTC
NM_000252	MTM1	9093	ACGACGGTCATTGTGCGTTGC
NM_000276	OCRL	9094	ACTTCCCATCTGGCTGCACAC
NM_001587	OCRL	9094	ACTTCCCATCTGGCTGCACAC
NM_000276	OCRL	9095	ACCAATGGACAGGTTCCCTGC
NM_001587	OCRL	9095	ACCAATGGACAGGTTCCCTGC
NM_000296	PKD1	9096	ACTAAACCTGAGTGGGAACCC
NM_000296	PKD1	9097	ACGGTCAAGGAGTTCGCCAC
NM_000446	PON1	9098	ACGATAATGCCATGTACCTCC
NM_000446	PON1	9099	ACGTGAAGTTCGAGTGGTGGC
NM_000446	PON1	9100	ACTGGCACAGTGTGCAAGGC
NM_000478	ALPL	9101	ACATCTGTGGGCATTGTGACC
NM_000507	FBP1	9102	ACCTCGCTCTGCACAGCAGTC
NM_000945	PPP3R1	9103	ACAGAATTCATTGAGGGCGTC

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NM_000945	PPP3R1	9104	ACTTCATTGAGGGCGTCTCTC
NM_000945	PPP3R1	9105	ACGACGTCCAGCAATGCTCTC
NM_001108	ACYP2	9106	ACGAATACAAGCAAAGGCACC
NM_001108	ACYP2	9107	ACAGCTAAGCAGCTGTACGTC
NM_001246	ENTPD2	9108	ACCTACCTGCTGGAGAACTTC
NM_001247	ENTPD6	9109	ACATATCCAACCACGGGAGCC
NM_001247	ENTPD6	9110	ACACAGGACATTCCGTTTCGAC
NM_001248	ENTPD3	9111	ACGATGGATCTGAACACCAGC
NM_001248	ENTPD3	9112	ACCTCCAGCACCTGGAATTTTC
NM_001249	ENTPD5	9113	ACCACAAAGCCAAGGCTCTGC
NM_001249	ENTPD5	9114	ACGCTGCAAGACTAGCAACCC
NM_001467	G6PT1	9115	ACCATATTCTTTGCCCTGGAGC
NM_001467	G6PT1	9116	ACCCTGCTGATGTTGGACTCC
NM_001467	G6PT1	9117	ACCTTGTGTGGCACCTCCAC
NM_001567	INPPL1	9118	ACTAACCCTGCCTACTACGTC
NM_001610	ACP2	9119	ACGCACAGACTTTGACCGGAC
NM_001610	ACP2	9120	ACCCTGACCCTAATGGCGACC
NM_001611	ACP5	9121	ACGATCTCCAAGCGCTGGAAC
NM_001631	ALPI	9122	ACGTCAGTAGGAGTGGTGACC
NM_001631	ALPI	9123	ACTATGAGATCCTCCGAGACC
NM_001632	ALPP	9124	ACATACGAGATCCACCGAGAC
NM_031313	ALPPL2	9124	ACATACGAGATCCACCGAGAC
NM_001776	ENTPD1	9125	ACTGCTCTGCAATTCGCCTC
NM_002194	INPP1	9126	ACGCATTAGCCAGGGTTGTTT
NM_002194	INPP1	9127	ACGGGAGGACTCATTGCATAC
NM_002452	NUDT1	9128	ACAGTGCAAGAAGGAGAGACC
NM_002452	NUDT1	9129	ACATGCGCCCATGCTGGTTCC
NM_002452	NUDT1	9130	ACGAAATTCCACGGGTACTTC
NM_002481	PPP1R12B	9131	ACAGCTTCTGGCAAGAGGTGC
NM_032105	PPP1R12B	9131	ACAGCTTCTGGCAAGAGGTGC
NM_002481	PPP1R12B	9132	ACGGAGACACGGAATAAACTC
NM_032105	PPP1R12B	9132	ACGGAGACACGGAATAAACTC
NM_002481	PPP1R12B	9133	ACCAGATTCTCTGTGGAAGC
NM_032105	PPP1R12B	9133	ACCAGATTCTCTGTGGAAGC
NM_002706	PPM1B	9134	ACGGAATGCCTGATCTTGCCC
NM_002708	PPP1CA	9135	ACTGTACAGCTGACAGAGAAC
S57501	S57501	9135	ACTGTACAGCTGACAGAGAAC
NM_002708	PPP1CA	9136	ACGTTCTCCACAAGCACGAC
S57501	S57501	9136	ACGTTCTCCACAAGCACGAC
NM_002709	PPP1CB	9137	ACGAGGAAACCATGAGTGTGC
NM_002710	PPP1CC	9138	ACTGAAATCAGAGGACTGTGC
NM_002710	PPP1CC	9139	ACCCATGAATGTGCCAGCATC
NM_002710	PPP1CC	9140	ACTGACAGAGGAGTGTCTTC
NM_002712	PPP1R7	9141	ACGTGAAGACTCTCTGCCTCC
NM_002712	PPP1R7	9142	ACCTTCAGAACCTGGATGCGC
NM_002716	PPP2R1B	9143	ACGTGATTGGAATCCGTCAGC

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NM_002716	PPP2R1B	9144	ACTGGCAGGAGACCAAGTAGC
NM_002717	PPP2R2A	9145	ACCAGGCCTGTGGAAACATAC
NM_002717	PPP2R2A	9146	ACATCCTTCACACAGCCTGGC
NM_002718	PPP2R3A	9147	ACGCTGTCCAGGTCCAATCAC
NM_002718	PPP2R3A	9148	ACCAGATGAACCTGCCTCTCC
NG_001307	NG_001307	9149	ACGGTGTTACTACCTTTGCAC
NM_002719	PPP2R5C	9149	ACGGTGTTACTACCTTTGCAC
NM_002719	PPP2R5C	9150	ACAGACCCATTGGAACAAGAC
NM_002720	PPP4C	9151	ACGGTTCGCTATCCTGATCGC
NM_002721	PPP6C	9152	ACCTGTTTCAGAACTGGAGGTC
NM_002721	PPP6C	9153	ACTGCCTGGAGATACTGTACC
NM_002721	PPP6C	9154	ACCTCATCTGCAGAGCACATC
NM_002827	PTPN1	9155	ACCCGAAATAGGTACAGAGAC
NM_002827	PTPN1	9156	ACTGCGCACAATACTGGCCAC
NM_002827	PTPN1	9157	ACGAGGAAAGACCCCTTCTCC
NM_002828	PTPN2	9158	ACGGTGGTTATATTGGCAACC
NM_002832	PTPN7	9159	ACGACCATCTTGCCAAATCCC
NM_080588	PTPN7	9159	ACGACCATCTTGCCAAATCCC
NM_080589	PTPN7	9159	ACGACCATCTTGCCAAATCCC
NM_002833	PTPN9	9160	ACTGTGGCTGTCAAGTTCCTC
NM_002833	PTPN9	9161	ACCCCTGTTGGCACTTTCCAC
NM_002834	PTPN11	9162	ACCCATCCAGATGGTGCGGTC
XM_067153	LOC131015	9162	ACCCATCCAGATGGTGCGGTC
NM_002835	PTPN12	9163	ACAGATATATCCCACAGCCAC
NM_002835	PTPN12	9164	ACATACTGCAGCCACCGGAAC
NM_002835	PTPN12	9165	ACCTCTGATGGTGCTGTGACC
NM_002837	PTPRB	9166	ACTGATTCTGTGGTGCTGCTC
NM_002837	PTPRB	9167	ACGAGGTACCTGGTGCTCCATC
NM_002838	PTPRC	9168	ACGCCAGGTCTGGAACATGAC
NM_080921	PTPRC	9168	ACGCCAGGTCTGGAACATGAC
NM_080922	PTPRC	9168	ACGCCAGGTCTGGAACATGAC
NM_002838	PTPRC	9169	ACGCTAAGGCGACAGAGATGC
NM_080921	PTPRC	9169	ACGCTAAGGCGACAGAGATGC
NM_080922	PTPRC	9169	ACGCTAAGGCGACAGAGATGC
NM_002839	PTPRD	9170	ACGTGTATCCACCAGACTCAC
NM_130391	PTPRD	9170	ACGTGTATCCACCAGACTCAC
NM_130392	PTPRD	9170	ACGTGTATCCACCAGACTCAC
NM_130393	PTPRD	9170	ACGTGTATCCACCAGACTCAC
NM_002840	PTPRF	9171	ACCTCCACTGCTGTGCATGTC
NM_130440	PTPRF	9171	ACCTCCACTGCTGTGCATGTC
NM_002840	PTPRF	9172	ACGCAGAATGCCTACATCGCC
NM_130440	PTPRF	9172	ACGCAGAATGCCTACATCGCC
NM_002840	PTPRF	9173	ACCCTGCCCTGCAACAAGTTC
NM_130440	PTPRF	9173	ACCCTGCCCTGCAACAAGTTC
NM_002841	PTPRG	9174	ACATGGAAATGGTCCCATGAC
NM_002842	PTPRH	9175	ACTGTCAGCATCTCCACAGTC

NM_002842	PTPRH	9176	ACGCAGCAGAAACCAGAACTC
NM_002843	PTPRJ	9177	ACCGCAGATCAGCAGTACAGC
NM_002843	PTPRJ	9178	ACGGACGGGCACCTTTCATTGC
NM_002845	PTPRM	9179	ACTATCAGCACCCCTCTATGCC
NM_002845	PTPRM	9180	ACTTCCAGTTCCTGGGCTGGC
NM_002846	PTPRN	9181	ACGACTCTGGGCTGCTCTATC
NM_002846	PTPRN	9182	ACGGAGATTGACATCGCTGCC
NM_002847	PTPRN2	9183	ACCTCAAGTTCCTGCCTCCTC
NM_130842	PTPRN2	9183	ACCTCAAGTTCCTGCCTCCTC
NM_130843	PTPRN2	9183	ACCTCAAGTTCCTGCCTCCTC
NM_002848	PTPRO	9184	ACATCACTCTTCGCAGTGAAC
NM_030667	PTPRO	9184	ACATCACTCTTCGCAGTGAAC
NM_030668	PTPRO	9184	ACATCACTCTTCGCAGTGAAC
NM_030669	PTPRO	9184	ACATCACTCTTCGCAGTGAAC
NM_030670	PTPRO	9184	ACATCACTCTTCGCAGTGAAC
NM_030671	PTPRO	9184	ACATCACTCTTCGCAGTGAAC
NM_002849	PTPRR	9185	ACGAGTGGGAAGCCGGTATTC
NM_002849	PTPRR	9186	ACACCAGGAGATCCACCTATC
NM_130846	PTPRR	9186	ACACCAGGAGATCCACCTATC
NM_002849	PTPRR	9187	ACGACAGTCCACAGCATGGTC
NM_130846	PTPRR	9187	ACGACAGTCCACAGCATGGTC
NM_002850	PTPRS	9188	ACACGTGTACGAGTGTGTGGC
NM_130853	PTPRS	9188	ACACGTGTACGAGTGTGTGGC
NM_130854	PTPRS	9188	ACACGTGTACGAGTGTGTGGC
NM_130855	PTPRS	9188	ACACGTGTACGAGTGTGTGGC
NM_003584	DUSP11	9189	ACTTGGAATTCCAGTGTACCC
NM_003620	PPM1D	9190	ACATCGTTGTGGAGCCCGAAC
NM_003620	PPM1D	9191	ACGTGTCCACACTCTTGACCC
NM_003626	PPFIA1	9192	ACCAGTTGATGGTCTCCATGC
NM_003671	CDC14B	9193	ACCAAGCAAATGCTGCCTTCC
NM_033331	CDC14B	9193	ACCAAGCAAATGCTGCCTTCC
NM_033332	CDC14B	9193	ACCAAGCAAATGCTGCCTTCC
NM_003671	CDC14B	9194	ACACGCTTTACGGATGCTGGC
NM_033331	CDC14B	9194	ACACGCTTTACGGATGCTGGC
NM_033332	CDC14B	9194	ACACGCTTTACGGATGCTGGC
NM_003672	CDC14A	9195	ACTGGTTATCCTCTTCACGCC
NM_033312	CDC14A	9195	ACTGGTTATCCTCTTCACGCC
NM_033313	CDC14A	9195	ACTGGTTATCCTCTTCACGCC
NM_003672	CDC14A	9196	ACTGGTATAACCCAGGGAGAC
NM_033312	CDC14A	9196	ACTGGTATAACCCAGGGAGAC
NM_003712	PPAP2C	9197	ACACACCACTGGAGCGATGTC
NM_003713	PPAP2B	9198	ACATGACGCTGTGCTCTGTGC
NM_003800	RNGTT	9199	ACAGCAGATGGTACTCGGTAC
NM_003832	PSPHL	9200	ACGAAGGAATCGGATGCTTTC
NM_003832	PSPHL	9201	ACGTTGGTACAGATGATCTGC
NM_003837	FBP2	9202	ACCTCAATGCTGACGGCCATC

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NM_003837	FBP2	9203	ACTATTGACTGCCTGGCCTCC
NM_003837	FBP2	9204	ACGAAATTCCTGAGGATGGC
NM_003866	INPP4B	9205	ACGAATGCAGGTACACAGCCC
NM_003866	INPP4B	9206	ACGTGCCAAAGACAGGACATC
NM_003895	SYNJ1	9207	ACTGGTGGGAAGCAATTTTCGC
NM_003895	SYNJ1	9208	ACGTGGAGGAACCTTCTTCCTC
NM_003895	SYNJ1	9209	ACCCCGAAAGGATGGGTAACC
NM_003912	MTMR2	9210	ACATGGAAGAACCACCCTTGC
NM_016156	MTMR2	9210	ACATGGAAGAACCACCCTTGC
NM_003978	PSTPIP1	9211	ACGACATACGAGCAGAAGTGC
NM_004090	DUSP3	9212	ACGCTGCAGAACTAGGCATC
NM_004156	PPP2CB	9213	ACTGTGCAAGAGGTTTCGTTGC
NM_004156	PPP2CB	9214	ACGGTGCGTTATCCAGAACGC
NM_004419	DUSP5	9215	ACACCAGTGGTAAATGTCAGC
NM_004420	DUSP8	9216	ACGGTGACCATTGCGGAGCTC
NM_004420	DUSP8	9217	ACTAAGCTACGTCTCAACGC
M64930	HUMPROP2AB	9218	ACCCCAATAGGTTTGGGACAC
NM_004576	PPP2R2B	9218	ACCCCAATAGGTTTGGGACAC
NM_004577	PSPH	9219	ACGCTCAATATCCCAGCAACC
NM_004687	MTMR4	9220	ACGCAGTGCCAAGAGTGGCTC
NM_004687	MTMR4	9221	ACAGAGACTGAGGTGACTCGC
NM_004715	CTDP1	9222	ACGCCAGACGAGAGGGACATC
NM_048368	CTDP1	9222	ACGCCAGACGAGAGGGACATC
NM_004901	LYSAL1	9223	ACGGTACCTGGCAGGAGTTAC
NM_004901	LYSAL1	9224	ACGACCTTCTGACCGATATCC
NM_005134	PPP4R1	9225	ACATGGTGGCCCCGAGTTTGC
NM_005398	PPP1R3C	9226	ACGAGTTTCTCTGGGCCCCGTAC
NM_005398	PPP1R3C	9227	ACCTTTGTCTGTCTGGAGAAC
NM_005401	PTPN14	9228	ACAGCACAGGGCAAGAATGCC
NM_005401	PTPN14	9229	ACAGTTTCATCCAGGCCTCCC
NM_005536	IMPA1	9230	ACGTATCTTAACCGACAACCC
NM_005536	IMPA1	9231	ACGGCAGCCTCATAGTCAATC
NM_005539	INPP5A	9232	ACCTACAAATCCCAGGAGCAC
NM_005539	INPP5A	9233	ACCAAGCCCTTCCGTGTACTC
NM_005539	INPP5A	9234	ACCTGGACATCTCGTTCCCTC
NM_005541	INPP5D	9235	ACATTCACTGTTTCAGGCATCC
NM_005541	INPP5D	9236	ACGATCACGTCTCTGGTTTCTC
NM_005541	INPP5D	9237	ACGCCCCGAGATGTTTGAGAAC
NM_005670	EPM2A	9238	ACTATTGCAGGCCACCAAGCC
NM_005670	EPM2A	9239	ACGGCCGAGTACAGATGCTGC
NM_005704	PTPRU	9240	ACCACCAACTCCATCATTGGC
NM_133177	PTPRU	9240	ACCACCAACTCCATCATTGGC
NM_133178	PTPRU	9240	ACCACCAACTCCATCATTGGC
NM_005765	ATP6M8-9	9241	ACGACCTTTCTTGGCCAGGAC
NM_006239	PPEF2	9242	ACTGAGTTCTTGGAGGCCTTC
NM_006240	PPEF1	9243	ACCGTTGAATACATGTCCAGC

NM_006241	PPP1R2	9244	ACTGTCGACGAGGAGCTGAGC
NG_001026	NG_001026	9245	ACTAGATGAACCAAGCACTCC
NM_006241	PPP1R2	9245	ACTAGATGAACCAAGCACTCC
NM_006241	PPP1R2	9246	ACATTAGCTGCAGCTGAAGGC
NM_006247	PPP5C	9247	ACAGCCAAGGACTACGAGAAC
NM_006247	PPP5C	9248	ACTGCCATCTACTATGGCAAC
NM_006247	PPP5C	9249	ACCATGGCACTGGGCAAGTTC
NM_006264	PTPN13	9250	ACCAGTGCGGACTTCAACTAC
NM_080683	PTPN13	9250	ACCAGTGCGGACTTCAACTAC
NM_080684	PTPN13	9250	ACCAGTGCGGACTTCAACTAC
NM_080685	PTPN13	9250	ACCAGTGCGGACTTCAACTAC
NM_006264	PTPN13	9251	ACGCTGAGATTCTGAAGAGGC
NM_080683	PTPN13	9251	ACGCTGAGATTCTGAAGAGGC
NM_080685	PTPN13	9251	ACGCTGAGATTCTGAAGAGGC
NM_006264	PTPN13	9252	ACGAACATGTCCCGGTAACCC
NM_080683	PTPN13	9252	ACGAACATGTCCCGGTAACCC
NM_080684	PTPN13	9252	ACGAACATGTCCCGGTAACCC
NM_080685	PTPN13	9252	ACGAACATGTCCCGGTAACCC
NM_006305	ANP32A	9253	ACCAGTCGGTCGAATGAAGGC
NM_012403	ANP32C	9253	ACCAGTCGGTCGAATGAAGGC
NM_006504	PTPRE	9254	ACGAAGATGCCCAACGGAATC
NM_130435	PTPRE	9254	ACGAAGATGCCCAACGGAATC
NM_006504	PTPRE	9255	ACCGACTTCTGGAGAATGGTC
NM_130435	PTPRE	9255	ACCGACTTCTGGAGAATGGTC
NM_006504	PTPRE	9256	ACGGAGAACATGAGGACGGGC
NM_130435	PTPRE	9256	ACGGAGAACATGAGGACGGGC
NM_006741	PPP1R1A	9257	ACCAGCAGCAAGGAGAGGAAC
NM_006903	SID6-306	9258	ACTACCTCGGTGGACAAATGC
NM_006903	SID6-306	9259	ACTGCGAATGATCCTGAAGCC
NM_007026	DUSP14	9260	ACATCACCTCCTCTCTATTCC
NM_007026	DUSP14	9261	ACGTGCCTCTGGCTGACATGC
NM_007026	DUSP14	9262	ACTTCCACAACGTGTGCCTGC
NM_007039	PTPN21	9263	ACGGATGTCTCTGCCTAAACC
NM_007050	PTPRT	9264	ACGGAGAATGACACCCACTGC
NM_133170	PTPRT	9264	ACGGAGAATGACACCCACTGC
NM_007079	PTP4A3	9265	ACGGCCAAGTTCTGTGAGGCC
NM_032611	PTP4A3	9265	ACGGCCAAGTTCTGTGAGGCC
NM_007207	DUSP10	9266	ACTGCAGCAAGAGTCACCTGC
NM_007207	DUSP10	9267	ACTGAGCAGGATGCTCAGGAC
NM_144728	DUSP10	9267	ACTGAGCAGGATGCTCAGGAC
NM_144729	DUSP10	9267	ACTGAGCAGGATGCTCAGGAC
NM_007240	DUSP12	9268	ACCTGGTATGGTGAACAGTGC
NM_007254	PNKP	9269	ACCTCAAGTGGAGCTGGTCGC
NM_007254	PNKP	9270	ACGCGTATGCGGAAGTCAAAC
NM_007254	PNKP	9271	ACGAAAGACTTCTCCTGCGCC
NM_012404	ANP32D	9272	ACCAGTCAGTCAAATGAAGGC

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NM_013239	PR48	9273	ACCCAGCTGACCGAATTCTTC
NM_013239	PR48	9274	ACCGTCTTCTTCGACACCTTC
NM_013315	TPTE	9275	ACGTGTGTTAGCACGACTTTC
NM_013315	TPTE	9276	ACGTAAATGAGTGGATGGCTC
NM_130785	TPIP	9276	ACGTAAATGAGTGGATGGCTC
NM_002713	PPP1R8	9277	ACACCCTGCAGTCTATAACCC
NM_014110	PPP1R8	9277	ACACCCTGCAGTCTATAACCC
NM_138558	PPP1R8	9277	ACACCCTGCAGTCTATAACCC
NM_014214	IMPA2	9278	ACGTGTGTGCTCACCCACAGC
NM_014369	PTPN18	9279	ACCGTGAGGAAGAACCGCTAC
NM_014369	PTPN18	9280	ACGTGGCTGAATGAGGACATC
NM_014634	FEM-2	9281	ACCATCACGGTCATGGTGGTC
NM_014659	KIAA0377	9282	ACGAGAGTGACAGCGAGCTCC
NM_014659	KIAA0377	9283	ACCGGTTCCATGTGGAGCTAC
NM_014787	DNAJC6	9284	ACCCATCAGGTCAGGATTTGC
NM_014787	DNAJC6	9285	ACACCAGTTGGCATGGCAGAC
NM_014906	POPX1	9286	ACATTGGCCCCGTTCTGTCTTC
NM_014906	POPX1	9287	ACTAGGCACTAGCCTGTCCCTC
NM_015216	KIAA0433	9288	ACCGTTGTCAATGAGCTCAAC
NM_015216	KIAA0433	9289	ACGAGCACTAAAGCAAGCAGC
NM_016086	LOC51657	9290	ACAGCCATGTGATCACTGCCC
NM_016086	LOC51657	9291	ACGGTCTTCGTTGGCAATTTTC
NM_016147	PME-1	9292	ACTGGAGTGTGAAGAGTGGCC
NM_016147	PME-1	9293	ACGGTAGCTGAAGCTGTTGCC
NM_016340	RA-GEF-2	9294	ACGGCTCCATGGTCTTGCCCTC
NM_016340	RA-GEF-2	9295	ACGGTGACCCTGCTATGACTC
NM_016340	RA-GEF-2	9296	ACATGGCAAGGAAGGTGAAGC
NM_016361	LOC51205	9297	ACATGGTGCAAGGTGCTGTTTC
NM_016532	SKIP	9298	ACGGTGGAGTCAACATCTGCC
NM_130766	SKIP	9298	ACGGTGGAGTCAACATCTGCC
NM_016532	SKIP	9299	ACCTCCAACGACTATGACACC
NM_130766	SKIP	9299	ACCTCCAACGACTATGACACC
NM_017607	PPP1R12C	9300	ACGACAGGGGAGTTCTGGTGCC
NM_017677	FLJ20126	9301	ACGTTGAATGCCATGGCCAAC
NM_017677	FLJ20126	9302	ACCTTGGGTATTTCTGAGGCC
NM_017813	FLJ20421	9303	ACCGTCCTCCACGAGAAGTCC
NM_017813	FLJ20421	9304	ACCCCATGCTAGGAGTTATAC
NM_018159	NUDT11	9305	ACGCGAGAGTGGTTCAAAGTC
NM_018276	SSH-3	9306	ACCTTCTACCCTGAGCGCTTC
NM_018461	MDS026	9307	ACGTTTGAGTGTGCTGGAAC
NM_018461	MDS026	9308	ACCGGTTTCGGATAGCGCCATC
NM_018984	SSH1	9309	ACCCTCAGCTTAAGTGAGAGC
NM_018984	SSH1	9310	ACTGAAGGAATTCGGCTGGCC
NM_018984	SSH1	9311	ACAGTCCTGCCAAAGTCCCTC
NM_019061	3-PAP	9312	ACTTCATCATACCCAGGCTCC
NM_019061	3-PAP	9313	ACGACCTGTCAAGCAACTTCC

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NM_019892	PPI5PIV	9314	ACAGGGTCCATCTTCAAGGGC
NM_019892	PPI5PIV	9315	ACCATTCCGTTGGCAGCTGGC
NM_020185	MKPX	9316	ACTTCATTACGAGTGCCGGC
NM_020185	MKPX	9317	ACTATGGAGAGAGCCCTTTGC
NM_020354	LALP1	9318	ACGAAGCTGCCAAGATCCTGC
NM_020354	LALP1	9319	ACCAGCGAGTTCTACGGCTTC
NM_021003	PPM1A	9320	ACTGGAGGATGCACATACGGC
XM_070180	LOC137012	9320	ACTGGAGGATGCACATACGGC
NM_021003	PPM1A	9321	ACTTCAGAATGCAGGTGGCTC
NM_021129	PP	9322	ACTTGAAGCAAGGTATGTGC
NM_021131	PPP2R4	9323	ACAGGAGATCCACACAGTTCC
NM_021131	PPP2R4	9324	ACCTTGGTGGCCACAGTGGTC
NM_021131	PPP2R4	9325	ACGTCCCTGTGATCCAGCAC
NM_021132	PPP3CB	9326	ACTTATCAATGAGGGTGCTGC
NM_021132	PPP3CB	9327	ACGAGCCACCTGCATTTGGAC
NM_021132	PPP3CB	9328	ACTGCCACCTCGGAAAGATGC
NM_021176	IGRP	9329	ACCCAAGATGATATGGGTAGC
NM_021176	IGRP	9330	ACCATTGACCTGCTGTGGTCC
NM_002287	LAIR1	9331	ACGATGTGTCTCAAGCTAGTC
NM_021706	LAIR1	9331	ACGATGTGTCTCAAGCTAGTC
NM_021708	LAIR1	9331	ACGATGTGTCTCAAGCTAGTC
NM_002287	LAIR1	9332	ACTGAGCATGCACCTGCTTCC
NM_021706	LAIR1	9332	ACTGAGCATGCACCTGCTTCC
NM_021708	LAIR1	9332	ACTGAGCATGCACCTGCTTCC
NM_022076	LOC63904	9333	ACCGACAACTCCTTCTGTCC
NM_022076	LOC63904	9334	ACCACCGTGCGCATGATCAAC
NM_022126	LHPP	9335	ACGGTGAGGTTCTGCACCAAC
NM_022126	LHPP	9336	ACTAACGCCTTCCAGGTGCTC
NM_022648	TNS	9337	ACGAAGAAAGACTCCCTGCAC
NM_024025	MGC1136	9338	ACGACAGCCTGTAACCATGCC
NM_030768	ILKAP	9339	ACAGACTGAAGGGAAAGGAGC
NM_030768	ILKAP	9340	ACACATGCAGCCTTAAGCCTC
NM_030791	LOC81537	9341	ACGTTGGAGGTCTTCTACAAC
NM_030791	LOC81537	9342	ACGATCACCATTCTTTAGCC
NM_030949	PPP1R14C	9343	ACTACGATCGTAAGGAGCTTC
NM_030949	PPP1R14C	9344	ACAGAGTCCCTGGGATTTGTAC
NM_032781	FLJ14427	9345	ACCGCCACAAACCTCGTCTCC
NM_033068	ACPT	9346	ACGCCCACGGTCTTCCACTAC
NM_080789	ACPT	9346	ACGCCCACGGTCTTCCACTAC
NM_080791	ACPT	9346	ACGCCCACGGTCTTCCACTAC
NM_033068	ACPT	9347	ACTGTCACCGTCTCCCTCTTC
NM_080789	ACPT	9347	ACTGTCACCGTCTCCCTCTTC
NM_080790	ACPT	9347	ACTGTCACCGTCTCCCTCTTC
NM_080791	ACPT	9347	ACTGTCACCGTCTCCCTCTTC
NM_033256	PPP1R14A	9348	ACCCTGTGAGGACTTCATCC
NM_033313	CDC14A	9349	ACGAAGCAGAGGAAAGAAACC

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NM_057158	DUSP4	9350	ACGGTCCAGGTGTCTGTGTTC
NG_001182	NG_001182	9351	ACTCCACGTTCTAGATTGGCC
NM_003479	PTP4A2	9351	ACTCCACGTTCTAGATTGGCC
NM_080391	PTP4A2	9351	ACTCCACGTTCTAGATTGGCC
NM_003479	PTP4A2	9352	ACACCAGCAGAACATTAGGCC
NM_080391	PTP4A2	9352	ACACCAGCAGAACATTAGGCC
NM_080392	PTP4A2	9352	ACACCAGCAGAACATTAGGCC
NM_080422	PTPN2	9353	ACAGCAAGACCTGAAGCCCAC
NM_080423	PTPN2	9353	ACAGCAAGACCTGAAGCCCAC
NM_080611	DUSP15	9354	ACAGACCTGGATCAGCTGGGC
NM_080611	DUSP15	9355	ACCTTCATCCACTGCTGCCGC
NM_080611	DUSP15	9356	ACCTGCCTTGTGCACTGCACC
NM_006264	PTPN13	9357	ACGCTGAAGTTATCCAGTCTC
NM_080683	PTPN13	9357	ACGCTGAAGTTATCCAGTCTC
NM_080684	PTPN13	9357	ACGCTGAAGTTATCCAGTCTC
NM_080685	PTPN13	9357	ACGCTGAAGTTATCCAGTCTC
NM_004648	PTPNS1	9358	ACACGTGTCCCGGACAGAAAC
NM_080792	PTPNS1	9358	ACACGTGTCCCGGACAGAAAC
NM_130785	TPIP	9359	ACAGGAGGCAAAGGAAGAACC
XM_166267	LOC220115	9359	ACAGGAGGCAAAGGAAGAACC
NM_006750	SNTB2	9360	ACCCGGATGCCGATCCTCATC
NM_130845	SNTB2	9360	ACCCGGATGCCGATCCTCATC
NM_006750	SNTB2	9361	ACCTAGATGGTGGAAGACAGC
NM_130845	SNTB2	9361	ACCTAGATGGTGGAAGACAGC
NM_002849	PTPRR	9362	ACGGAGAAAGCCTTCATTGCC
NM_130846	PTPRR	9362	ACGGAGAAAGCCTTCATTGCC
NM_030764	SPAP1	9363	ACGTTCTGCCACTAATGAACC
NM_138738	SPAP1	9363	ACGTTCTGCCACTAATGAACC
NM_030764	SPAP1	9364	ACGCTCAGCAAACATCAGGAC
NM_138738	SPAP1	9364	ACGCTCAGCAAACATCAGGAC
NM_138739	SPAP1	9365	ACTGGCTGTGTCTCACCAGCC
NM_139283	TA-PP2C	9366	ACGGACTTCCGTAAGGGCCTC
NM_147180	PPP3R2	9367	ACGTTGAGGTTTGC GTTCAGC
NM_147180	PPP3R2	9368	ACGATGATGGTGGGCAACAAC
NM_005605	PPP3CC	9369	ACATCTGTAACCTCAGCACAC
S46622	S46622	9369	ACATCTGTAACCTCAGCACAC
XM_030846	SSH2	9370	ACGACTCAGGGATGTGCAACC
XM_038489	PIB5PA	9371	ACGTTTGCCATCGACAGTGAC
XM_038489	PIB5PA	9372	ACCCACAGCATCCTCATCGGC
XM_044665	LOC92370	9373	ACAGAGAATCATGCCCGACCC
XM_044665	LOC92370	9374	ACGACCACCACAAGCGTTCTC
XM_044727	MTMR7	9375	ACATGCTGGAAGTGTGTGAAC
XM_044727	MTMR7	9376	ACTGGAACAATTTCCCTGTGC
XM_044727	MTMR7	9377	ACTGGCAGTGAAGGAAGAAAC
XM_046577	MTMR1	9378	ACGCTTTGGACACAGGTTTGC
XM_054936	LOC114971	9379	ACGATCCGGTCATACATCCAC

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XM_058886	LOC124997	9380	ACTGACTCTCGGCCTGAGAAC
XM_058886	LOC124997	9381	ACCAAGATTGGCGTCTGCTCC
XM_059988	LOC138639	9382	ACAGATGGCCCTAAGCCTGGC
XM_059988	LOC138639	9383	ACTGGTCGTCCGTATTTGAAC
XM_060772	LOC127993	9384	ACGCTCAGCCATATCTCCCGC
XM_061101	LOC118707	9385	ACAGCCAAGCTGTCCAGCTGC
XM_114902	LOC203688	9385	ACAGCCAAGCTGTCCAGCTGC
XM_171375	LOC256242	9385	ACAGCCAAGCTGTCCAGCTGC
XM_061101	LOC118707	9386	ACGCTGTCCAGCTGCCAAGTC
XM_089436	LOC159193	9386	ACGCTGTCCAGCTGCCAAGTC
XM_114902	LOC203688	9386	ACGCTGTCCAGCTGCCAAGTC
XM_171375	LOC256242	9386	ACGCTGTCCAGCTGCCAAGTC
XM_061101	LOC118707	9387	ACGCCCTCCTTCTCTCTGGAC
XM_114902	LOC203688	9387	ACGCCCTCCTTCTCTCTGGAC
XM_171375	LOC256242	9387	ACGCCCTCCTTCTCTCTGGAC
XM_061191	LOC118879	9388	ACTGTCAGGAATCTTCTGGGC
XM_061191	LOC118879	9389	ACGAATGCCTACTCATCTGCC
XM_062692	LOC121554	9390	ACGCTGTGGGCAGGTATGGTC
XM_069073	LOC134897	9391	ACCCATCCACACAGTGCAGTC
XM_071015	LOC138654	9392	ACTTCCAGCTGCAGCACGCTC
XM_071015	LOC138654	9393	ACGATTCTGGAAGGACCCTTC
XM_071015	LOC138654	9394	ACTTCTGGCCAACGGAGATGC
XM_086863	LOC150290	9395	ACCTCACGTCTCTGTGACTTC
XM_087562	LOC152926	9396	ACATGGCAGGCTTGCAATGAC
XM_089436	LOC159193	9397	ACGACGTTCTGAACAAGGATC
XM_093300	LOC165582	9398	ACGGCCTCTATTGCTGAACGC
XM_095533	LOC169142	9399	ACTCACTCTTGGTGACCGAGC
XM_095533	LOC169142	9400	ACGAGTTTGAGGAAATCACGC
XM_114343	LOC201562	9401	ACAGAGGTACAGAGTGAAGAC
XM_115330	LOC197099	9402	ACGAAAGGTGCTGTGCATCCC
XM_166125	KIAA1274	9403	ACCAGCAAGGCCAAGTCCATC
XM_167349	LOC223021	9404	ACACGGTATGTTTCAGTTCCTC
XM_167970	MTMR6	9405	ACCACTGTATCTTACGGCTAC
XM_167970	MTMR6	9406	ACAGCCAATCCAGTCAATCGC
XM_167970	MTMR6	9407	ACCTATAGAGGGCAGCAGCCC
XM_171208	LOC257019	9408	ACGAGGAGAACATTTCTGCTC
XM_171312	LOC256415	9409	ACGATGTTAGGAAAGACGTGC
XM_171336	LOC256840	9410	ACCTCTATTCACTGGTGTGC
XM_171336	LOC256840	9411	ACTGAGAGAGCTCTCATCAGC
XM_171336	LOC256840	9412	ACGAAAGGCAAGGTCCTGGTC
XM_171634	LOC255048	9413	ACGCAGTTGTTGTGCTGAACC
NM_000283	PDE6B	9414	ACCATGGAGCGCGTGGTCTTC
NM_000283	PDE6B	9415	ACATGTGGCATCCAGATGTAC
NM_000440	PDE6A	9416	ACGTCATCCCGAATCCACCTC
NM_000921	PDE3A	9417	ACGGTCGCCTGGAGACCTTAC
NM_000921	PDE3A	9418	ACCAACAGTGACAGCAGTGAC

NM_000922	PDE3B	9419	ACCGGCTACGTGAAGAGCTGC
NM_000922	PDE3B	9420	ACTGGGTGCTTTCTCAGGTTT
NM_000922	PDE3B	9421	ACTCAGGAAGGATTCTCAGTC
NM_000923	PDE4C	9422	ACTGCCTAGGAGCAGCCAAGC
NM_000923	PDE4C	9423	ACGTTCAAGCGGATCCTGAAC
NM_000924	PDE1B	9424	ACGTTCCGAAGCATTGTGCAC
NM_000924	PDE1B	9425	ACCAGCTTCCACATCCAGACC
NM_001083	PDE5A	9426	ACCTGTATGAGGCCCTGACCC
NM_033430	PDE5A	9426	ACCTGTATGAGGCCCTGACCC
NM_033431	PDE5A	9426	ACCTGTATGAGGCCCTGACCC
NM_033437	PDE5A	9426	ACCTGTATGAGGCCCTGACCC
NM_002599	PDE2A	9427	ACCCTCAGCAACGCAGAGATC
NM_002600	PDE4B	9428	ACTGCTGAACCGGGAGCTGAC
NM_002600	PDE4B	9429	ACCATGGTACACTGTGCAGAC
NM_002606	PDE9A	9430	ACGTACTGCAACTCCAGCGAC
NM_002606	PDE9A	9431	ACGAAGTTGACTCCTCGACGC
NM_005019	PDE1A	9432	ACGAAGCTGAATTAGGGCTTC
NM_005020	PDE1C	9433	ACGCCTTATCCCTTATGCTGC
NM_005021	ENPP3	9434	ACAGACCGAGGTGATTGCTGC
NM_005021	ENPP3	9435	ACGAACCTGATTCTCTGGAC
NM_006204	PDE6C	9436	ACGCCAGATCCTTATGTGGTC
NM_006208	ENPP1	9437	ACCCTAGACACCTTAGCTTTC
NM_006661	PDE10A	9438	ACCATCCTGTGCATGCCCATC
NM_006661	PDE10A	9439	ACCAGCTACCTGCAGAAGTTC
NM_014936	ENPP4	9440	ACCAATTCTGAACCCACCAGTC
NM_015474	SAMHD1	9441	ACCGAGATGTTCTCTGTGTTC
NM_016641	MIR16	9442	ACCAGCATTAATCACAGACC
NM_016641	MIR16	9443	ACGTGGTCAGCTAAAGGAATC
NM_016953	PDE11A	9444	ACGTTTAAAGGCAGCCAACATC
NM_017711	FLJ20207	9445	ACTGAATTCCTCTTCCGCCGC
NM_018945	PDE7B	9446	ACGGCTTCTTGCTCATTTGCC
NM_018945	PDE7B	9447	ACCAAGGCCCAGTGGAAGAGC
NM_021572	ENPP5	9448	ACTATGGTGTTCACGTGAAGC
NM_021572	ENPP5	9449	ACGAGCCCATAAATCTTGGTC
NM_021572	ENPP5	9450	ACGACGTTCCAGAAAGGTGGC
NM_024307	MGC4171	9451	ACGGAGAAGCTGGAGGTTTAC
NM_030792	PP1665	9452	ACCCTGAGTGTGAACCTCTAC
XM_031443	PDE8A	9453	ACGTTTCCAGCCAGAGACGAC
XM_031443	PDE8A	9454	ACGTAGTCCCATGCCTGTGAC
XM_037534	PDE7A	9455	ACTTGAAGTGTCTGTCTCTGC
XM_037534	PDE7A	9456	ACATCACCCTGGAGATCTGC
XM_045585	KIAA1434	9457	ACCTCATGGACCTCAGATCTC
XM_045585	KIAA1434	9458	ACCGCCTGAAGCAGGAATTGC
NM_000068	CACNA1A	9459	ACCTCAGGCCTTCTACTGGAC
NM_023035	CACNA1A	9459	ACCTCAGGCCTTCTACTGGAC
NM_000068	CACNA1A	9460	ACTAACTTCCGGACCTTCTTC

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NM_023035	CACNA1A	9460	ACTAACTTCCGGACCTTCTTC
XM_059898	LOC137057	9461	ACAGCATGGCCATCATCTCCC
XM_093333	LOC165622	9462	ACTCAACAGGACCATCGGACC
XM_093333	LOC165622	9463	ACTGTTCTGTGAATGCGCCC
XM_115430	LOC204524	9464	ACCTACGACCAGGATGTGGAC
XM_115430	LOC204524	9465	ACATGAGACGGAGTGGAGAGC
XM_166251	LOC220032	9466	ACGGAACACCAAGGCCATTTC
XM_166251	LOC220032	9467	ACGTGAGGCTACCTTTCAAAC
NM_000069	CACNA1S	9468	ACGATCCGTGTCTGTGTTCAC
NM_000069	CACNA1S	9469	ACGATCTGGAAGAGAACCAGC
NM_000079	CHRNA1	9470	ACGACTACAGCAGCGTGGTGC
NM_000079	CHRNA1	9471	ACCAGAACTGCAGCATGAAGC
NM_000079	CHRNA1	9472	ACGTCAGACCAGGAGTCTAAC
NM_000080	CHRNE	9473	ACTGCCGAAGAGGTGGAGTTC
NM_000080	CHRNE	9474	ACTTGCGTCATCGTGCTCAAC
NM_000080	CHRNE	9475	ACTGCCCTTGACAACATCTGC
NM_000083	CLCN1	9476	ACCAAGGATGCTGTCACCATC
NM_000083	CLCN1	9477	ACGCTACCCTACTTGCCTGAC
NM_000083	CLCN1	9478	ACCTGGAACCTGCCTGAGGAC
NM_000084	CLCN5	9479	ACGCAAAGAGTCAACATGGGC
NM_000087	CNGA1	9480	ACCTGGACAATGGTTATTGCC
NM_000087	CNGA1	9481	ACTCTTGGCTGAGTATGAGTC
NM_000171	GLRA1	9482	ACCCAAGCCTATGTCACCCTC
NM_000171	GLRA1	9483	ACCACAGGTAAATTACCTGC
NM_000171	GLRA1	9484	ACATATCCCGCATTGGCTTCC
NM_000217	KCNA1	9485	ACCCCTAAGAAACGCATGCGC
NM_000217	KCNA1	9486	ACCAATTGCCCTGCCCGTACC
NM_000218	KCNQ1	9487	ACGCCCATTTCATCATCGAC
NM_000218	KCNQ1	9488	ACGCACTTCAACCGGCAGATC
NM_000218	KCNQ1	9489	ACGCCCTCACTGTTTCATCTCC
NM_000219	KCNE1	9490	ACGAAGCTGGAGACTCGAAC
NM_000219	KCNE1	9491	ACCGACCCATTCAACGTCTAC
NM_000220	KCNJ1	9492	ACGCTTCTGAAGACCACAGTC
NM_000220	KCNJ1	9493	ACGACAGTGGAGTGGAGACC
NM_000297	PKD2	9494	ACGTACGACCAAGATGGAGAC
NM_000334	SCN4A	9495	ACGGTGTACTTCACCAACGCC
NM_000335	SCN5A	9496	ACGCTGCCAGATCTCTATGGC
NM_000335	SCN5A	9497	ACCTTGTGGTCCTGAATCTC
NM_000335	SCN5A	9498	ACCTACACCATCGTGAACAAC
NM_000335	SCN5A	9499	ACCAGCATGCTGTGCCTCTTC
NM_006514	SCN10A	9499	ACCAGCATGCTGTGCCTCTTC
NM_000336	SCNN1B	9500	ACAGCCATGTGGTTCTGCTC
NM_000336	SCNN1B	9501	ACCTTCTCCATCTGGAACCAC
NM_000338	SLC12A1	9502	ACTTAACCACAGTGGAGACC
NM_000342	SLC4A1	9503	ACACTCTCGGTGCCTGATGGC
NM_000492	CFTR	9504	ACGAGGTGCAAGATACAAGGC

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NM_000525	KCNJ11	9505	ACCGCCATCATGCTTGGCTGC
NM_000525	KCNJ11	9506	ACAGTGCCACACCACTCTGC
NM_000540	RYR1	9507	ACTGTCTACCACTGCTGCC
NM_000540	RYR1	9508	ACTCGTAGCAACTGTGCCCTC
NM_000701	ATP1A1	9509	ACTGGCTGCAAGGTGGATAAC
NM_000702	ATP1A2	9510	ACTGGATGACCACAAGCTGTC
NM_000703	ATP1A3	9511	ACGCAGGCAGCTGACATGATC
NM_000704	ATP4A	9512	ACCATCGCCTTCTTCTCCACC
NM_000704	ATP4A	9513	ACCATCTTCAACTTCATGCCC
NM_000718	CACNA1B	9514	ACGCAGAACTGCTTCACCGTC
NM_000718	CACNA1B	9515	ACGGTGATGTCTGAATGCAGC
NM_000721	CACNA1E	9516	ACACATGCACTGCAGAAGGCC
NM_000721	CACNA1E	9517	ACCCTCTCACCCGCTACATGC
NM_000742	CHRNA2	9518	ACGAACCAAATGATGACCACC
NM_000742	CHRNA2	9519	ACGTATGTTGCCATGGTCATC
NM_000743	CHRNA3	9520	ACCGTGTCTGACCCAGTCATC
NM_000743	CHRNA3	9521	ACTCGACGTGACCTACTTCCC
NM_000743	CHRNA3	9522	ACCCTTGTCATCGTCATCAC
NM_000744	CHRNA4	9523	ACACTCTTCTCCGGTTACAAC
NM_000744	CHRNA4	9524	ACTGTCACCTCCATCCGCATC
NM_000745	CHRNA5	9525	ACTACCCTGTATTGGGCTCTC
NM_000745	CHRNA5	9526	ACGCTGCGCTCGATTCTATTC
NM_000747	CHRNA1	9527	ACGCCTCTCTTCTACCTGGTC
NM_000748	CHRNA2	9528	ACCAATGCTGACGGCATGTAC
NM_000748	CHRNA2	9529	ACCTACACCACCACCACCTTC
NM_000749	CHRNA3	9530	ACCGGAACGTGTGTCTGGACC
NM_000749	CHRNA3	9531	ACGTTCTTGACCGAATCTTCC
NM_000750	CHRNA4	9532	ACGGTGTCAGCTTCATCGCCC
NM_000751	CHRNA5	9533	ACGGGCTACAACAAGGAGCTC
NM_000751	CHRNA5	9534	ACCAGGATGCCAAGGAGAACC
NM_000751	CHRNA5	9535	ACCATCCACTTCCGAACACCC
NM_000806	GABRA1	9536	ACGACTGATATCTTCGTACC
NM_000807	GABRA2	9537	ACTGCACTTGGAGGATTTCCC
NM_000807	GABRA2	9538	ACAGTGGCTTATGCAACTGCC
NM_000808	GABRA3	9539	ACTATGTCGTCATGACAACCC
NM_000809	GABRA4	9540	ACTGAGACTCACCATAAGTGC
NM_000810	GABRA5	9541	ACTTTGGCAGCTATGCGTACC
NM_000812	GABRB1	9542	ACGGATATGACATTCGCTTGC
NM_000812	GABRB1	9543	ACCTATGATGCATCTGCAGCC
NM_000813	GABRB2	9544	ACTGCCATAGATCGGTGGTCC
NM_021911	GABRB2	9544	ACTGCCATAGATCGGTGGTCC
NM_000814	GABRB3	9545	ACGCTGTTGAAAGGCTACGAC
NM_021912	GABRB3	9545	ACGCTGTTGAAAGGCTACGAC
NM_000814	GABRB3	9546	ACTGCCATAGACAGATGGTCC
NM_021912	GABRB3	9546	ACTGCCATAGACAGATGGTCC
NM_000815	GABRD	9547	ACCCTGGAGATCTCCTGGCTC

NM_000815	GABRD	9548	ACCGCCATTGTCCTCTTCTCC
NM_000816	GABRG2	9549	ACAGTTCCTGAGGGTGATGTC
NM_000816	GABRG2	9550	ACTGGATGAACACTCCTGCCC
NM_000826	GRIA2	9551	ACATGGACGTGTTATGACTCC
NM_000827	GRIA1	9552	ACGCCATACGGACATCGACCC
NM_000829	GRIA4	9553	ACTTTGGTACCTCATGTGGAC
NM_000829	GRIA4	9554	ACCAGAACAGTGGTTGTAACC
NM_000829	GRIA4	9555	ACGGGCAAATTTGCCTTTCTC
NM_000830	GRIK1	9556	ACCCCTCACGTGTCATCCATC
NM_000830	GRIK1	9557	ACCTGCAACCTCACTCAGATC
NM_000832	GRIN1	9558	ACCGACCACTTCACTCCCACC
NM_007327	GRIN1	9558	ACCGACCACTTCACTCCCACC
NM_021569	GRIN1	9558	ACCGACCACTTCACTCCCACC
NM_000832	GRIN1	9559	ACGCCCTTCAAGTACCAGGGC
NM_007327	GRIN1	9559	ACGCCCTTCAAGTACCAGGGC
NM_021569	GRIN1	9559	ACGCCCTTCAAGTACCAGGGC
NM_000832	GRIN1	9560	ACCCTGCAGCAGTACCATCCC
NM_000869	HTR3A	9561	ACCTACAGGAAGGGTGTGCGC
NM_000890	KCNJ5	9562	ACACAGGCCCGCGATTATGTC
NM_000891	KCNJ2	9563	ACGATGGCCACTGTAATGTTT
NM_000891	KCNJ2	9564	ACAGCACTAGTACGGACACGC
NM_001036	RYR3	9565	ACGGCCTTATACTGCAAGACC
NM_001036	RYR3	9566	ACGATGAGATTGGAGCCTGTC
NM_001038	SCNN1A	9567	ACCCGCATGAAGACGGCCTTC
NM_001038	SCNN1A	9568	ACGGACTGGAAGATCGGCTTC
NM_001038	SCNN1A	9569	ACCGTGGAGTACTGTGACTAC
NM_001039	SCNN1G	9570	ACTGAGACCATTCTCAGCACC
NM_001046	SLC12A2	9571	ACCGTGAGCTTCCAGAACGGC
NM_001046	SLC12A2	9572	ACGCCAAATATCAGCGATGGC
NM_001094	ACCN1	9573	ACGGATATGATGCTCTACTGC
NM_001094	ACCN1	9574	ACGGACAGCAATTACTGTCTC
NM_001094	ACCN1	9575	ACTGCCAAACCACTCTGAAAC
NM_001095	ACCN2	9576	ACATGCCTTGCAACCTGACCC
NM_020039	ACCN2	9576	ACATGCCTTGCAACCTGACCC
NM_001194	HCN2	9577	ACCACGGAGATCATCCTGGAC
NM_001194	HCN2	9578	ACCGAGGTGCTGGAGGAGTAC
NM_001285	CLCA1	9579	ACTGGCACAGTGATCGTGGAC
NM_001286	CLCN6	9580	ACGTGGATGGTGGTGTGTTGCC
NM_021735	CLCN6	9580	ACGTGGATGGTGGTGTGTTGCC
NM_021736	CLCN6	9580	ACGTGGATGGTGGTGTGTTGCC
NM_021737	CLCN6	9580	ACGTGGATGGTGGTGTGTTGCC
NM_001286	CLCN6	9581	ACACCTAAGCTCGTCAGAGTC
NM_001286	CLCN6	9582	ACGGAGTTCATGAAGGGCAAC
NM_001286	CLCN6	9583	ACCCTGTTTCAAGACGATGGGC
NM_001288	CLIC1	9584	ACGAATTCGCTTCGACCTGTC
NM_001289	CLIC2	9585	ACGCCTGAAGAACTAAAGGAC

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NM_001289	CLIC2	9586	ACGGTACCCTCACCTGAGTCC
NM_001289	CLIC2	9587	ACGAATTTACCCACACGTGTC
NM_001297	CNGB1	9588	ACGGAGGCTGCCCTTACTTCC
NM_001297	CNGB1	9589	ACCCGCGTCAAGACCTGGTAC
NM_001298	CNGA3	9590	ACGATGAAGCAGCGTCTCAGC
NM_001426	EN1	9591	ACCATCCTGAGGCCGGACTTC
NM_001426	EN1	9592	ACATACCCGGAGCACGGCAAC
NM_001426	EN1	9593	ACGATCAAGAAAGCCACAGGC
NM_001542	IGSF3	9594	ACCTCGTTCAGCCTGGGCATC
NM_001678	ATP1B2	9595	ACGACTGAGAACCTTGATGTC
NM_001678	ATP1B2	9596	ACGATGAACCGGGTCATCAAC
NM_001679	ATP1B3	9597	ACCTGCATGTTGGGTATCTAC
NM_001679	ATP1B3	9598	ACGATTGATGGATCAGCCAAC
NM_001682	ATP2B1	9599	ACGAGGGTGGATTACCTCGTC
NM_001682	ATP2B1	9600	ACTGAACAAGTCTGCTACCTC
NM_001683	ATP2B2	9601	ACGGCATCATCGACAGCACAC
NM_001683	ATP2B2	9602	ACGAAGATGCCGCGCTCAAGC
NM_001684	ATP2B4	9603	ACCTGAGGAAGCTCATGGAGC
NM_001684	ATP2B4	9604	ACGCTCTACAAGGTGTACACC
NM_001829	CLCN3	9605	ACGAGAGGGATAAATGTCCAC
NM_001829	CLCN3	9606	ACGGTTCCATCAGGCTTGTTTC
NM_002043	GABRR2	9607	ACGAGCATGACCTTCGATGGC
NM_002063	GLRA2	9608	ACTGAGAAGGGTGCCAACTTC
NM_002063	GLRA2	9609	ACGTTTACCTGCATTGAGGTC
NM_002088	GRIK5	9610	ACGTAGACATCTTTGAGCTGC
NM_002088	GRIK5	9611	ACTGCCACCACCCTGGACATC
NM_002222	ITPR1	9612	ACCCCAGGCTGCAATGAGGTC
NM_002223	ITPR2	9613	ACGAATGCCATGCGTGTGTCC
NM_002223	ITPR2	9614	ACCCTCTTTGCAAGGATGTGC
NM_002223	ITPR2	9615	ACCTGACATTTGAGGTGGTCC
NM_002224	ITPR3	9616	ACACTCAACGAGGGCTTCATC
NM_002224	ITPR3	9617	ACTGGGCAGAATGTCTTGAC
NM_002232	KCNA3	9618	ACCCTGATCGACATTGTGGCC
NM_002232	KCNA3	9619	ACGTCGGAGTATATGGTGATC
NM_002233	KCNA4	9620	ACCTCAGGGCACACAATATTC
NM_002233	KCNA4	9621	ACTGCAGTCAGTTGTCCATAC
NM_002235	KCNA6	9622	ACTGGTGGTGTGAGTCGAGTC
NM_002236	KCNF1	9623	ACGCGCGAGTTCTACTTTGAC
NM_002236	KCNF1	9624	ACCATTGTGGACGTGCTGGCC
NM_002237	KCNG1	9625	ACCGTAGGCGGCATCAAGTAC
NM_002238	KCNH1	9626	ACCAGGACACCTGTGTGGTTC
NM_002238	KCNH1	9627	ACCTTATCCGCATGAACTACC
NM_002239	KCNJ3	9628	ACTTTGCCACGTGATCGATGC
NM_002239	KCNJ3	9629	ACGAGCAGGAGGAAATGCTTC
NM_002241	KCNJ10	9630	ACGTTGTGAAAGTGGCCTCTC
NM_002243	KCNJ15	9631	ACACTCACCTGTTCGCTGCC

NM_002243	KCNJ15	9632	ACCTCGAGGAGAAGTACAGGC
NM_002245	KCNK1	9633	ACGGCCTTCTGCATCATCTAC
NM_002246	KCNK3	9634	ACGGTGTCTGCATGTTCTAC
NM_002246	KCNK3	9635	ACCATGGTGCTCATCGGCTTC
NM_002247	KCNMA1	9636	ACGAGTCAAGATAGAGTCAGC
NM_002247	KCNMA1	9637	ACGTCGGGCTGATTTAAGGGC
NM_002247	KCNMA1	9638	ACTTTACCGGCTGAGAGATGC
NM_002248	KCNN1	9639	ACACCCTCAAATGTGGGCCAC
NM_002248	KCNN1	9640	ACGACACTCATGACCATCTGC
NM_002248	KCNN1	9641	ACGCTGAACGACCAGGCTAAC
NM_002249	KCNN3	9642	ACAGCGACTGAGTGACTATGC
NM_002249	KCNN3	9643	ACGCTGAGTGACCAAGCCAAC
NM_002251	KCNS1	9644	ACTTCTACTTCGACCGGCACC
NM_002251	KCNS1	9645	ACCTTCTTCTGCCACCCGCTC
NM_002251	KCNS1	9646	ACCTCTCAGGAGGGACAGTC
NM_002420	TRPM1	9647	ACCATCACAGATCTCGTGGCC
NM_002558	P2RX1	9648	ACGAAGGTGGGCGTTATCTTC
NM_002558	P2RX1	9649	ACCAGCATCAGCTTTCACGC
NM_002560	P2RX4	9650	ACGGGCTACCAGGAACTGAC
NM_002560	P2RX4	9651	ACGAACAACATCTGGTATCCC
NM_002560	P2RX4	9652	ACCTGGGACTGCAACCTGGAC
NM_002561	P2RX5	9653	ACGGAGGCCGAAGACTTCACC
NM_002561	P2RX5	9654	ACGTCTGTCTCCTCCGGGTAC
NM_002976	SCN7A	9655	ACTAAGAGTCGGTGTGAAAGC
NM_002978	SCNN1D	9656	ACCATCGTCTACCAGGAGCTC
NM_003040	SLC4A2	9657	ACGCAATTCCACGAGGCAGCC
NM_003040	SLC4A2	9658	ACATTCAAGAACAGCCGGTTC
NM_003048	SLC9A2	9659	ACGGACCAGTTCATCATTGCC
NM_003052	SLC34A1	9660	ACGCTCATCATCCAGCTGGAC
NM_003052	SLC34A1	9661	ACGATGCTCAACTCCCTGCTC
NM_003304	TRPC1	9662	ACCAGTTCAGGTGACTTGAAC
NM_003304	TRPC1	9663	ACGTGATGTGCTGCCTAGTGC
NM_003305	TRPC3	9664	ACCTGCGTGGACTIONTACATGGGC
NM_003305	TRPC3	9665	ACGCCATTCTGAATGGAGATC
NM_003305	TRPC3	9666	ACGTCCAGGTTAAACCTCTTC
NM_003307	TRPM2	9667	ACGCAGGATTGTGAGTGGAC
NM_003307	TRPM2	9668	ACCATCCTCTCCTACTTCGCC
NM_003740	KCNK5	9669	ACGGACGTCAACATCTTCAGC
NM_004070	CLCNKA	9670	ACGACCAATCGGTACAGCTCC
NM_004137	KCNMB1	9671	ACGCGTGTGGACCCAGGAATC
NM_004137	KCNMB1	9672	ACATTCCAAGAGCAGCAGGTC
NM_004174	SLC9A3	9673	ACGATCGGGTTCCACCTGTCC
NM_004198	CHRNA6	9674	ACACCATCCCATCCACATCTC
NM_004320	ATP2A1	9675	ACTCTGGAGAAATACGGCCTC
NM_004320	ATP2A1	9676	ACGATGTTTGTCAAGGGTGCC
NM_004320	ATP2A1	9677	ACTGCACTGAACAGCCTGTCC

NM_004366	CLCN2	9678	ACGAGGAAGCTGCTCGGATTC
NM_004518	KCNQ2	9679	ACCTCAGAAGAAGCAAGCCTC
NM_004519	KCNQ3	9680	ACCAATAAAGAGCGTTTCCGC
NM_004594	SLC9A5	9681	ACCATCTCCCATAAGTCACGC
NM_004594	SLC9A5	9682	ACACTTCTGTCCACCAACCTGC
NM_004594	SLC9A5	9683	ACGGACCACACCCATCTCAGC
NM_004621	TRPC6	9684	ACGTTTGTAGCACACGCAGCC
NM_004621	TRPC6	9685	ACGCAGGACATCTCAAGTCTC
NM_004669	CLIC3	9686	ACGACAGACACGCTGCAGATC
NM_004700	KCNQ4	9687	ACCTTGCCAACGAGTGTCTCC
NM_004700	KCNQ4	9688	ACGAGCTACCAGTGTGAGCTC
NM_004727	SLC24A1	9689	ACGAACAGCCAAGATGATCCC
NM_004727	SLC24A1	9690	ACTCCTTGCGAGGCACATC
NM_004770	KCNB2	9691	ACCAAGAGCGTGCTGCAGTTC
NM_004770	KCNB2	9692	ACTAAGTACCAGGAGGTTAGC
NM_004823	KCNK6	9693	ACGGTGCTGGTCACAGTCTAC
NM_004858	SLC4A8	9694	ACGCTCAAGAAAGGCTGTGGC
NM_004909	TRAG3	9695	ACTGCACTGTGAGTTTCATGC
NM_004961	GABRE	9696	ACCCAGATGGTCCGCATCTAC
NM_021984	GABRE	9696	ACCCAGATGGTCCGCATCTAC
NM_021987	GABRE	9696	ACCCAGATGGTCCGCATCTAC
NM_021990	GABRE	9696	ACCCAGATGGTCCGCATCTAC
NM_004961	GABRE	9697	ACTGGATTCTCACTCTTGCCC
NM_021984	GABRE	9697	ACTGGATTCTCACTCTTGCCC
NM_021987	GABRE	9697	ACTGGATTCTCACTCTTGCCC
NM_021990	GABRE	9697	ACTGGATTCTCACTCTTGCCC
NM_004961	GABRE	9698	ACGAATTTCCCGCGTGTCTCC
NM_021984	GABRE	9698	ACGAATTTCCCGCGTGTCTCC
NM_021987	GABRE	9698	ACGAATTTCCCGCGTGTCTCC
NM_021990	GABRE	9698	ACGAATTTCCCGCGTGTCTCC
NM_004974	KCNA2	9699	ACCCGCCCTAGCTTTGATGCC
NM_004975	KCNB1	9700	ACGAGCAGATGAACGAGGAGC
NM_004770	KCNB2	9701	ACTCCAACAAGAGCGTGTCTGC
NM_004975	KCNB1	9701	ACTCCAACAAGAGCGTGTCTGC
NM_004975	KCNB1	9702	ACACACACAGCAATAGCGTTC
NM_004976	KCNC1	9703	ACCATCATTGACTTTGTGGCC
NM_004977	KCNC3	9704	ACGATCGTGATCAACGTGGGC
NM_004977	KCNC3	9705	ACACCCATGAGGGCTTCATCC
NM_004977	KCNC3	9706	ACCCACACCTACTTCAAGAAC
NM_004978	KCNC4	9707	ACGATCATCATCAACGTGGGC
NM_004979	KCND1	9708	ACCTCCACTGCCCTCAGTCAGC
NM_004980	KCND3	9709	ACCGAGGACACCAAGGAGTAC
NM_004980	KCND3	9710	ACCAACCAGGAGTCCATGCCC
NM_004981	KCNJ4	9711	ACCGAGCTGGCCCTTATGAGC
NM_004982	KCNJ8	9712	ACGCATGATCATTAGTGCCCTC
NM_004982	KCNJ8	9713	ACTTCTCTGAGGAAGCGCAAC

NM_004983	KCNJ9	9714	ACGCCACGGGAATGACATGCC
NM_005070	SLC4A3	9715	ACCGATGACAAGGACAGTGGC
NM_005070	SLC4A3	9716	ACGCCTTCTTCAAGTTCTGCC
NM_005074	SLC17A1	9717	ACCCCTTCATCCTGATGGCAGC
NM_005135	SLC12A6	9718	ACGGTGTCTTCCCTCCTCAAC
NM_005135	SLC12A6	9719	ACCCTACCTGGGCTTTACTTC
NM_005136	KCNE2	9720	ACTCTAGAAGAATCGAAGGCC
NM_005136	KCNE2	9721	ACGGCCACCATCCATGAGAAC
NM_005173	ATP2A3	9722	ACGCAATTCATCCGCTACCTC
NM_005183	CACNA1F	9723	ACGTTCAACTTTGACCAGACC
NM_005183	CACNA1F	9724	ACGGAGAAGGTGGTACCCATC
NM_005183	CACNA1F	9725	ACCATGGTCTTCACTGGCCTC
NM_005199	CHRNA1	9726	ACTGGGAATGAGGAGTGGTTC
NM_005446	P2RX1	9727	ACCTTCAGGACAGCCACTCAC
NM_005472	KCNE3	9728	ACGAACCGTGTGTCTATGATC
NM_005477	HCN4	9729	ACGGATGAGAACACCACACCC
NM_005477	HCN4	9730	ACTGAGGTGCTGGAGGAGTAC
NM_005549	KCNA10	9731	ACGACCCTGAAACACTGCTAC
NM_005832	KCNMB2	9732	ACCAGTCACAGCACTGAAGGC
NM_006028	HTR3B	9733	ACGACGTAGACCTGGCCTTTC
NM_006028	HTR3B	9734	ACTTCTCCATGATGAGCAGC
NM_006071	PKDREJ	9735	ACTTTCACGGTGTCCATCACC
NM_006359	SLC9A6	9736	ACTAGTGGCATAACCAGCCAGC
NM_006359	SLC9A6	9737	ACATGATGTTTCAGCACCACGC
NM_006424	SLC34A2	9738	ACCATCTCTGCCAAGTATCGC
NM_006514	SCN10A	9739	ACCTACACCAGCTTTGATTCC
NM_006514	SCN10A	9740	ACGATGCTCAGAGCTTCCAGC
NM_006529	GLRA3	9741	ACGTGCTCCAATGTACCTTC
NM_006536	CLCA2	9742	ACTACCTGCCACATGGAAAGC
NM_006536	CLCA2	9743	ACAGTGACAGTGACCTCTCGC
NM_006536	CLCA2	9744	ACTTCTGATCCTGTACCTGCC
NM_006920	SCN1A	9745	ACCTTTGAGACCTTTGGCAAC
NM_006922	SCN3A	9745	ACCTTTGAGACCTTTGGCAAC
NM_021007	SCN2A2	9745	ACCTTTGAGACCTTTGGCAAC
NM_007327	GRIN1	9746	ACAGAGTGGTAGAGCAGAGCC
NM_007332	ANKTM1	9747	ACGATCGATTCTGAAGGACGC
NM_012069	ATP1B4	9748	ACGGCCTGCCAATTTAAGCGC
NM_012069	ATP1B4	9749	ACGATGAACCGGATTGTAGGC
NM_012128	CLCA4	9750	ACTTCTTCTGTGCCTCCAATC
NM_012226	P2RX2	9751	ACGATCAATGGCACCACCACC
NM_016318	P2RX2	9751	ACGATCAATGGCACCACCACC
NM_012226	P2RX2	9752	ACGATGGTGGACACTCCTGCC
NM_016318	P2RX2	9752	ACGATGGTGGACACTCCTGCC
NM_012285	KCNH4	9753	ACAGCTCTGACCTACTGTGGC
NM_012471	TRPC5	9754	ACAGAGTTTGTGTGCTCAGCCC
NM_012471	TRPC5	9755	ACTGAACCTCCCTCTACCTGGC

NM_013348	KCNJ14	9756	ACGAAAGACGGGCACTGCAAC
NM_013348	KCNJ14	9757	ACTGAACCTTGCTCTGAGCTGC
NM_013943	CLIC4	9758	ACGGCCAGAGGCTAATGAAGC
NM_014139	SCN12A	9759	ACTTGAAGTCCTTCCGGACTC
NM_014191	SCN8A	9760	ACGAGTCTCAGAGAAAGTGCC
NM_014191	SCN8A	9761	ACCACAGAGGATGTTAGCAGC
NM_014191	SCN8A	9762	ACGTGCTGCCAGGTCAACATC
NM_014211	GABRP	9763	ACCAGGCTCATCCGCCTCTTC
NM_014211	GABRP	9764	ACGAACCTGCATTGGAGTGAC
NM_014217	KCNK2	9765	ACGACGGTCTCCACGATATTC
NM_014274	ABP/ZF	9766	ACGCCCAGGACCAATAACCGC
NM_018646	TRPV6	9766	ACGCCCAGGACCAATAACCGC
NM_014274	ABP/ZF	9767	ACGACAGGCAAGATCTCAACC
NM_018646	TRPV6	9767	ACGACAGGCAAGATCTCAACC
NM_014379	KCNV1	9768	ACCATCATAGACCTCCTTGCC
NM_014379	KCNV1	9769	ACGAAGTCGGCCTACTGCTCC
NM_014382	ATP2C1	9770	ACGCTGATCTTCAGAATGGTC
NM_014386	PKD2L2	9771	ACTGTCTCAGCTGTCAAC
NM_014386	PKD2L2	9772	ACTTCAAGATGACTACCAGCC
NM_014407	KCNMB3	9773	ACGAAGAGAGAGACAGACTAC
NM_014407	KCNMB3	9774	ACGAGGCTGTCCAGATAAATC
NM_014505	KCNMB4	9775	ACGTGCTCCTATATCCCTCCC
NM_014505	KCNMB4	9776	ACAGACCAGATGATGTGCTTC
NM_014619	GRIK4	9777	ACGTGGACATCTTTGAGCTTC
NM_014619	GRIK4	9778	ACTTCCCGCTACCAGACCTAC
NM_014861	KIAA0703	9779	ACGGGACTGTGTGTCTTCTAC
NM_014861	KIAA0703	9780	ACGTCTGCAGACATTGGGATC
NM_014861	KIAA0703	9781	ACGATGTGTAGTGGACCGCAC
NM_016112	PKD2L1	9782	ACGAAGCCTGAAGATGAACCC
NM_016121	LOC51133	9783	ACGGATGTAGGTGGTCCAACC
NM_016121	LOC51133	9784	ACCTGACTCACCTGGTACTGC
NM_016179	TRPC4	9785	ACGTTTATCTGCCACACAGCC
NM_016179	TRPC4	9786	ACGGAGGTACTCTGCCTACTC
NM_016601	KCNK9	9787	ACAGCCGAGGAGATCCGGATC
NM_016601	KCNK9	9788	ACGTGCTGTGGCATGCGCAAC
NM_016611	KCNK4	9789	ACGCCATCTTCTTGAAGTGGC
NM_033310	KCNK4	9789	ACGCCATCTTCTTGAAGTGGC
NM_033311	KCNK4	9789	ACGCCATCTTCTTGAAGTGGC
NM_016611	KCNK4	9790	ACCTGGCTGCGAGTAGTGTCC
NM_033310	KCNK4	9790	ACCTGGCTGCGAGTAGTGTCC
NM_033311	KCNK4	9790	ACCTGGCTGCGAGTAGTGTCC
NM_016929	CLIC5	9791	ACAGGAGTCGTGTTCAATGTC
NM_016929	CLIC5	9792	ACAGAGGCCTAACCAAGGCTC
NM_017915	FLJ20641	9793	ACTACCAAACCCAAGCATTGC
NM_017915	FLJ20641	9794	ACCGCATCTGTGTGTCAATGC
NM_018298	MCOLN3	9795	ACCCATGGAACTTGCCATAC

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NM_018558	GABRQ	9796	ACCTATGATTCTCTGCAGCC
NM_018558	GABRQ	9797	ACGCCTCAGCCCACTCACTTC
NM_018658	KCNJ16	9798	ACGCTTTGCCTCATGTGGCGC
NM_018896	CACNA1G	9799	ACCATCGTCTTCACCAGCCTC
NM_018896	CACNA1G	9800	ACTGACAGTGAAGGTGGTGGC
NM_018992	FLJ20040	9801	ACGTGGGTCCGACTCAACGTC
NM_018992	FLJ20040	9802	ACCGAAGACCAAGCCGAGTTC
NM_019098	CNGB3	9803	ACGGCTCTCACCCAAGTAATC
NM_019842	KCNQ5	9804	ACGTACAAGAACAACACCGCC
NM_019842	KCNQ5	9805	ACCATGAGACCACAGACGATC
NM_019842	KCNQ5	9806	ACCTGATGAAGAGGTGGGTCC
NM_020344	SLC24A2	9807	ACGCTTGCTTCTCTTAACAGC
NM_020344	SLC24A2	9808	ACTGACACCATCCAGTGATGC
NM_003305	TRPC3	9809	ACTGCTGGAGGAGTCCAAGAC
NM_020389	trp7	9809	ACTGCTGGAGGAGTCCAAGAC
NM_020389	trp7	9810	ACGTCAAGAAGTTCGTTGCTC
NM_020533	MCOLN1	9811	ACGAGGAAGACCTTCGCCGTC
NM_020533	MCOLN1	9812	ACTCAGCTGGCTGTGACATTC
NM_020689	NCKX3	9813	ACCGCTTGCATACATCAGTGC
NM_021007	SCN2A2	9814	ACTCCAGACAGAAATGCCAC
NM_021012	KCNJ12	9815	ACCTCCTTCTGCTACGAGAAC
NM_021096	CACNA1I	9816	ACCTTCGGCATGGCCTTCCTC
NM_021098	CACNA1H	9816	ACCTTCGGCATGGCCTTCCTC
NM_021098	CACNA1H	9817	ACCATCGTCCTCATCTGCTGC
NM_021137	TNFAIP1	9818	ACGCAGACCAAGGTGGAATTC
NM_021161	KCNK10	9819	ACCTCCGCGCCTGTCCATTTC
NM_138317	KCNK10	9819	ACCTCCGCGCCTGTCCATTTC
NM_138318	KCNK10	9819	ACCTCCGCGCCTGTCCATTTC
NM_021161	KCNK10	9820	ACTTGGAGACCAACTTGGAAC
NM_138317	KCNK10	9820	ACTTGGAGACCAACTTGGAAC
NM_138318	KCNK10	9820	ACTTGGAGACCAACTTGGAAC
NM_021196	SLC4A5	9821	ACACTGACCAGAAGGGACATC
NM_033323	SLC4A5	9821	ACACTGACCAGAAGGGACATC
NM_133478	SLC4A5	9821	ACACTGACCAGAAGGGACATC
NM_133479	SLC4A5	9821	ACACTGACCAGAAGGGACATC
NM_021196	SLC4A5	9822	ACGAAGGAGTGTCTGAGCTAC
NM_033323	SLC4A5	9822	ACGAAGGAGTGTCTGAGCTAC
NM_133478	SLC4A5	9822	ACGAAGGAGTGTCTGAGCTAC
NM_133479	SLC4A5	9822	ACGAAGGAGTGTCTGAGCTAC
NM_021614	KCNN2	9823	ACATGCCTTATCAGTCTCTCC
NM_021614	KCNN2	9824	ACTTATGGGTGCTGGTTGCAC
NM_021625	TRPV4	9825	ACAGTCTTCAACCGGCCCATC
NM_021625	TRPV4	9826	ACACACTACGTGGAACCTTCTC
NM_021625	TRPV4	9827	ACTGCCCTGGAGTGAATTCTC
NM_021625	TRPV4	9828	ACCAAGAACTCGAACCCGGAC
NM_021949	ATP2B3	9829	ACGGAGGCCTCCGACATCATC

NM_021949	ATP2B3	9830	ACTTCTCTCTGCTGCCAATCC
NM_021956	GRIK2	9831	ACTACCCAAGTCTCCTCCATC
NM_021956	GRIK2	9832	ACTGGTACAAACCCAGGCGTC
NM_021956	GRIK2	9833	ACGGTTGCCAGGTAAAGAAAC
NM_022054	KCNK13	9834	ACCAGTCCTTGAAGTGGATCC
NM_022054	KCNK13	9835	ACGCAACTGTCTGAGATGGCC
NM_022055	KCNK12	9836	ACCCATAGGTTTCGGCATGAC
NM_022058	SLC4A10	9837	ACATGCAGGTCAGGTTGTTTC
NM_022058	SLC4A10	9838	ACGACTGCCTTGTGGAGGAAC
NM_022358	KCNK15	9839	ACGGTCTTCTGCATGTTCTAC
NM_023930	MGC2376	9840	ACAGCTGGCAGAGATGTTCTC
NM_023930	MGC2376	9841	ACATCAAGCCTTTGGTCAAGC
NM_023930	MGC2376	9842	ACGTCCAGCGTGCTTGTGTGC
NM_024076	MGC2628	9843	ACCATGTCCCGGCTGTCTCTC
NM_024076	MGC2628	9844	ACGCTGCTGCTTCCGGATGAC
NM_024080	TRPM8	9845	ACCACCCAACCTGGTCATTTTC
NM_024681	FLJ12242	9846	ACGCTGGTGCTGGACAAGGAC
NM_024681	FLJ12242	9847	ACGGAAGAAGCACCCCTCTCCC
NM_030779	KCNH6	9848	ACTGCTCAGATGGAGAAGTGC
NM_030779	KCNH6	9849	ACGGGCTGGTTTCCTCATTGAC
NM_030779	KCNH6	9850	ACGCTGGAGGTCACCTTCAAC
NM_031460	KCNK17	9851	ACGGATGCTATCCAGAGGGAC
NM_031886	KCNA7	9852	ACGAACGTGATGAACCTCATC
NM_031886	KCNA7	9853	ACGAGGCTGGGATGTTTCAGCC
NM_031954	MSTP028	9854	ACGCTGAATGTGGGTGGAGCC
NM_031954	MSTP028	9855	ACGTACTACCTAGTCCAAGGC
NM_031954	MSTP028	9856	ACGCTGTCTCTGCGCTTTAAC
NM_032115	KCNK16	9857	ACCGTGATCTTCCTCAACCAC
NM_033223	GABRG3	9858	ACTTCAGTGGAGGCAGCTGAC
NM_033272	KCNH7	9859	ACCCTCAACAAATACAGCACC
NM_005714	KCNK7	9860	ACGCGTCAGGTGACCGAGTTC
NM_033347	KCNK7	9860	ACGCGTCAGGTGACCGAGTTC
NM_033348	KCNK7	9860	ACGCGTCAGGTGACCGAGTTC
NM_033455	KCNK7	9860	ACGCGTCAGGTGACCGAGTTC
NM_033456	KCNK7	9860	ACGCGTCAGGTGACCGAGTTC
NM_054020	CATSPER2	9861	ACGGCTTGAGCCAAGCTGTGC
NM_054020	CATSPER2	9862	ACGCTGACATGTTCAAGCGGC
NM_080671	KCNE4	9863	ACTGGCAACGAGTACTTCTAC
NM_080671	KCNE4	9864	ACGAGGCGGGAGAAGAAGTCC
NM_018727	TRPV1	9865	ACGTTTCCTGCTGCAGAACTCC
NM_080704	TRPV1	9865	ACGTTTCCTGCTGCAGAACTCC
NM_080705	TRPV1	9865	ACGTTTCCTGCTGCAGAACTCC
NM_080706	TRPV1	9865	ACGTTTCCTGCTGCAGAACTCC
NM_018727	TRPV1	9866	ACGTTACCATCGGCATGGGC
NM_080704	TRPV1	9866	ACGTTACCATCGGCATGGGC
NM_080705	TRPV1	9866	ACGTTACCATCGGCATGGGC

NM_080706	TRPV1	9866	ACGTTTACCATCGGCATGGGC
NM_133490	Kv6.3	9867	ACGAAGGAGATCCTGATCAAC
NM_133490	Kv6.3	9868	ACACTCAGGCTCTGTCTGGAGC
NM_133490	Kv6.3	9869	ACGGTCTTCGCTTGCCCTCTCC
NM_133497	Kv11.1	9870	ACCCTCATGGAGAAGCCATTC
NM_133497	Kv11.1	9871	ACGGCTTATGAGTATACCACC
NM_138392	LOC92799	9872	ACGACCAGTGACAGTGGGAAC
NM_138444	LOC115207	9873	ACAGGCCGCTTCTTTCTGGAC
NM_138444	LOC115207	9874	ACCTTCCTGGAGCAGGCCTTC
NM_139075	TPC2	9875	ACCCTGCTGACAGCCATCATC
NM_139075	TPC2	9876	ACCGTGTGTTGACGGGCTCCTC
XM_030524	KIAA0939	9877	ACTGTTCTTTGGCTCTGCAGC
SK423	ChaK1	9878	ACAGAAGTTGGAGATCGTGTC
XM_030709	TRPM7	9878	ACAGAAGTTGGAGATCGTGTC
SK423	ChaK1	9879	ACTTCAACAACAGAGAGCAGC
XM_030709	TRPM7	9879	ACTTCAACAACAGAGAGCAGC
XM_032835	INAC	9880	ACTGTGAATCAGGAGGCATTC
XM_032835	INAC	9881	ACCACATAACTCTAGCTGCCC
XM_032835	INAC	9882	ACATGACCCAGTGGACTCCTC
XM_035483	KCNH3	9883	ACGTCCATTTGCCTCCACTAC
XM_035483	KCNH3	9884	ACCAATGGCATCGACACCACC
XM_035483	KCNH3	9885	ACGGACTGCAGTCACTTCGCC
XM_036123	TRPM3	9886	ACGAACATCTTCTACATGCCC
XM_036123	TRPM3	9887	ACGTGCGCCATATGCACACAC
XM_038736	SLC4A9	9888	ACCTCCTCTGGCTGGATGAGC
XM_043106	KCNS2	9889	ACGTGGGACGAGCAGAGTGAC
XM_043106	KCNS2	9890	ACCCTTATTGACCTCATGTCC
XM_043106	KCNS2	9891	ACGAAGTAGGGCTGCTCTTGC
XM_044785	KCNJ13	9892	ACTGGCAAACCTCTACCAGACC
XM_046881	SLC9A1	9893	ACGAGATCCACACACAGTTCC
XM_046881	SLC9A1	9894	ACGGAGGACCTGCCTGTCTATC
XM_059638	LOC133308	9895	ACCTGTAGGAAGCGCGGATTC
XM_062645	LOC121456	9896	ACGAGGACCACAACGAACACC
XM_062909	LOC122032	9897	ACATCTACCAGGGATCCCTTC
XM_062909	LOC122032	9898	ACCATCAATGTCAGTGGCCAC
XM_063451	SLC24A4	9899	ACGGTCAAGTGGGTGTTTACC
XM_063919	LOC123948	9900	ACTGCCTCTGCTCTGATAGGC
XM_066360	LOC128997	9901	ACCATCTCAGAGCAGTTGGCC
NM_001337	CX3CR1	9902	ACGGCCAATGGCAAAGATGAC
XM_066668	LOC139390	9902	ACGGCCAATGGCAAAGATGAC
XM_066668	LOC139390	9903	ACTGTGGGCTCCATGATCTCC
XM_066809	LOC139649	9904	ACGCTTTGGACCTCTGCAGAC
XM_069849	LOC136363	9904	ACGCTTTGGACCTCTGCAGAC
XM_066809	LOC139649	9905	ACGACATCTTCAGGTTTCATGC
XM_066809	LOC139649	9906	ACGCTGCCACCAAGAACAAGC
XM_069035	LOC134829	9907	ACGCTCAGAGATAGGCAGAAC

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XM_069035	LOC134829	9908	ACCTCACACCAAGTATGCTGC
XM_069035	LOC134829	9909	ACGGAAGTAGAGAAGGAACTC
XM_069849	LOC136363	9910	ACCCGCCTCTGAAGAGAAAGC
XM_070698	LOC137979	9911	ACGGGTATCTGCAAGCACTTC
XM_070698	LOC137979	9912	ACGTTGGCAGCTCTCTTAAGC
XM_071144	LOC138850	9913	ACGTTTGTATGACGCGTGGTC
XM_071144	LOC138850	9914	ACTCCATACACCAGGGTAAAC
XM_072244	LOC130535	9915	ACCCAACAGTTTGGGTTCCTCC
XM_084997	bA430M15.1	9916	ACGAAGTGCCTGAAGCGCATC
XM_084997	bA430M15.1	9917	ACGTTAAGAAGTGGTGGACCC
XM_085367	LOC146212	9918	ACTATGGCCGATGCATGGACC
XM_086379	MGC25056	9919	ACTGACCTGGAGGACAGCTAC
XM_086379	MGC25056	9920	ACGTTGTGGAGTTTCACATGCC
XM_086565	KIAA1535	9921	ACCATGACAGAGACATGGCTC
XM_088063	LOC154881	9922	ACAGAGGCCCCAGTACTATGCC
XM_088063	LOC154881	9923	ACGCGTTTCTGGGACTCATGC
XM_088063	LOC154881	9924	ACGCACCTCGTGAACCACTAC
XM_088998	KCNT2	9925	ACGGTTACCCACCTTATTCTC
XM_088998	KCNT2	9926	ACGACTCCAAAGAACAAGGGC
XM_088998	KCNT2	9927	ACCAGCCCATATGGCATCTGC
XM_090201	LOC160297	9928	ACCACAATGGTCTTCCCAGTC
XM_090201	LOC160297	9929	ACGATGACCAACGAGGTAGCC
XM_090201	LOC160297	9930	ACGAGCCTAGGTTATTTCAGAC
XM_090298	LOC160434	9931	ACGATTCAGGGCATTCTGGCC
XM_090298	LOC160434	9932	ACTTATGCCAGGAAGCAGGGC
XM_090298	LOC160434	9933	ACTTCTCTGCTTGGCAGAGCC
XM_091397	LOC162163	9934	ACTCCAGAGCATCTGCAGCAC
XM_091397	LOC162163	9935	ACGTGAACCTCTGCTGCGACTC
XM_092804	CLIC6	9936	ACGATTGTGGCCAAGAAGTAC
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XM_093929	LOC166538	9938	ACGTACACGTCCCGCTTCTAC
XM_094080	LOC166765	9939	ACGGATACACATACGCATTGC
XM_094383	LOC167293	9940	ACTGAAGCTGACAGATGGCTC
XM_094383	LOC167293	9941	ACGTTCCAGAAGGATCTGAAC
XM_094383	LOC167293	9942	ACATGAAGTGCACAAGAGCAC
XM_095739	LOC206980	9943	ACGCTGCAACTACAGAGACAC
XM_095739	LOC206980	9944	ACCAAGGAAGAGCTTGTGCGC
XM_095780	LOC169572	9945	ACTCGTGGGCTCCTTGATGTC
XM_095780	LOC169572	9946	ACGGTATGCAGTCTGCAGCTC
XM_098368	KIAA1317	9947	ACTGATCTAGCCAAGGACTCC
XM_098368	KIAA1317	9948	ACGCAGAGACCCTGATCGAGC
XM_098368	KIAA1317	9949	ACAGCGACTTACTCCGGACTC
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XM_100072	LOC159479	9951	ACCTTCTTCTGTTCTTCTCC
XM_100072	LOC159479	9952	ACTCGAGGTGCTGACCCAGAC
XM_114305	LOC200845	9953	ACCGCAACTAACCATCACCAC

XM_114305	LOC200845	9954	ACGTTTCTCTTAGGGTCCACC
XM_116036	LOC200959	9955	ACCTGGAAAGCTGTAAGTCTC
XM_116036	LOC200959	9956	ACGAGTTTCCCTGGGAATCAC
XM_116036	LOC200959	9957	ACACGTGCCAGTTTCTTCTCC
XM_166742	LOC219896	9958	ACATCTGCAAGGGCCAAACTC
XM_170731	LOC254387	9959	ACCCATGGGTTCACTCTTTGTC
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XM_170803	LOC253980	9961	ACCAAGTACTCCTACACCAGC
XM_170815	LOC256412	9962	ACAGAGGCTTCAGCCTTGACC
XM_170815	LOC256412	9963	ACAGCCCAGCCTTTACAGGCC
XM_170908	LOC255231	9964	ACACGGATTTGCAGGAATTCC
XM_171197	LOC253971	9965	ACACATCTTTACCATCCCACC
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XM_171384	LOC256342	9968	ACGCTCTGTGATGACATCAGC
XM_171720	LOC253188	9969	ACCAGCGGATTGCAATTGCCC
XM_171749	LOC255087	9969	ACCAGCGGATTGCAATTGCCC
XM_171828	LOC254633	9970	ACGAACCTGTACAAGATCGAC
XM_171828	LOC254633	9971	ACGATCGACTACTCGCACTTC
XM_172164	LOC253355	9972	ACGTGGCAAGGAGACCCATAC
XM_172164	LOC253355	9973	ACGTCCTTGCCATGAGAGTC
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SK013	ADCK4	9974	ACCCAGATTTGCTTCCAGCTC
NM_024876	FLJ12229	9975	ACGTCCAGGGACCTCAAATTC
SK013	ADCK4	9975	ACGTCCAGGGACCTCAAATTC
SK015	BRSK2	9976	ACCCAGAGCAGCCCATTCCCTC
XM_113646	STK29	9976	ACCCAGAGCAGCCCATTCCCTC
SK015	BRSK2	9977	ACGAGGGTGGTGGAGACCATC
XM_113646	STK29	9977	ACGAGGGTGGTGGAGACCATC
SK016	Wnk2	9978	ACGACATACCTGAAGCGGTTTC
SK016	Wnk2	9979	ACGAAGGGTACCTTCACGGAC
SK060	CaMK2g	9980	ACTACCAAGAAGTTGTCTGCC
SK060	CaMK2g	9981	ACACCTGTGGATATCTGGGCC
SK112	DMPK2	9982	ACGAGGAAACCCTGGACATCC
SK183	IRR	9983	ACATCAAGCACTCCTTTGCCC
XM_043563	INSRR	9983	ACATCAAGCACTCCTTTGCCC
SK183	IRR	9984	ACTCCAGAGTACTTCAGCGCC
XM_043563	INSRR	9984	ACTCCAGAGTACTTCAGCGCC
SK200	PIM3	9985	ACGGCGGACAAGGAGAGCTTC
SK200	PIM3	9986	ACTCTGCTTGTGGACCTGCGC
SK440	ZC4/NRK	9987	ACCCAGCAGCAGATGCAGACC
SK440	ZC4/NRK	9988	ACTGGGTAGGCTATAATGCAC
SK453	TTBK2	9989	ACGCCAGACACTGACAAGTTC
SK458	MLKL	9990	ACTTCGAATCTCCCAACATCC
SK458	MLKL	9991	ACGACTGCCCTTCAGAGCTGC
XM_113849	LOC197259	9991	ACGACTGCCCTTCAGAGCTGC

SK459	DCAMKL3	9992	ACGGCTCTGAAAGGAGACCAC
XM_047355	KIAA1765	9992	ACGGCTCTGAAAGGAGACCAC
SK466	CDKL4	9993	ACGAAACCCAAATGGAGTTGC
SK466	CDKL4	9994	ACCAGAATCAACTGTTGCCTC
BC015792	BC015792	9995	ACCAAAGGCCGTCTGCACTGC
SK469	YANK3	9995	ACCAAAGGCCGTCTGCACTGC
SK476	NEK8	9996	ACCAGATGACCAAGGAAGAGC
XM_170826	LOC255185	9996	ACCAGATGACCAAGGAAGAGC
SK500	NDR2	9997	ACTACCACAGAACCGGACTAC
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ENSG00000165117	ENSG00000165117	9998	ACGATCGTGCCACTGCACTCC
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ENSG00000173314	ENSG00000173314	9998	ACGATCGTGCCACTGCACTCC
ENSG00000174027	ENSG00000174027	9998	ACGATCGTGCCACTGCACTCC
ENSG00000174931	ENSG00000174931	9998	ACGATCGTGCCACTGCACTCC
NG_000002	NG_000002	9998	ACGATCGTGCCACTGCACTCC
NG_000004	NG_000004	9998	ACGATCGTGCCACTGCACTCC
NG_000006	NG_000006	9998	ACGATCGTGCCACTGCACTCC
NG_000007	NG_000007	9998	ACGATCGTGCCACTGCACTCC
NG_000008	NG_000008	9998	ACGATCGTGCCACTGCACTCC
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NG_000016	NG_000016	9998	ACGATCGTGCCACTGCACTCC
NG_000017	NG_000017	9998	ACGATCGTGCCACTGCACTCC
NG_000018	NG_000018	9998	ACGATCGTGCCACTGCACTCC
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NG_001334	NG_001334	9998	ACGATCGTGCCACTGCACTCC
NG_001337	NG_001337	9998	ACGATCGTGCCACTGCACTCC
NM_000243	MEFV	9998	ACGATCGTGCCACTGCACTCC
NM_000843	GRM6	9998	ACGATCGTGCCACTGCACTCC
NM_001432	EREG	9998	ACGATCGTGCCACTGCACTCC
NM_001450	FHL2	9998	ACGATCGTGCCACTGCACTCC

NM_001544	ICAM4	9998	ACGATCGTGCCACTGCACTCC
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NM_003082	SNAPC1	9998	ACGATCGTGCCACTGCACTCC
NM_003190	TAPBP	9998	ACGATCGTGCCACTGCACTCC
NM_003417	ZNF264	9998	ACGATCGTGCCACTGCACTCC
NM_004153	ORC1L	9998	ACGATCGTGCCACTGCACTCC
NM_005044	PRKX	9998	ACGATCGTGCCACTGCACTCC
NM_005373	MPL	9998	ACGATCGTGCCACTGCACTCC
NM_006085	BPNT1	9998	ACGATCGTGCCACTGCACTCC
NM_006455	SC65	9998	ACGATCGTGCCACTGCACTCC
NM_006588	SULT1C2	9998	ACGATCGTGCCACTGCACTCC
NM_007181	MAP4K1	9998	ACGATCGTGCCACTGCACTCC
NM_014130	PRO0483	9998	ACGATCGTGCCACTGCACTCC
NM_014681	DDX34	9998	ACGATCGTGCCACTGCACTCC
NM_014851	KIAA0469	9998	ACGATCGTGCCACTGCACTCC
NM_014864	KIAA0475	9998	ACGATCGTGCCACTGCACTCC
NM_014947	KIAA1041	9998	ACGATCGTGCCACTGCACTCC
NM_016123	IRAK4	9998	ACGATCGTGCCACTGCACTCC
NM_017595	KBRAS2	9998	ACGATCGTGCCACTGCACTCC
NM_017638	FLJ20045	9998	ACGATCGTGCCACTGCACTCC
NM_017961	FLJ20813	9998	ACGATCGTGCCACTGCACTCC
NM_018073	SS-56	9998	ACGATCGTGCCACTGCACTCC
NM_018283	FLJ10956	9998	ACGATCGTGCCACTGCACTCC
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NM_145014	FLJ32915	9998	ACGATCGTGCCACTGCACTCC
NM_145060	MGC10200	9998	ACGATCGTGCCACTGCACTCC
NM_145273	LOC146894	9998	ACGATCGTGCCACTGCACTCC
NM_145309	LOC220074	9998	ACGATCGTGCCACTGCACTCC
SK443	CDK11	9998	ACGATCGTGCCACTGCACTCC
SK513	QIK	9998	ACGATCGTGCCACTGCACTCC
U63721	HSU63721	9998	ACGATCGTGCCACTGCACTCC
XM_087239	LOC151556	9998	ACGATCGTGCCACTGCACTCC
XM_166324	KIAA1028	9998	ACGATCGTGCCACTGCACTCC
SK516	SgK496	9999	ACCTCTCTGAGAGGGATGAGC

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SK516	SgK496	10000	ACTGCTGCATCCGACAGATCC
AL137662	HSM801974	10001	ACTGTGGTGGAGGAGAAGACC
SK520	NRBP2	10001	ACTGTGGTGGAGGAGAAGACC
AL137662	HSM801974	10002	ACCCTGGAGAGAAGCGAGGAC
SK520	NRBP2	10002	ACCCTGGAGAGAAGCGAGGAC
SK521	SgK071	10003	ACTATTCGTGCGGAGGAAGAC
SK521	SgK071	10004	ACACTAGGGAAGCTGTTGGGC
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ENSG00000139908	ENSG00000139908	10006	ACAGCAGAAGGTTATGGTGGC
SK534	TSSK4	10006	ACAGCAGAAGGTTATGGTGGC
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SK534	TSSK4	10007	ACGTGGTTCTCCAGCTGACC
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SK534	TSSK4	10008	ACCCCTTTCTGTCTGACACC
SK558	NEK5	10009	ACATTGCTGCTGTCTGTGGAC
XM_166970	LOC220435	10009	ACATTGCTGCTGTCTGTGGAC
SK558	NEK5	10010	ACCAGAAGAGGCCTCCAGTAC
XM_166970	LOC220435	10010	ACCAGAAGAGGCCTCCAGTAC
SK592	SgK110	10011	ACCACATTGCACTCTCCCTAC
SK601	Obscn	10012	ACGATTGCCATGGAGAAGCAC
XM_047536	OBSCN	10012	ACGATTGCCATGGAGAAGCAC
SK601	Obscn	10013	ACGACCAGTGACAGTTCTTC
XM_047536	OBSCN	10013	ACGACCAGTGACAGTTCTTC
NM_031480	AD034	10014	ACGGAAGCAGATATGTATCGC
SK615	RIOK1	10014	ACGGAAGCAGATATGTATCGC
NM_031480	AD034	10015	ACGATGACATGCCTGCACCAC
SK615	RIOK1	10015	ACGATGACATGCCTGCACCAC
NM_031480	AD034	10016	ACACACACCACGGACCCTGAC
SK615	RIOK1	10016	ACACACACCACGGACCCTGAC
SK627	EphA10	10017	ACGCTGAACACAGAGGTGCGC
SK641	Wnk3	10018	ACCTACCCTTCAACCCACTAC
XM_029183	PRKWINK3	10018	ACCTACCCTTCAACCCACTAC
SK643	SgK223	10019	ACCATCAGCAGCAAGGAGGGC
SK645	NEK10	10020	ACAGAGCAGCTTTATCATCCC
XM_171056	LOC256519	10020	ACAGAGCAGCTTTATCATCCC
SK646	EphA6	10021	ACAGATCGACACAATTGCTGC
XM_114973	LOC203806	10021	ACAGATCGACACAATTGCTGC
SK646	EphA6	10022	ACGAAATTGAGGGTTCTTGCC
XM_114973	LOC203806	10022	ACGAAATTGAGGGTTCTTGCC
SK646	EphA6	10023	ACGACCCATCCCTAGCAGTCC
XM_172246	LOC256595	10023	ACGACCCATCCCTAGCAGTCC
SK650	SBK	10024	ACGACATGCAGGCCCTGACTC
XM_171786	LOC254078	10024	ACGACATGCAGGCCCTGACTC
SK650	SBK	10025	ACACCAAGCTGAAGAACTTCC
XM_171786	LOC254078	10025	ACACCAAGCTGAAGAACTTCC
SK650	SBK	10026	ACGGAGGTGTTCCGCTTCCTC

SK658	SgK288	10027	ACCCTGAGAACACCACTGCAC
XM_171494	LOC255239	10027	ACCCTGAGAACACCACTGCAC
SK658	SgK288	10028	ACGCAGGGCATCATGTCCTTC
XM_171494	LOC255239	10028	ACGCAGGGCATCATGTCCTTC
SK690	LRRK2	10029	ACCAGATAGAAAACGCTGGTCC
SK690	LRRK2	10030	ACAGGCTCGCGCTTCTTCTTC
ENSG00000174931	ENSG00000174931	10031	ACGAATGCAGTCAGCCTGCTC
SK695	CRIK	10031	ACGAATGCAGTCAGCCTGCTC
SK695	CRIK	10032	ACGAGCAGGAGTACCAGGCTC
SK712	ADCK2	10033	ACCGTATGAAGAGAGTGTGCC
SK712	ADCK2	10034	ACGCTTGAGAGCAACTTTGCC
NM_014299	BRD4	10035	ACTGCGCTTTGCCAAGATGCC
NM_058243	BRD4	10035	ACTGCGCTTTGCCAAGATGCC
SK763	BRD4	10035	ACTGCGCTTTGCCAAGATGCC
SK780	ADCK5	10036	ACCACCGTGCGCGCTATCAAC
XM_114612	LOC203054	10036	ACCACCGTGCGCGCTATCAAC
SK781	TAF1L	10037	ACGCCAAAGACACCAGCAGAC
NM_004606	TAF1	10038	ACGGAAGAGGGCCACCTCTAAC
NM_138923	TAF1	10038	ACGGAAGAGGGCCACCTCTAAC
SK781	TAF1L	10038	ACGGAAGAGGGCCACCTCTAAC
SK781	TAF1L	10039	ACGAGTCGAATTCTCTTGGGC
NM_005762	TRIM28	10040	ACGATGGCCATCCTGCAGATC
SK784	TIF1b	10040	ACGATGGCCATCCTGCAGATC
NM_005762	TRIM28	10041	ACGGTCTTCCCAGGCAGTACC
SK784	TIF1b	10041	ACGGTCTTCCCAGGCAGTACC
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NM_000222	KIT	10043	ACGCAGATTTTCAAGAGCACC
NM_001184	ATR	10044	ACGGTTCGACATGATCTTGCC
NM_001726	BRDT	10045	ACGCTGTACATCAACAGCTCC
NM_001726	BRDT	10046	ACCTCTGGCTTCTCAAAGACC
NM_002944	ROS1	10047	ACTACAACGTGTGCGGTCCAGAC
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NM_007313	ABL1	10048	ACGACATCATGGAGTCCAGCC
NM_005158	ABL2	10049	ACCTGCAGGACAGTCCACATC
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NM_014916	KIAA1079	10055	ACTGCAGAACTTAGCAGCGGC
NM_015906	TRIM33	10056	ACAGCTGCAAACAGTCAGGGC
NM_033020	TRIM33	10056	ACAGCTGCAAACAGTCAGGGC
NM_015906	TRIM33	10057	ACTCCCGGATGACTTTGTGGC
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NM_017433	MYO3A	10058	ACACGAAGACCAAGGAAAGAC

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NM_018343	FLJ11159	10059	ACCCATGAAATTGTTCCCGGC
NM_018343	FLJ11159	10060	ACGCTGTTCAACAATTCCTCC
NM_020198	GK001	10061	ACTGTGCCTGGCTCAGGTAAC
NM_031272	TEX14	10062	ACCAGAAGGAACAGGAAGAGC
NM_004606	TAF1	10063	ACCTGACACAGACAGCAGCTC
NM_138923	TAF1	10063	ACCTGACACAGACAGCAGCTC
NM_004606	TAF1	10064	ACCGTGCGTAAACGCCTCTAC
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NM_138995	MYO3B	10065	ACGCAACTCTCCTGCTGTAC
XM_035920	KIAA1811	10066	ACGGAGGCCCGAAAGTTCTTC
XM_035920	KIAA1811	10067	ACGTCCATGGAAGTCCTGAGC
XM_035920	KIAA1811	10068	ACGGACAAACCTCTCAGCAGC
SK134	Erk1	10069	ACCATGAAGGCCCGAAACTAC
XM_055766	MAPK3	10069	ACCATGAAGGCCCGAAACTAC
XM_059368	LOC129607	10070	ACGTTCCAGGTTGTTGCCATC
XM_059368	LOC129607	10071	ACCCTGACCTTATCCTGCTGC
XM_062445	LOC121064	10072	ACTCAGCCAAGGAAGCTTCAC
XM_062850	LOC121908	10073	ACAGATCCTCTCGGTGGAGTC
XM_062850	LOC121908	10074	ACGTGAACATCTTCTGCGGAC
XM_065311	LOC129602	10075	ACTAGTGACAAACCCAGGGAC
XM_065311	LOC129602	10076	ACCATCCAACCTCAACAACCGC
XM_066264	LOC128968	10077	ACGCTGTTCTACTTCAGGTTT
XM_066534	LOC139189	10078	ACGCCATATCTTGGACAAGGC
XM_066604	LOC139270	10079	ACGGTGGTAGAAGTGGGCAGC
XM_066604	LOC139270	10080	ACGATGATGATTGGGTGCTGC
XM_066604	LOC139270	10081	ACCTTGGCTATGAATGTTGGC
XM_066968	LOC139932	10082	ACCGGTCATTTCTGCTTGATC
XM_066968	LOC139932	10083	ACTCCAGGGTCTTGCCACCTC
XM_066977	LOC139952	10084	ACGTGACTGTGGACCCATTCC
XM_067723	LOC132187	10085	ACAGGAGGTGGGTCTCCATAC
XM_067723	LOC132187	10086	ACGGAAGGTATTTTACGCTCCC
XM_067723	LOC132187	10087	ACGGGCAGGTTACCTACGAC
XM_069722	LOC136126	10088	ACCAATGTCCACTGCGAGAAC
XM_070335	LOC137298	10089	ACTTCCCGAGTCACAGTTTCC
XM_086946	LOC150537	10090	ACTTGGACAGGAGCTTCTGGC
XM_086946	LOC150537	10091	ACGGCGTGCGGAAACATGTTT
XM_090535	LOC160848	10092	ACGAGCTCTGTCTGATGTCAC
XM_095399	LOC168921	10093	ACGTGCTTCGAGATCTCAGAC
XM_095399	LOC168921	10094	ACTTGTGCTTGGCTGCCAACC
XM_095455	LOC169014	10095	ACTGTACTGCACAGAGATCCC
XM_095725	LOC169505	10096	ACGGCATAACCGCTCAATGACC
XM_095725	LOC169505	10097	ACGCAGGCTGAGATGCAGCTC
XM_095725	LOC169505	10098	ACTCATTGTGCCATCCCAAAC
XM_095990	LOC169874	10099	ACGTACTTCGACGAGCACTAC
XM_095990	LOC169874	10100	ACCAAGCACCTGAAACTCATC
XM_114099	LOC200047	10101	ACGAAGATCCACAGTACCAGC

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SK169	HIPK1	10102	ACACAGGACTGTGGTGGGTGC
XM_114728	LOC204851	10102	ACACAGGACTGTGGTGGGTGC
SK169	HIPK1	10103	ACAGCTGTGTGCTCAACCTAC
XM_114728	LOC204851	10103	ACAGCTGTGTGCTCAACCTAC
XM_166672	LOC220231	10104	ACAGAGGCCTGGTCCATTATC
XM_167020	LOC222521	10105	ACACTGATGCAATTGAGCGCC
XM_167020	LOC222521	10106	ACTACTGCAGGTGTTGTATC
XM_167220	LOC222816	10107	ACGTGAAGCAGAAGGATGCTC
XM_167220	LOC222816	10108	ACTCGTCCTCACCAGTCTGC
XM_167231	LOC221757	10109	ACTGCTGACCAGACAGAGTGC
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XM_170826	LOC255185	10111	ACGGGTTAGAGTTCTGGTCCC
XM_171030	LOC256356	10112	ACGTTGGCAAGACTTAAGAGC
XM_171056	LOC256519	10113	ACGAAACTGTGGCAGGCTAAC
XM_171520	LOC255376	10114	ACCTGGACAGAGTTAGGCTCC
XM_171520	LOC255376	10115	ACGCATTTGATGCTCACATCC
XM_171744	LOC256238	10116	ACTGAATCCACAGCTCTACTC
XM_171862	LOC253603	10117	ACCACCTGTGAGAGGCGCTTC
XM_172116	LOC254665	10118	ACTGGTACAGATCTCCACATC
XM_172246	LOC256595	10119	ACAGGGAGCTTCTGACATGGC
XM_172550	LOC256248	10120	ACGACAGTACAAAGATGTGGC
XM_172550	LOC256248	10121	ACAGATGTGGCAAAGCCAGTC
XM_172605	LOC255992	10122	ACGGAGGTTGACATCCTGCAC
XM_172741	LOC253939	10123	ACCTATCAAGGCCTCCCACCC
ENSG00000172441	ENSG00000172441	10124	ACGCTCTATGCCATGCCCGAC
NM_000066	C8B	10125	ACGGCCACATTCTTTGGGTC
NM_000121	EPOR	10126	ACGCAGAAGATCTGGCCTGGC
NM_000163	GHR	10127	ACGTGAGATGGGAAGCACCAC
NM_000163	GHR	10128	ACGGAATCGATCCAGATCTCC
NM_000163	GHR	10129	ACTGACATACATGAGGGTACC
NM_000264	PTCH	10130	ACGGTGCTTTCTCTCACCACC
NM_000264	PTCH	10131	ACGCAGACTACCCGAATATCC
NM_000416	IFNGR1	10132	ACCCACATGTGCTAGTGGATC
NM_000527	LDLR	10133	ACGACCACAGAGGATGAGGTC
NM_000562	C8A	10134	ACTCTTCACAAAGGTGCAGAC
NM_000564	IL5RA	10135	ACATGTGTAACCATCCTCCAC
NM_000564	IL5RA	10136	ACGGAACCTCGTCTCTCTATCC
NM_000564	IL5RA	10137	ACCTATGAGAAAGCTGGGTCC
NM_000565	IL6R	10138	ACCTATTGCTGCTACCGGGCC
NM_000577	IL1RN	10139	ACCCAACTAGTTGCCGGATAC
NM_000577	IL1RN	10140	ACGATGTGCCTGTCTGTGTC
NM_000587	C7	10141	ACCACAGTCCTGTGAACCTAC
NM_000587	C7	10142	ACATGTGATGCTGAGAGCAGC
NM_000629	IFNAR1	10143	ACCAGGAGCGATGAGTCTGTC
NM_000640	IL13RA2	10144	ACGTTCTCTGGGCAGAACTAC
NM_000640	IL13RA2	10145	ACTGGAGCATACCTTTGGGAC

NM_000756	CRH	10146	ACGCTCACAGCAACAGGAAAC
NM_000760	CSF3R	10147	ACTCAGAAGTGTGAGCTGCGC
NM_000803	FOLR2	10148	ACCTTTAACTGGGACCACTGC
NM_000803	FOLR2	10149	ACGAACGCTTCCTGGATGTGC
NM_000803	FOLR2	10150	ACCGAGGAAGTGGCGAGGTTT
NM_000804	FOLR3	10151	ACGAGCGCATTCTGAACGTGC
XM_169247	LOC245804	10151	ACGAGCGCATTCTGAACGTGC
NM_000804	FOLR3	10152	ACTGAGGAGGTGGCCAAGTTC
NM_000833	GRIN2A	10153	ACGTCCAGCTGAAGAAGATCC
NM_000833	GRIN2A	10154	ACACTTAGCCAAAGGGAAAGC
NM_000834	GRIN2B	10155	ACGAACTGGAAGCTCTCTGGC
NM_000834	GRIN2B	10156	ACCCTGCAGCTGAAGGACAGC
NM_000835	GRIN2C	10157	ACCTCATCCCAGCTGGACTTC
NM_000836	GRIN2D	10158	ACGGAGAAGGGCTCCACCTTC
NM_000836	GRIN2D	10159	ACTCATGGTGCTGGTGTGGGC
NM_000877	IL1R1	10160	ACTTGATGTTTGGTCCCTGTCC
NM_000877	IL1R1	10161	ACACATCAGGCTTCAGCTGGC
NM_000878	IL2RB	10162	ACGCCCTTTGAGAACCTTCGC
NM_000878	IL2RB	10163	ACGCAGCAACCACTCGCTGAC
NM_000908	NPR3	10164	ACGAGAGGAGACAAACACGAC
NM_000949	PRLR	10165	ACACTGGTTGGTTTACGCTCC
NM_000949	PRLR	10166	ACGGGCTATAGCATGGTGACC
NM_001496	GFRA3	10167	ACGACACAGTGACCAGCAAAC
NM_001496	GFRA3	10168	ACCTTGTCGAACAGAGCAGTC
NM_001510	GRID2	10169	ACGAAATACCAGGGCTTCTCC
NM_001558	IL10RA	10170	ACTAGCACAGACAGCGGGATC
NM_001559	IL12RB2	10171	ACCATCACAGGACACACCTCC
NM_001560	IL13RA1	10172	ACTGAGAGTGAGAAGCCTAGC
NM_001842	CNTFR	10173	ACTGTGACTGTGCTGCATGGC
NM_147164	CNTFR	10173	ACTGTGACTGTGCTGCATGGC
NM_002183	IL3RA	10174	ACCTCCACCCAACATGACTGC
NM_002184	IL6ST	10175	ACCAGTTGGCATGGAGGCTGC
NM_002185	IL7R	10176	ACGAATCTGAGAAGCAGAGGC
NM_002186	IL9R	10177	ACACACACAGAGCTCTGGGCC
NM_002187	IL12B	10178	ACAGAGTTTGGAGATGCTGGC
NM_002187	IL12B	10179	ACACCTGACCCACCCAACAAC
NM_002310	LIFR	10180	ACGAGTGGAGTGACTGGAGCC
NM_002310	LIFR	10181	ACATTCTGTGGGCTCATCACC
NM_002310	LIFR	10182	ACACTGCGGGTTACAGACCTC
NM_002333	LRP3	10183	ACTACAGGGCCTTCGAGACCC
NM_002335	LRP5	10184	ACGAAGCTGTACTGGACGGAC
NM_002335	LRP5	10185	ACACAGCAGTGCGACTCCTTC
NM_002336	LRP6	10186	ACGTGGGTTTACTGTACTGGAC
NM_002336	LRP6	10187	ACTGGGACCATGAGGAAGATC
NM_002445	MSR1	10188	ACTGACAGCTTTGCTTCCTCC
NM_138715	MSR1	10188	ACTGACAGCTTTGCTTCCTCC

NM_138716	MSR1	10188	ACTGACAGCTTTGCTTCCTCC
NM_002445	MSR1	10189	ACTTCAAGGTCCCTCGGACC
NM_138715	MSR1	10189	ACTTCAAGGTCCCTCGGACC
NM_138716	MSR1	10189	ACTTCAAGGTCCCTCGGACC
NM_002659	PLAUR	10190	ACGAAGGAGAAGAGCTGGAGC
NM_002659	PLAUR	10191	ACTGGTTTCCACAACAACGAC
NM_002659	PLAUR	10192	ACCCACCCAGACCTGGATGTC
NM_003105	SORL1	10193	ACTATGGATGGTTCTGCTGCC
NM_003105	SORL1	10194	ACGTGCAATGGATTCCGCTGC
NM_003383	VLDLR	10195	ACAGTCTCTGGAGTTCCTAGC
NM_003383	VLDLR	10196	ACCCACTGAAGAGGACCTCTC
NM_003604	IRS4	10197	ACGTCTGCAAACGCGGCTACC
NM_003604	IRS4	10198	ACGTTGGAGCTCCTACTTCTC
NM_003738	PTCH2	10199	ACCGCGCCCTCTTTGATCTGC
NM_003738	PTCH2	10200	ACAGCCCAGAGATCCTGAGTC
NM_003749	IRS2	10201	ACGCATGGCCACAAGCGCTTC
NM_003749	IRS2	10202	ACCATCGACTTTGGCGAGCCC
NM_003749	IRS2	10203	ACTGGTCTCAAGTACATCGCC
NM_003818	CDS2	10204	ACGAACTGGTGGGTGAGAGGC
NM_003999	OSMR	10205	ACGTGAACTGGAACCTGCCAC
NM_003999	OSMR	10206	ACCAAACCCAGTAGAGGCACC
NM_004525	LRP2	10207	ACCGGTGACTGCAGCCACTTC
NM_004525	LRP2	10208	ACCTGGGTCTGTGACACAGAC
NM_004631	LRP8	10209	ACTAAGACCATCTCAGTGGCC
NM_017522	LRP8	10209	ACTAAGACCATCTCAGTGGCC
NM_033300	LRP8	10209	ACTAAGACCATCTCAGTGGCC
NM_004631	LRP8	10210	ACTACCTGTGCCTTCCTGCTC
NM_017522	LRP8	10210	ACTACCTGTGCCTTCCTGCTC
NM_033300	LRP8	10210	ACTACCTGTGCCTTCCTGCTC
NM_004633	IL1R2	10211	ACTGACTCTGCTAGGACGGTC
NM_004633	IL1R2	10212	ACGGAAGCCTCCTCCACGTTT
NM_004750	CRLF1	10213	ACACCCGGCACCGTGTACTTC
NM_004750	CRLF1	10214	ACGTGCGACAAGACCCGCAAC
NM_005137	DGCR2	10215	ACCGACAACGTGTTCTGTGCC
NM_005137	DGCR2	10216	ACCTTGCAACCACTTCAACCTC
NM_005174	ATP5C1	10217	ACATTCAGGTCTGTCTATCTCC
NM_005264	GFRA1	10218	ACTTACATCTGCAGATCTCGC
NM_145793	GFRA1	10218	ACTTACATCTGCAGATCTCGC
NM_005264	GFRA1	10219	ACTGCAATTCAAGCCTTTGGC
NM_145793	GFRA1	10219	ACTGCAATTCAAGCCTTTGGC
NM_005373	MPL	10220	ACCTTGCACTGGAGGGAGATC
NM_005515	HLXB9	10221	ACGATGCCCGACTTCAACTCC
NM_005529	HSPG2	10222	ACCTGGGATTCTCCTCCTTCC
NM_005529	HSPG2	10223	ACTGGCATCCTGACCATTTCGC
NM_005534	IFNGR2	10224	ACTAGCACGAGGCCTGTTGTC
NM_005534	IFNGR2	10225	ACTCCAACAGGTCAAAGGCCC

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NM_005534	IFNGR2	10226	ACAGGATGACGTCTGGGACTC
NM_005535	IL12RB1	10227	ACTTTGGTCCTGGCCTGAACC
NM_005544	IRS1	10228	ACCTATATCTGCATGGGTGGC
NM_005544	IRS1	10229	ACGCCAGTCCTCTCCTACTAC
NM_006140	CSF2RA	10230	ACTTCAGGAAGGGAGGGTACC
NM_006140	CSF2RA	10231	ACTAGAACGATTCAACCCTCC
NM_006653	SNT-2	10232	ACGTGCACCTACGAGAACGTC
NM_006653	SNT-2	10233	ACGACCGTGGCCATGTCCAAC
NM_006654	SNT-1	10234	ACTGGCACTACCTCTGCCTGC
NM_012275	IL1F5	10235	ACGGAATCCAAGAGCTTCACC
NM_012275	IL1F5	10236	ACGCCGATCAGCCTGTCAGAC
NM_013437	ST7	10237	ACCTGCTTGTGGAGAGACTCC
NM_013437	ST7	10238	ACGAAGAGAAGCTCCTCCCTC
NM_013437	ST7	10239	ACCAAATCCTGGAGTAAGGCC
NM_014045	DKFZP564C1940	10240	ACTGATAACTCAGTGCTGGGC
NM_014045	DKFZP564C1940	10241	ACAGTTAAGTGTCCCTCAGGC
NM_014138	PRO0659	10242	ACTGTCGATACTGCCAGAGCC
NM_014439	IL1F7	10243	ACCTACATACGCCAGAGATC
NM_014439	IL1F7	10244	ACACTGATGAAGCTGGCTGCC
NM_014779	KIAA0669	10245	ACCTGACAGCTCCTTGACTGC
NM_014779	KIAA0669	10246	ACGCGTGCCTAGTGTGTCTAC
NM_016579	8D6A	10247	ACTGCCACATCCTCCTCTGCC
NM_000802	FOLR1	10248	ACACGGCATTTTCATCCAGGAC
NM_016724	FOLR1	10248	ACACGGCATTTTCATCCAGGAC
NM_016725	FOLR1	10248	ACACGGCATTTTCATCCAGGAC
NM_016729	FOLR1	10248	ACACGGCATTTTCATCCAGGAC
NM_016730	FOLR1	10248	ACACGGCATTTTCATCCAGGAC
NM_016731	FOLR1	10248	ACACGGCATTTTCATCCAGGAC
NM_017416	IL1RAPL2	10249	ACGCCTCCCAAGCCATTGTTC
NM_017416	IL1RAPL2	10250	ACAGCAGACTCCATAACATGC
NM_017581	CHRNA9	10251	ACGATGTGGAATGGGAGGTCC
NM_017581	CHRNA9	10252	ACTGGTGGCAGAAATCATGCC
NM_017581	CHRNA9	10253	ACGGTGGCGAAAGTCATAGAC
NM_018110	DOK4	10254	ACGGTGACTGAGATCAGCAAC
NM_018557	LRP1B	10255	ACATCTGGTAAACCCTCGTGC
NM_019618	IL1F9	10256	ACGTGTGGACCCCTTCAGGGTC
NM_019618	IL1F9	10257	ACGAGCAGAAGATCATGGATC
NM_005691	ABCC9	10258	ACCAGCTTCCATTGACATGGC
NM_020297	ABCC9	10258	ACCAGCTTCCATTGACATGGC
NM_020298	ABCC9	10258	ACCAGCTTCCATTGACATGGC
NM_021258	IL22R	10259	ACCATCCTGACGTGGGACAGC
NM_021258	IL22R	10260	ACCCGCACCTACCAAATGCAC
NM_022139	GFRA4	10261	ACCTACGTGGACAACGTGAGC
NM_145762	GFRA4	10261	ACCTACGTGGACAACGTGAGC
NM_145763	GFRA4	10261	ACCTACGTGGACAACGTGAGC
NM_022139	GFRA4	10262	ACGTCCCTTTATTACAGACC

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NM_145762	GFRA4	10262	ACGTCCCTTTATTACAGACC
NM_145763	GFRA4	10262	ACGTCCCTTTATTACAGACC
NM_022148	CRLF2	10263	ACGAAGTTTCTCATTCCCAGC
NM_024872	FLJ22570	10264	ACTGAGCACCTCTATGAGAAC
NM_031429	RTBDN	10265	ACGATGATATCACCTGCGGCC
NM_032556	IL1F10	10266	ACCTGCTGTGCAGAGAAGATC
NM_032556	IL1F10	10267	ACGATCTGCACACTTCCTAAC
NM_032556	IL1F10	10268	ACGGTGGTGAAGAGGCCACAC
NM_032777	TEM5	10269	ACCATCCACAACCTACCGGGAC
NM_032832	FLJ14735	10270	ACGGTGCCTCAATCAGGAACC
NM_032832	FLJ14735	10271	ACAGTCTCAGAAAGCCACTGC
NM_052962	IL22RA2	10272	ACCTCAGACATACAGGAACC
NM_133445	GRIN3A	10273	ACGGGCTGCTACCCTACAACC
NM_138966	NETO1	10274	ACAGCAAACCACCTCAGAAAC
NM_138999	NETO1	10274	ACAGCAAACCACCTCAGAAAC
NM_138966	NETO1	10275	ACGGCAACACATTCTTCTGCC
NM_138966	NETO1	10276	ACTCGAAGAGGTGCCGACCAC
NM_139017	CRL3	10277	ACCATTGGCGTGAAGACGGTC
NM_139017	CRL3	10278	ACTACCTACGTTTCGAGGATGC
XM_035037	LRP4	10279	ACACTCCACTTCCCTATGGAC
XM_043613	GRID1	10280	ACGAGAGCAGACTTGGCCATC
XM_061180	LOC118851	10281	ACCCAATCCCAGTACATTGTC
XM_061180	LOC118851	10282	ACATTTGGTGACACGGCTGAC
XM_061852	LOC120086	10283	ACACACCACAAGAGAGTGCCC
XM_061852	LOC120086	10284	ACGCACTTCATCCAGGCTATC
XM_063677	LOC123482	10285	ACGATCCTCCTCTTTGTGGTC
XM_064862	LOC125915	10286	ACCTGTACGGCCACCATCATC
XM_068013	LOC132745	10287	ACGGCTCTGATGTGACCTCTC
XM_071152	LOC138883	10288	ACGCTGTCTGTTCTGACACC
XM_071152	LOC138883	10289	ACTGTACACCATAGTGA CTCC
XM_084524	LOC143458	10290	ACATGTGGCCCCAACCTTCTTC
XM_084524	LOC143458	10291	ACTGTGGCCCCAACCTTCTTCC
XM_084524	LOC143458	10292	ACTGGGTTTGAGGACTGTCCC
XM_088463	LOC158056	10293	ACTTACTGCTCCTTTGAGGAC
XM_090812	LOC161327	10294	ACTGATCGAGGACTGTGTGGC
XM_116009	LOC205527	10295	ACTTCCGTAAAGGGATCCTGC
XM_166294	LOC220164	10296	ACCAGAGTGAAGAGGCCCAGC
XM_166723	LOC222361	10297	ACCGGGATGGACATATGGCTC
XM_166723	LOC222361	10298	ACTGAAGATGAGCTCATCTGC
XM_167059	LOC222582	10299	ACACTCGCATACAGTGTATGC
XM_169246	LOC220075	10300	ACGAGTGGGTGCTGAATGTGC
XM_169246	LOC220075	10301	ACTGGGTGAGCAACTACAACC
XM_169247	LOC245804	10302	ACGAATGCCTGCTGCATGACC
XM_171429	LOC254104	10303	ACCTGCACCCTCCTTCTCATC
XM_171429	LOC254104	10304	ACCACATGGCTGTGGCAGTTC
XM_171429	LOC254104	10305	ACGACCAAGCAGATCCGTGAC

XM_172003	LOC253809	10306	ACAGACTTTGGCCACTCCATC
XM_172003	LOC253809	10307	ACGACTTTGGCCACTCCATCC
XM_174355	LOC254502	10308	ACGCAGAGCCAAATATCAGCC
NM_000033	ABCD1	10309	ACCATCAGGGTGGAGGAAGGC
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NM_000033	ABCD1	10310	ACTACCACACACACTTGCTAC
NM_000052	ATP7A	10311	ACGTGGATGTGGAACCTGTAC
NM_000053	ATP7B	10312	ACGTATGACCCAGAGGTCATC
NM_000053	ATP7B	10313	ACTACCATGGCTGATGAGTCC
NM_000053	ATP7B	10314	ACGACAGCCAGAGCTATTGCC
NM_000111	SLC26A3	10315	ACGTGTGTTGTAGCTGTTCCC
NM_000111	SLC26A3	10316	ACCACCGTAGGAGATTGCTTC
NM_000112	SLC26A2	10317	ACGTGTCCTTGGTGTGATCAC
NM_000324	RHAG	10318	ACTGCAGACTTCAGTGCAGCC
NM_000339	SLC12A3	10319	ACTGTTCTCCATCTTCTTCCC
NM_000339	SLC12A3	10320	ACCAAGAGGAAGATCAAGGCC
NM_000340	SLC2A2	10321	ACCAGTACAGATGAACTGCCC
NM_000340	SLC2A2	10322	ACGAAGAGTGGCTCAGCCCAC
NM_000350	ABCA4	10323	ACGTATCGCTCAGGCAGAACC
NM_000370	TTPA	10324	ACTAAGTGCAGATCTACACCC
NM_000370	TTPA	10325	ACGCTTGCTTCAGCATTTCCC
NM_000392	ABCC2	10326	ACCCTGGACATTATGGCAGGC
NM_000392	ABCC2	10327	ACTGGCAGGCATCTGAAGTCC
NM_000441	SLC26A4	10328	ACTACCGAGTCAAGGAATGGC
NM_000443	ABCB4	10329	ACACTCAATGTCCAGTGGCTC
NM_018849	ABCB4	10329	ACACTCAATGTCCAGTGGCTC
NM_018850	ABCB4	10329	ACACTCAATGTCCAGTGGCTC
NM_000452	SLC10A2	10330	ACCTGCCTCCAATATCTTGGC
NM_000452	SLC10A2	10331	ACAGCGCTGGATCATTGCTC
NM_000452	SLC10A2	10332	ACGGCAGAAATCCAGAGAGC
NM_000593	TAP1	10333	ACTGGCTAGCTCTAGGTGTCC
NM_000927	ABCB1	10334	ACATGTTGTCTGGACAAGCAC
NM_000927	ABCB1	10335	ACAGCGCCAGTGAACCTCTGAC
NM_001042	SLC2A4	10336	ACGGTGATTGAACAGAGCTAC
NM_001043	SLC6A2	10337	ACAGGTGGTGTGGATCACAGC
NM_001044	SLC6A3	10338	ACCTGGCCTACGCCATTGCAC
NM_001045	SLC6A4	10339	ACTATCCAATGGGTACTCAGC
NM_001045	SLC6A4	10340	ACCTCCTGGAACACTGGCAAC
NM_001089	ABCA3	10341	ACCCTGTACGAGGGACAGATC
NM_001090	ABCF1	10342	ACACATCCTCCTAAGCCTGCC
NM_001090	ABCF1	10343	ACTCGACCCACACAGAAGTTC
NM_001090	ABCF1	10344	ACGGATTTGCATTGTGGGCCC
NM_001171	ABCC6	10345	ACGATGGTGTCTGGATTGCGC
NM_001171	ABCC6	10346	ACGGACAGCATCCAATACGGC
NM_001606	ABCA2	10347	ACCTACGTGTGGGACATGCTC
NM_002858	ABCD3	10348	ACCATCATGAGTACTACCTGC

NM_002940	ABCE1	10349	ACCTTCACAGGTTGCCTATCC
NM_003003	SEC14L1	10350	ACGCTGGATGTAGATGCACCC
NM_003003	SEC14L1	10351	ACGCCAGAGAGATCATGTGTC
NM_003039	SLC2A5	10352	ACCGTGGCTGCTGTCAACTCC
NM_003039	SLC2A5	10353	ACCTTCACCGTGGGCTTGATC
NM_003042	SLC6A1	10354	ACACCTTGGTGGTCAAGGTGC
NM_003042	SLC6A1	10355	ACCACTACCAACATGACCAGC
NM_003043	SLC6A6	10356	ACTGGTGGAGGTGCGTTTCTC
NM_003043	SLC6A6	10357	ACGGGTATCGTCGGGAAATC
NM_003044	SLC6A12	10358	ACTTCTGGGAGAGACGAGTTC
NM_003046	SLC7A2	10359	ACCGTTGGCTGGTGTGCAAC
NM_003046	SLC7A2	10360	ACGATGGTCTGGGATCGTCTC
NM_003046	SLC7A2	10361	ACTTCTAACACTTGCAGGAGC
NM_003049	SLC10A1	10362	ACCTCAGCATTGTGATGACC
NM_003051	SLC16A1	10363	ACCTTGAATCCAGCTCTGACC
NM_003051	SLC16A1	10364	ACGAACAGAAAGCAAACGAGC
NM_003053	SLC18A1	10365	ACGCGTACCTAGTGAATAGC
NM_003053	SLC18A1	10366	ACAGTCTCTCCTGAGAGTGCC
NM_003053	SLC18A1	10367	ACCATCGTCTATGCTCCACTC
NM_003057	SLC22A1	10368	ACCCTGGTGTGTGCTGACTCC
NM_003058	SLC22A2	10369	ACCCTGGTATGTGCCAACTCC
NM_003058	SLC22A2	10370	ACTCTCTACCCGCCTCCCTTC
NM_003058	SLC22A2	10371	ACAGCTTTGCCTGAGACCATC
NM_003059	SLC22A4	10372	ACTGGTATGTGAGTCGTGTTC
NM_003059	SLC22A4	10373	ACCCCTGGTCAGGAACATGGC
NM_003060	SLC22A5	10374	ACGAGGCAGAGGTGATCATCC
NM_003060	SLC22A5	10375	ACGTCTGACCATCCTGACAGC
NM_003486	SLC7A5	10376	ACGCTCTGGATCGAGCTGCTC
NM_031211	LAT1-3TM	10376	ACGCTCTGGATCGAGCTGCTC
NM_003486	SLC7A5	10377	ACTGGGTCCCTGTTTACATCC
NM_003486	SLC7A5	10378	ACCAAGCCCAAGTGGCTCCTC
NM_003742	ABCB11	10379	ACTGGAAGACATAGTCCAAGC
NM_003742	ABCB11	10380	ACCGTCACTGTGGCCATGATC
NM_004207	SLC16A3	10381	ACCTTCCAGCCCTCGCTCATC
NM_004207	SLC16A3	10382	ACGTTCTCCAGTGCCATTGGC
NM_004212	SLC28A2	10383	ACGGAGTTCACTGCTATGGCC
NM_004213	SLC28A1	10384	ACGCATCATTGCGCAGTGTC
NM_004213	SLC28A1	10385	ACCTGACCTATGGAGATGCTC
NM_004213	SLC28A1	10386	ACCGCCTGTATGGCAGGGATC
NM_004254	SLC22A8	10387	ACCCTGCAGAAGGAGATCTCC
NM_004254	SLC22A8	10388	ACATCACGGGTGAGGTACAGC
NM_004256	ORCTL3	10389	ACCTTCTGTCTCCCTTCTAC
NM_004256	ORCTL3	10390	ACCAGAGGCCAAGGGAAGAAC
NM_004695	SLC16A5	10391	ACCCTCAGCCAGCTCTACTTC
NM_004695	SLC16A5	10392	ACCACAGGCTACTGCGTGTAC
NM_004695	SLC16A5	10393	ACGACGGTCTGGGAAGCAAC

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NM_004731	SLC16A7	10394	ACAGCTGTCACCGTATTCTTC
NM_004731	SLC16A7	10395	ACGTCCAGAGAATCTGAACCC
NM_004790	SLC22A6	10396	ACTGGCACAGAAGCCAATGGC
NM_004790	SLC22A6	10397	ACTTGAGTATGGAGGTACTCC
NM_004790	SLC22A6	10398	ACGGGAAACAGACGCGACAGC
NM_004803	ORCTL4	10399	ACAGGGAAGGTGAAGGAGGCC
NM_004827	ABCG2	10400	ACGACTTATGTTCCACGGGCC
NM_005164	ABCD2	10401	ACGCCTCGGACTTTTCATCATC
NM_005164	ABCD2	10402	ACGGAGGTTGGCGCTTTGAAC
NM_005415	SLC20A1	10403	ACCCCATTTGTATTGTTGGTGC
NM_005415	SLC20A1	10404	ACTGGGAACCTTGTCCAGTTC
NM_005415	SLC20A1	10405	ACGGCTGTTGACTGGCGTCTC
NM_005445	CSPG6	10406	ACTTGACCAGGCTCTGGATGC
NM_005496	SMC4L1	10407	ACAGATGGATGTAGCCCAGTC
NM_005496	SMC4L1	10408	ACGGAAGAATGGGTTCCCTCAC
NM_005496	SMC4L1	10409	ACGATCTTCGGAAACAAAGGC
NM_005502	ABCA1	10410	ACCTGGCTGTGTCCATGATC
NM_005502	ABCA1	10411	ACGTTAGGAAACCTGCTGCCC
NM_005629	SLC6A8	10412	ACGGCCGGCAGCATCAATGTC
NM_005629	SLC6A8	10413	ACCAACTGCTACAAGGACGCC
NM_005660	SLC35A2	10414	ACTGCCTCCCTCATCCTCAGC
NM_005660	SLC35A2	10415	ACCCTCCAGTATGTTGCCATC
NM_005660	SLC35A2	10416	ACCCTGCAACTGGGCCTCTTC
NM_005688	ABCC5	10417	ACAGCCATTTCGAGGAGTTGTC
NM_005689	ABCB6	10418	ACCCTCTGAAGACACTAAGCC
NM_006516	SLC2A1	10419	ACGTCCTTTGAGATGCTGATC
NM_006516	SLC2A1	10420	ACCGCTGTCTTCTATTACTCC
NM_006598	SLC12A7	10421	ACGGATGCACAGAAGTCCATC
NM_006598	SLC12A7	10422	ACCATACGGTCCCTAATGAGC
NM_006598	SLC12A7	10423	ACGCTCAATGGCGTCGTCTC
NM_006672	SLC22A7	10424	ACCAGAGCTGCGTCCACTTTC
NM_006749	SLC20A2	10425	ACGGTTCAGGAAGCAGAGTCC
NM_006749	SLC20A2	10426	ACCAGTTACACCTGCTACACC
NM_006762	LAPTM5	10427	ACGCTCTCCCAGATGGGCTAC
NM_006762	LAPTM5	10428	ACCTTCAAGTCCATGAACCAC
NM_006762	LAPTM5	10429	ACGATGCTCCAGAAGGTGGTC
NM_006931	SLC2A3	10430	ACGTCGGTTGAAATGCTGATC
NM_006931	SLC2A3	10431	ACCTTCCTAGTCGGATTGCTC
NM_004211	SLC6A5	10432	ACAGTGGTGTACTTCACGGCC
NM_006934	SLC6A9	10432	ACAGTGGTGTACTTCACGGCC
NM_006934	SLC6A9	10433	ACCCACTACCAGTACCCAGGC
NM_006979	HKE4	10434	ACCCTCATTTCTCACCACACTC
NM_006979	HKE4	10435	ACGATGGGCCAGTGAGACCTC
NM_007168	ABCA8	10436	ACTGGCTGAATTCATTGCTCC
NM_007256	SLC21A9	10437	ACCCTGACTGTGATCCAGTTC
NM_012089	ABCB10	10438	ACCAGCGGATTGCGATTGCCC

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NM_012243	SLC35A3	10439	ACGAAGAAGGACCTCGTTATC
NM_012244	SLC7A8	10440	ACGAAAGAGATCGGATTGGTC
NM_012429	SEC14L2	10441	ACGCTTCGACCTGCAGAAGTC
NM_013356	SLC16A8	10442	ACAGCCGTGAGCGTCTTCTTC
NM_013356	SLC16A8	10443	ACCTTCCAGCCGTCGCTCATC
NM_014229	SLC6A11	10444	ACCATCTACACCTACCCAGCC
NM_014437	SLC39A1	10445	ACCCATGAAGGCTCAGCTTCC
NM_014437	SLC39A1	10446	ACCAAGGGCTCTGCTGGGAAC
NM_014579	SLC39A2	10447	ACTTCTTCCACGGGAGCTAGC
NM_014580	SLC2A8	10448	ACGCTGAGCCTCTTGCTGTGC
NM_014713	LAPTM4A	10449	ACCTCCATGCCAGCTGTCAAC
NM_014848	SV2B	10450	ACGCAAGTCCATGACACCAAC
NM_014848	SV2B	10451	ACGCATTGCAGCCTGGAATGC
NM_014849	SV2	10452	ACCAAAGGCATGCTAGGCCTC
NM_015559	SETBP1	10453	ACCGTGCACAGATCACTCTCC
NM_015657	ABCA12	10454	ACTCTAAGACTCCTGCAGTCC
NM_015657	ABCA12	10455	ACGAATTCTGCAACCTGTCTC
NM_015657	ABCA12	10456	ACGATGATGGGTGTGAACCTCC
NM_016321	RHCG	10457	ACTCTGCATGGCATTCTTGGC
NM_016582	PHT2	10458	ACCCTCGTGCTGTACCTCAAC
NM_016582	PHT2	10459	ACCATCAGCTTCCTGCTGGGC
NM_016582	PHT2	10460	ACGGACTTTGGGAACATCAAC
NM_016609	LOC51310	10461	ACCGGCAGATTGAGGAAGCCC
NM_016609	LOC51310	10462	ACTCTGCTTATCCTGGGCTTC
NM_020372	LOC57100	10462	ACTCTGCTTATCCTGGGCTTC
NM_017767	SLC39A4	10463	ACGACGGCCTGCGTAGATATC
NM_130849	SLC39A4	10463	ACGACGGCCTGCGTAGATATC
NM_017836	FLJ20473	10464	ACTTCCATGTGCTGAGTCC
NM_017945	FLJ20730	10465	ACCTACTGTGAATGTGTGCTC
NM_017945	FLJ20730	10466	ACCTGGATCCAGTGGGCTTCC
NM_017945	FLJ20730	10467	ACGCCTCAAGTTCCGGAATAC
NM_018057	NTT73	10468	ACCTACAATACATCCTGGCCC
NM_018057	NTT73	10469	ACCTGGAAGATGACCATCTGC
NM_018358	FLJ11198	10470	ACCGTTACTGAAGATGCTGGC
NM_018358	FLJ11198	10471	ACCTCAAGATGCTGGAGAAGC
NM_018358	FLJ11198	10472	ACGGAGGATTTGACCAGTACC
NM_018375	FLJ11274	10473	ACTCATGCTACATAAGGCACC
NM_018375	FLJ11274	10474	ACTAGGGCACAGCCACAAGCC
NM_018407	LC27	10475	ACTACATACGGCAACTGCCTC
NM_018484	SLC22A11	10476	ACGCCAGTCCATCTTCATGTC
NM_019848	P3	10477	ACGAACGTGAGTGCTATAACC
NM_019848	P3	10478	ACCAAGTGTTGTTTTGGGTGC
NM_019848	P3	10479	ACGCCCTTCAGCTTTGTGCTC
NM_020041	SLC2A9	10480	ACGGAGAAGAAAGGACTGGTC
NM_020041	SLC2A9	10481	ACGGAGAGTACCTGGCCATAC
NM_020208	XT3	10482	ACGGCCTGGATCAATGCAGCC

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NM_022405	XT3	10482	ACGGCCTGGATCAATGCAGCC
NM_020309	SLC17A7	10483	ACGTACATCGAGGACGCCATC
NM_020309	SLC17A7	10484	ACGTTGATGAACTGCGGAGGC
NM_020309	SLC17A7	10485	ACTGGAGGATGAGGCTGAGCC
NM_020407	RHBG	10486	ACGCTACCCTTTCTGGACTCC
NM_016124	RHD	10487	ACCGGCAATGGCATGATTGGC
NM_020485	RHCE	10487	ACCGGCAATGGCATGATTGGC
NM_138616	RHCE	10487	ACCGGCAATGGCATGATTGGC
NM_020708	SLC12A5	10488	ACTGTACAGAGATCCAGGGC
NM_020708	SLC12A5	10489	ACGGTGCATCTCACCTGGACC
NM_021082	SLC15A2	10490	ACGAAGCCATCTCCGACAATC
NM_021082	SLC15A2	10491	ACATGGCTGTTGGTATGATCC
NM_021977	SLC22A3	10492	ACACTTGGCAGTCCACATTCC
NM_022042	SLC26A1	10493	ACGAGCCTGGTGAAGACAGCC
NM_022127	SLC28A3	10494	ACTCTGATTGCCTTCCTGGCC
NM_022169	ABCG4	10495	ACGGTCTTCAACAACACCGGC
NM_022436	ABCG5	10496	ACGCAATGTGCTAAAGGGTGC
NM_022436	ABCG5	10497	ACCCTGCCCAGGTGCAACATC
NM_022437	ABCG8	10498	ACCAGCCTGTACTTCACCTAC
NM_022437	ABCG8	10499	ACCCTGGTGAAGACCTTGTC
NM_022736	FLJ14153	10500	ACATTCATGCTGCTGTATGCC
NM_022736	FLJ14153	10501	ACCATCATCTGGGTTCTTTGC
NM_022911	SLC26A6	10502	ACTCGGGCGGATCTGCTTATC
NM_134263	SLC26A6	10502	ACTCGGGCGGATCTGCTTATC
NM_134426	SLC26A6	10502	ACTCGGGCGGATCTGCTTATC
NM_024331	C20orf121	10503	ACGAGTTCGCCAACCTGTTC
NM_030807	SLC2A11	10504	ACGTCCCTCCTGGTGAATAAC
NM_030807	SLC2A11	10505	ACTGACTCGGTGTACGCCTAC
NM_030807	SLC2A11	10506	ACGACCTTCCAAGAGATCTCC
NM_032034	SLC4A11	10507	ACGAGGTCGACGGAGGAGATC
NM_032038	LOC83985	10508	ACCTACATGGACCGCTTCACC
NM_032148	DKFZP434K0427	10509	ACTAGCTGCCAAACATCCAGC
NM_032718	MGC11332	10510	ACGGTGACAGGCTACCTCATC
NM_032803	SLC7A3	10511	ACGCACCCCTGGATTTAGTGGC
NM_032803	SLC7A3	10512	ACGTGTTTACAGGCGTGAACC
NM_033125	OKB1	10513	ACTTGGAGTTTGGAGGACACC
NM_033125	OKB1	10514	ACGGTCTGGGAGGAGAACAGTC
NM_032583	ABCC11	10515	ACGAAGCCTGGGTCATTGTTC
NM_033151	ABCC11	10515	ACGAAGCCTGGGTCATTGTTC
NM_145186	ABCC11	10515	ACGAAGCCTGGGTCATTGTTC
NM_033226	ABCC12	10516	ACCAGGACCATGTGTGAGGTC
NM_145187	ABCC12	10516	ACCAGGACCATGTGTGAGGTC
NM_145188	ABCC12	10516	ACCAGGACCATGTGTGAGGTC
NM_145189	ABCC12	10516	ACCAGGACCATGTGTGAGGTC
NM_145190	ABCC12	10516	ACCAGGACCATGTGTGAGGTC
NM_052832	SLC26A7	10517	ACTGCCATATATATCCGGACC

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NM_134266	SLC26A7	10517	ACTGCCATATATATCCGGACC
NM_052832	SLC26A7	10518	ACTGAAGAAGCTTCACAGTCC
NM_134266	SLC26A7	10518	ACTGAAGAAGCTTCACAGTCC
NM_052885	SLC2A13	10519	ACCAACAAGGAGACACTGCTC
NM_052885	SLC2A13	10520	ACCAGGCTATGTACATGTGGC
NM_052934	SLC26A9	10521	ACATCATCACGTACTGCTCCC
NM_134325	SLC26A9	10521	ACATCATCACGTACTGCTCCC
NM_052961	SLC26A8	10522	ACGCGAATTCACCAGCATTC
NM_052961	SLC26A8	10523	ACTCTTCCAGTGCTGCAGCTC
NM_138718	SLC26A8	10523	ACTCTTCCAGTGCTGCAGCTC
NM_052961	SLC26A8	10524	ACTCAGAACAAGAGGCTGGGC
NM_138718	SLC26A8	10524	ACTCAGAACAAGAGGCTGGGC
NM_080282	ABCA10	10525	ACCTTCTCCCACAGGAAGACC
NM_080284	ABCA6	10526	ACGTGGAACAAGAGGTACAAC
NM_080284	ABCA6	10527	ACTGAGATGGAACTCCTCCC
NM_134425	SLC26A1	10528	ACCACCCATGGCAATTAACAC
NM_139177	C17orf26	10529	ACTCGGGATCCAGAATTTCCC
XM_029730	LOC222915	10530	ACGCACCTATGGAGTTGTACAC
XM_032693	KIAA0420	10531	ACGATCGCAGGTGTTGAGCAC
XM_032693	KIAA0420	10532	ACGTTCTCATCTACAGTGGC
XM_037173	LOC91252	10533	ACGTCAGCGGTACCTCAACC
XM_037173	LOC91252	10534	ACGATCGGGCTCCTGACAACC
XM_043493	KIAA1054	10535	ACCACCTACTTCAAGAACTGC
XM_043493	KIAA1054	10536	ACATGCGCTATGCAAGGCAGC
XM_046677	KIAA0062	10537	ACGCTCTCTTCTTCAACTTCC
XM_047707	KIAA1265	10538	ACCCTGATCGTGACATAACC
XM_047707	KIAA1265	10539	ACCATGCACATGGGCATGGAC
XM_060424	LOC127324	10540	ACGGAGATGAAGCCACAGCGC
XM_060969	LOC118461	10541	ACGCAGGACTTCAGAACACAC
XM_060969	LOC118461	10542	ACGCAATTGCAAGAGCGGTTT
XM_062680	LOC121524	10543	ACGTCGTCTGCAACATGATCC
XM_062680	LOC121524	10544	ACCATTTCCCTGCAGTGGAGC
XM_062680	LOC121524	10545	ACACACTGGTAAACCCAGCCC
XM_063138	LOC122438	10546	ACGTCAAGAGAGTCCCTGGAC
XM_063138	LOC122438	10547	ACGGAAGAGCTAGACAGTGGC
XM_064152	LOC124470	10548	ACGCCTCTGGAGCAGTCCTAC
XM_066420	LOC129255	10549	ACTGAGGTGCGGTCAGAACAC
XM_066420	LOC129255	10550	ACGCATCACACGTACCATGTC
XM_066420	LOC129255	10551	ACCAGACAAACCTGCCACATC
XM_066649	LOC139355	10552	ACCTTTAGGACTGTGGCCTCC
XM_066649	LOC139355	10553	ACCAGCTAGAAGAGCTAAGGC
XM_067219	LOC131136	10554	ACTGTGGAGTGTGAGAAGCTC
XM_069204	LOC135143	10555	ACCAGAGTGCTTCTTGGGACC
XM_070474	LOC137518	10556	ACACGGCCTAATTCCAGCCAC
XM_070474	LOC137518	10557	ACGACAGTCTACTCCAGGCAC
XM_086329	LOC148810	10558	ACGGTGACAGAGGTCTTCATC

XM_086889	LOC150287	10559	ACGTGCCTGACCAAGATCAAC
XM_087693	LOC153505	10560	ACCGCACATTCTCCAGAACCC
XM_091236	LOC161932	10561	ACCTGGCATGGACCCAGTAGC
XM_091236	LOC161932	10562	ACGTTCACTTGCTTGGGCAGC
XM_092895	LOC164636	10563	ACCCTCTGGTAGAAGTGTACC
XM_099966	LOC159361	10564	ACTACAGGAGCCAGCATTGTC
XM_108856	LOC169534	10565	ACGCTTGTTTCCTCTAGGTCC
XM_108856	LOC169534	10566	ACGGATTGTTTCAGGGACAGCC
XM_108856	LOC169534	10567	ACCTGTCAGGGAGTGCATGGC
XM_115387	LOC204461	10568	ACCTCTTCCTTGGCAAGGACC
XM_116595	LOC206568	10569	ACGTTCTCCAAGTATAGGAGACC
XM_116595	LOC206568	10570	ACTTCTGTCTTGGTCAAGGAC
XM_116595	LOC206568	10571	ACTGTCTTGGTTCTCCTCAGC
XM_166496	LOC221832	10572	ACCAGAGGATCGCAATTGCTC
XM_166496	LOC221832	10573	ACGCAAGTCAGCTGTTCAAGC
XM_166496	LOC221832	10574	ACTCGCTGACCTTGAACCAGC
XM_167663	LOC221074	10575	ACACCCCTCAGCCCAGGATAGC
XM_167663	LOC221074	10576	ACTAGTGAGCAGTGAAGGTGC
XM_170932	LOC254428	10577	ACTGGAATGCCCGGAGAGAAC
NM_031301	DKFZP564D0372	10578	ACACCCAGGTGAGACAGCACC
NM_015331	NCSTN	10579	ACGTCATCAAGCAGTGCTATC
NM_015331	NCSTN	10580	ACATCAGTCCCAGCCTCTCCC
NM_000015	NAT2	10581	ACTACAGCACTGGCATGGTTC
NM_000015	NAT2	10582	ACGAGAGAGGAATCTGGTACC
NM_000016	ACADM	10583	ACCAGAACCTGGAGCAGGCTC
NM_000016	ACADM	10584	ACCCAGACCTGTAGTAGCTGC
NM_000016	ACADM	10585	ACTGAGTTACCAGAGAGCAGC
NM_000017	ACADS	10586	ACGAAGACAAGCTGGGCATCC
NM_000018	ACADVL	10587	ACTGTTCAAAGGCCAGCTCAC
NM_000018	ACADVL	10588	ACTCTTTGGCTCGGAGGCAGC
NM_000019	ACAT1	10589	ACGCCATCATGATGGCCTCTC
NM_000019	ACAT1	10590	ACTGGCACAGTAACAGCTGCC
NM_000019	ACAT1	10591	ACGCCTTTAGTCTGGTTGTAC
NM_000108	DLD	10592	ACCAGTTATAGGTTCTGGTCC
NM_000110	DPYD	10593	ACCTCTGTGTTCCACTTCGGC
NM_000110	DPYD	10594	ACTGGCGTTACAGCCACCAAC
NM_000182	HADHA	10595	ACGTGCCGTCCTTATCTCATC
NM_000182	HADHA	10596	ACGGCCTTGATGGGACTCTAC
NM_000183	HADHB	10597	ACGCAATGTGGCTAGAGAGGC
NM_000183	HADHB	10598	ACCAGGATGAATATGCACTGC
XM_093031	LOC169988	10598	ACCAGGATGAATATGCACTGC
NM_000183	HADHB	10599	ACAGAAGGAGGCCAGTATGGC
NM_000194	HPRT1	10600	ACGGAGATGGGAGGCCATCAC
NM_000194	HPRT1	10601	ACTTGGTGGAGATGATCTCTC
NM_000196	HSD11B2	10602	ACGTAGTTGCTGATGCGGAGC
NM_000197	HSD17B3	10603	ACACGTGGACTCAATGTTGTC

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NM_000197	HSD17B3	10604	ACTGCTTCCAAACCTTCTCCC
NM_000229	LCAT	10605	ACCAATGGCTACGTGCGGGAC
NM_000229	LCAT	10606	ACCCTGACCCTGGAGCACATC
NM_000235	LIPA	10607	ACCCATTCTGACAAAGGTCCC
NM_000235	LIPA	10608	ACATATGACCTACCAGCTTCC
NM_000235	LIPA	10609	ACGGAGCTCTGTGGAATCTC
NM_000236	LIPC	10610	ACGAGCAAGAGGCTCTTCCTC
NM_000237	LPL	10611	ACTGTATGAGAGTTGGGTGCC
NM_000237	LPL	10612	ACCAATCTGGGCTATGAGATC
NM_000254	MTR	10613	ACGCTGGGTAAAGTGCTGCC
NM_000254	MTR	10614	ACGGCTGTTGGCCACCTTATC
NM_000254	MTR	10615	ACGCTCACCATGTGGAGACTC
NM_000274	OAT	10616	ACCAGTCCAAGGCCCTCCAAC
NM_000300	PLA2G2A	10617	ACGGATGCAACGGATCGCTGC
NM_000320	QDPR	10618	ACGGGTGCTGTTACCAGCTC
NM_000320	QDPR	10619	ACGCCTAATCCAGGTGGTAAC
NM_000348	SRD5A2	10620	ACTGGAGTCCTTCAAGGCTAC
NM_000348	SRD5A2	10621	ACGCCTGGAGAAATCAGCTAC
NM_000348	SRD5A2	10622	ACCAACATGACCCCTGGATGGC
XM_002471	SRD5A2	10622	ACCAACATGACCCCTGGATGGC
NM_000348	SRD5A2	10623	ACAGGACCTGCAGGCAGAGAC
XM_002471	SRD5A2	10623	ACAGGACCTGCAGGCAGAGAC
NM_000353	TAT	10624	ACTGAAAGATGCCCTGGACTC
NM_000353	TAT	10625	ACTATGAACCACTGGCCACCC
NM_000353	TAT	10626	ACTTTTCATCCGAGTGGTCATC
NM_000379	XDH	10627	ACGTTTACCACCCCTGTGTGTC
NM_000398	DIA1	10628	ACGGTTTACTTCAAGGACACC
NM_007326	DIA1	10628	ACGGTTTACTTCAAGGACACC
NM_000398	DIA1	10629	ACTGAGGAGATGATCCGGGAC
NM_007326	DIA1	10629	ACTGAGGAGATGATCCGGGAC
NM_000402	G6PD	10630	ACGGTCAAGGTGTTGAAATGC
NM_000408	GPD2	10631	ACAGTGGACAACCTATCGGTC
NM_000408	GPD2	10632	ACGGAAGGGTATCTGGAAGCC
NM_000413	HSD17B1	10633	ACTGACGTTTATTGCGCCAGC
NM_000413	HSD17B1	10634	ACTACCTCGCCACAGCAAGC
NM_000413	HSD17B1	10635	ACCTACGTCACCGCCATGCAC
NM_000414	HSD17B4	10636	ACTTACGCTGGGAGCGGACTC
NM_000414	HSD17B4	10637	ACGATTTTCATGGAGGTGGTCC
NM_000436	OXCT	10638	ACCAAAGATGGCAGTGTGCCC
NM_000463	UGT1A1	10639	ACGACGTACCCTGTGCCATTCT
NM_000463	UGT1A1	10640	ACGCATATGCAATGGCGTTCC
NM_001072	UGT1A6	10640	ACGCATATGCAATGGCGTTCC
NM_007120	UGT1A4	10640	ACGCATATGCAATGGCGTTCC
NM_019076	UGT1A8	10640	ACGCATATGCAATGGCGTTCC
NM_019093	UGT1A3	10640	ACGCATATGCAATGGCGTTCC
NM_021027	UGT1A9	10640	ACGCATATGCAATGGCGTTCC

NM_000482	APOA4	10641	ACTGAGGTGAGCCAGAAGATC
NM_000482	APOA4	10642	ACGGACCTGAGGGACAAGGTC
NM_000485	APRT	10643	ACGCTGGCACCTGTACCCTTC
NM_000531	OTC	10644	ACTAAAGTGACGTGAAGGGC
NM_000637	GSR	10645	ACAGGTAATGTGGAACACAGC
NM_000637	GSR	10646	ACTGATCAGCACCAACTGCAC
NM_000637	GSR	10647	ACCAACATCCCCAACTGTGGTC
NM_000662	NAT1	10648	ACCACCAGATCCGAGCTGTTC
NM_000663	ABAT	10649	ACGACCATCTTCATGTGGTAC
NM_000663	ABAT	10650	ACCCATGCATCCGATGACTTC
NM_000670	ADH4	10651	ACTTTGAGGGCCTAGCTTTCC
NM_000670	ADH4	10652	ACTCAACAATGCCAAGGTCAC
NM_000670	ADH4	10653	ACATCAGTGAGGCATTTGACC
NM_000671	ADH5	10654	ACGGCGGGTGACACTGTCATC
NM_000671	ADH5	10655	ACGGGCCAAAGAGTTTGGAGC
NM_000671	ADH5	10656	ACGTGTCCCAAAGTTGGTGTC
NM_000672	ADH6	10657	ACGGAGTAAGCACAGTGAAAC
NM_000672	ADH6	10658	ACGGTGACTCCAGGTTCTACC
NM_000672	ADH6	10659	ACATCTGGACGTTCTGGCAGC
NM_000673	ADH7	10660	ACCAATGGTGTCCAAGTTTCC
NM_000689	ALDH1A1	10661	ACGAGATCGTCTGCTGCTGGC
NM_000691	ALDH3A1	10662	ACCCAAATTGTGGAGAAGCTC
NM_000691	ALDH3A1	10663	ACTGATGAAGGCCTGAAGGTC
NM_000692	ALDH1B1	10664	ACTGAATGGCAAGATGCAGTC
NM_000692	ALDH1B1	10665	ACGTGGCATGGCAAGACCATC
NM_000692	ALDH1B1	10666	ACCGAGTCCTAGGCTACATCC
NM_000693	ALDH1A3	10667	ACGTGGAAGAAGGAGATAAGC
NM_000694	ALDH3B1	10668	ACCAAGCAGCTTCTGCACGAC
NM_000695	ALDH3B2	10669	ACGTTACCTTCGACACCTTC
NM_000696	ALDH9	10670	ACCCGGCCGAGTGATAGCTAC
NM_000709	BCKDHA	10671	ACGTTGGAATTCATCCAGCCC
NM_000712	BLVRA	10672	ACGAAGACCGGTTTGGCTTCC
NM_000712	BLVRA	10673	ACTGACAGTGTGTCTGGAGAC
NM_000791	DHFR	10674	ACGATCCACATACCCTTCAAC
NM_000791	DHFR	10675	ACGCTTCCTACGTGTATATCC
NM_000791	DHFR	10676	ACGCAGTGTATTTGCTAGGTC
NM_000819	GART	10677	ACAGCCACTTCCAGATCAGGC
NM_000819	GART	10678	ACTATCCACCCATCCTTGCTC
NM_000561	GSTM1	10679	ACATTCAAGCTGGGCCTGGAC
NM_000848	GSTM2	10679	ACATTCAAGCTGGGCCTGGAC
NM_000850	GSTM4	10679	ACATTCAAGCTGGGCCTGGAC
NM_000851	GSTM5	10679	ACATTCAAGCTGGGCCTGGAC
XM_167023	LOC221270	10679	ACATTCAAGCTGGGCCTGGAC
NM_000848	GSTM2	10680	ACGGAGCAGATTTCGGAAGAC
NM_000848	GSTM2	10681	ACCCTGAAGGACTTCATCTCC
XM_167023	LOC221270	10681	ACCCTGAAGGACTTCATCTCC

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NM_000849	GSTM3	10682	ACGAACAAGATCACCCAGAGC
NM_000853	GSTT1	10683	ACGGACTTCCCACCTGCAGAC
NM_000854	GSTT2	10684	ACTGGCTGGAGGACAAGTTCC
NM_000855	GUCY1A2	10685	ACGGTCTAAGGAAGCAGCTTC
NM_000855	GUCY1A2	10686	ACAGCCTTCTCTTTCTTCGTC
NM_000856	GUCY1A3	10687	ACCCACCTCCCTGATTCTTCC
NM_000856	GUCY1A3	10688	ACTCTTCAAGGGTTATGGACC
NM_000856	GUCY1A3	10689	ACCAATGTCACTCTGGCTAAC
NM_000857	GUCY1B3	10690	ACTGGTACCCAGGAATCACGC
NM_000857	GUCY1B3	10691	ACTACTGTCAACCTCACAAAGC
NM_000860	HPGD	10692	ACGACTCTGTTTCATCCAGTGC
NM_000860	HPGD	10693	ACTGGAGGTGAAGGCGGCATC
NM_000860	HPGD	10694	ACGCATGGCATAGTTGGATTTC
NM_000883	IMPDH1	10695	ACTGAGATCCTGCAGCGTAGC
XM_095828	LOC169633	10695	ACTGAGATCCTGCAGCGTAGC
XM_167188	LOC221654	10695	ACTGAGATCCTGCAGCGTAGC
NM_000884	IMPDH2	10696	ACTCGGGACTACCCACTAGCC
NM_000903	NQO1	10697	ACTTTGGCCTTTTCTGTGGGCC
NM_000918	P4HB	10698	ACGTACCTGCTGGTGGAGTTC
NM_000928	PLA2G1B	10699	ACCTACGGCTGCTACTGTGGC
NM_000928	PLA2G1B	10700	ACGTGCTGCCAGACACATGAC
NM_000928	PLA2G1B	10701	ACCAAAGAGTGTGAGGCCTTC
NM_000929	PLA2G5	10702	ACGGATGGCACCGATTGGTGC
NM_000929	PLA2G5	10703	ACCATTCGCACACAGTCCTAC
NM_000932	PLCB3	10704	ACGATGGCTGAGTACTGCCGC
NM_000932	PLCB3	10705	ACCAGCTGGCAGAAGAGGAGC
NM_000942	PPIB	10706	ACGAGCATCTACGGTGAGCGC
NM_000942	PPIB	10707	ACCGCAGGCAAAGACACCAAC
NM_001047	SRD5A1	10708	ACAGCCTATGCCACTGTTGGC
NM_001047	SRD5A1	10709	ACACCAGGAGATACTGGATAC
NM_001047	SRD5A1	10710	ACGAGCATCATGAGTGGTACC
NM_001054	SULT1A2	10711	ACGGTGGTCTATGTTGCCCCG
NM_001055	SULT1A1	10711	ACGGTGGTCTATGTTGCCCCG
NM_001054	SULT1A2	10712	ACCCCTATGACCAACTACACC
NM_001055	SULT1A1	10712	ACCCCTATGACCAACTACACC
NM_003166	SULT1A3	10712	ACCCCTATGACCAACTACACC
XM_051068	SULT1A2	10712	ACCCCTATGACCAACTACACC
NM_001056	SULT1C1	10713	ACGCAGGGACAACGTGGATTTC
NM_001072	UGT1A6	10714	ACGAGCTGAAGAACCGTTACC
NM_001080	ALDH5A1	10715	ACTTTCCTCTGTGGAGTGCCC
NM_001114	ADCY7	10716	ACGGACCTGAAGACCATGACC
NM_001115	ADCY8	10717	ACCAGAATACTCTGGCTGCCC
NM_001115	ADCY8	10718	ACGTCGATACCCCTTGAAGAAC
NM_001116	ADCY9	10719	ACCATCGCCAGCAGGATGGAC
NM_001179	ART3	10720	ACGCCACCAGCAATTAGATAC
NM_001179	ART3	10721	ACACCTTGTGAGGCCAGTTCC

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NM_001182	ALDH7A1	10722	ACCAACGCCATCGCCATGATC
NM_001236	CBR3	10723	ACCTGGACATCGACGACTTGC
NM_001303	COX10	10724	ACCGCATGTATGTCACACAGC
NM_001359	DECR1	10725	ACCACTGTGTGTCAGAACTGATC
NM_001359	DECR1	10726	ACATGGCACAGCCTTCGTGAC
NM_001359	DECR1	10727	ACACCAAAGGTGCCTTTAGCC
NM_001361	DHODH	10728	ACCCCTAGACCCAGAGTCTTC
NM_001361	DHODH	10729	ACCCATTTCGGGAGATGTATGC
NM_001379	DNMT1	10730	ACCGGTGCTCATGCTTACAAC
NM_001379	DNMT1	10731	ACCATCAAGCTGTCCAGTCCC
NM_001478	GALGT	10732	ACGTAACCACCAAGTACGTGC
NM_001482	GATM	10733	ACCTTTCCAGAGCACCCAGGC
NM_001482	GATM	10734	ACTTCCCTGGGAGGAGGCTTC
NM_001490	GCNT1	10735	ACACATGACCAGTGACTGTTC
NM_001490	GCNT1	10736	ACACGGAGAGGATGCCATCCC
NM_001490	GCNT1	10737	ACCTGGATGCTGCGCAAACAC
NM_001491	GCNT2	10738	ACGGCTAAATATCTCAGACCC
NM_001491	GCNT2	10739	ACCACCTGTGGGCAAGACTTC
NM_001491	GCNT2	10740	ACTGCCTAGAAGTGAAGGCATC
NM_145649	AlGnT	10740	ACTGCCTAGAAGTGAAGGCATC
NM_145655	CIgNt	10740	ACTGCCTAGAAGTGAAGGCATC
NM_001497	B4GALT1	10741	ACCCCAAATGTGAAGATGGGC
NM_001503	GPLD1	10742	ACTGGGACCAGTGACTGCAGC
NM_001503	GPLD1	10743	ACGAATCAAGTCGTCATTGCC
NM_001512	GSTA4	10744	ACGGAAGTGGTTAACATGGCC
NM_001512	GSTA4	10745	ACGAGATTCTCTTGAACCTGGC
NM_001513	GSTZ1	10746	ACGTGGGAGAGGAGATGCAGC
NM_145870	GSTZ1	10746	ACGTGGGAGAGGAGATGCAGC
NM_145871	GSTZ1	10746	ACGTGGGAGAGGAGATGCAGC
NM_001513	GSTZ1	10747	ACGATTCAAGGTGGATCTCAC
NM_145870	GSTZ1	10747	ACGATTCAAGGTGGATCTCAC
NM_145871	GSTZ1	10747	ACGATTCAAGGTGGATCTCAC
NM_001513	GSTZ1	10748	ACTTGAGGAGATGGGAGACTC
NM_145870	GSTZ1	10748	ACTTGAGGAGATGGGAGACTC
NM_145871	GSTZ1	10748	ACTTGAGGAGATGGGAGACTC
NM_001527	HDAC2	10749	ACCCTAGTGCTGTGGTATTAC
NM_001535	HRMT1L1	10750	ACCCCAAGTGTGGAGAAGGCAC
NM_001543	NDST1	10751	ACCTTCACCTTCAACCTGGGC
NM_001543	NDST1	10752	ACCTATCACAAAGGCATCGAC
NM_001543	NDST1	10753	ACGCTGCTGTATAAGATGGGC
NM_001607	ACAA1	10754	ACTGTGGCTGAGCGGTTTGGC
NM_001607	ACAA1	10755	ACGAGGAGCATCACTGTGACC
NM_001608	ACADL	10756	ACTGGAAGCAAGGTGTTTCATC
NM_001608	ACADL	10757	ACCAGTTGCTCACCTACAGAC
NM_001609	ACADSB	10758	ACTCTTCCAGTCAGAAGCTC
NM_001609	ACADSB	10759	ACGTATGCCATAGGGAGTCTC

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NM_001618	ADPRT	10760	ACGTCCAACAGAAGTACGTGC
NM_001618	ADPRT	10761	ACGGCCATGATTGAGAACTC
NM_001628	AKR1B1	10762	ACGTCTGTGACACCAGAACGC
NM_001644	APOBEC1	10763	ACGATCTGGCGAAGCTCAGGC
NM_005889	APOBEC1	10763	ACGATCTGGCGAAGCTCAGGC
NM_001644	APOBEC1	10764	ACTCGGCAAGGTCTCAGGGAC
NM_005889	APOBEC1	10764	ACTCGGCAAGGTCTCAGGGAC
NM_001713	BHMT	10765	ACACGTCATGCAGACCTTCAC
NM_001713	BHMT	10766	ACGCTCACCTGATGAGCCAGC
NM_001713	BHMT	10767	ACATACGCCAGAGAGGCCTAC
NM_017614	BHMT2	10767	ACATACGCCAGAGAGGCCTAC
NM_001757	CBR1	10768	ACGTTCCGCAGTGAGACCATC
NM_001757	CBR1	10769	ACGATCCTCCTGAATGCCTGC
NM_001818	AKR1C4	10770	ACCAGAGCTGTAGAGGTCAAC
NM_001818	AKR1C4	10771	ACCAAGCCAGGACTCAAGTAC
NM_003739	AKR1C3	10771	ACCAAGCCAGGACTCAAGTAC
NM_001876	CPT1A	10772	ACGAACGGCATCATCACTGGC
NM_001876	CPT1A	10773	ACCCCATGTTGTACAGCTTCC
NM_001889	CRYZ	10774	ACTGGAGCCCATGAAGTGTTT
NM_001933	DLST	10775	ACCAAGTGTCTTCAGTGTTTGC
NM_001933	DLST	10776	ACCCTACAGCAGCGGCAGTTC
NM_001933	DLST	10777	ACATGCAGTGATTGACGACAC
NM_001966	EHHADH	10778	ACGATTGGAGTCGTTGTAGGC
NM_001966	EHHADH	10779	ACACTGGCTTCTCAGGGAAAC
NM_002004	FDPS	10780	ACCAGGATGCTGATAGTCTCC
XM_066636	LOC139340	10780	ACCAGGATGCTGATAGTCTCC
NM_002004	FDPS	10781	ACGCATGTATCTACCGCCTGC
NM_002004	FDPS	10782	ACTGCAGCTGGCTGGTGGTTC
XM_089168	LOC163828	10782	ACTGCAGCTGGCTGGTGGTTC
XM_091043	LOC161674	10782	ACTGCAGCTGGCTGGTGGTTC
NM_002027	FNTA	10783	ACTGGCTAAGAGATCCATCTC
NM_002027	FNTA	10784	ACGGGACCCTGCAGGAGTTTC
NM_002028	FNTB	10785	ACGAGGCCTTCGACAACCTGAC
NM_002033	FUT4	10786	ACCCTCTTCAACTGGACGCTC
NM_002033	FUT4	10787	ACCTACGAGCGCTTTGTGCCC
NG_001123	NG_001123	10788	ACGCTCACTGGCATGGCCTTC
NM_002046	GAPD	10788	ACGCTCACTGGCATGGCCTTC
XM_060641	LOC127739	10788	ACGCTCACTGGCATGGCCTTC
XM_068131	LOC132990	10788	ACGCTCACTGGCATGGCCTTC
XM_069391	LOC135508	10788	ACGCTCACTGGCATGGCCTTC
XM_114787	LOC199972	10788	ACGCTCACTGGCATGGCCTTC
XM_171406	LOC254142	10788	ACGCTCACTGGCATGGCCTTC
NG_001123	NG_001123	10789	ACGCTCATTTTCTGGTATGAC
NM_002046	GAPD	10789	ACGCTCATTTTCTGGTATGAC
XM_068609	LOC133937	10789	ACGCTCATTTTCTGGTATGAC
XM_094687	LOC167821	10789	ACGCTCATTTTCTGGTATGAC

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XM_116493	LOC202432	10789	ACGCTCATTTCTGGTATGAC
XM_171289	LOC254592	10789	ACGCTCATTTCTGGTATGAC
NG_001013	NG_001013	10790	ACGAGATCCTCAGTCAATTGC
NM_002064	GLRX	10790	ACGAGATCCTCAGTCAATTGC
NG_001013	NG_001013	10791	ACAGATTGTATAGGCGGATGC
NM_002064	GLRX	10791	ACAGATTGTATAGGCGGATGC
NM_002153	HSD17B2	10792	ACTACAAGAAGAGCTCAGGGC
NM_002153	HSD17B2	10793	ACTATCGCAGGCACCAAGTGC
NM_002168	IDH2	10794	ACGGACATCTTCCAGGAGATC
NM_002168	IDH2	10795	ACCGAGCACTTCTGAACACC
NM_002225	IVD	10796	ACCCTGGGCGTATTGGGCATC
NM_002225	IVD	10797	ACTGGCAACAAGTTCTGGATC
NM_002225	IVD	10798	ACGATGGCTGACATGTACACC
NM_002300	LDHB	10799	ACGTACAGTCCTGATTGCATC
NM_002300	LDHB	10800	ACTCTATCCAGGATTCATCCC
NM_002301	LDHC	10801	ACATCTTAGGAGAGTGCACCC
NM_017448	LDHC	10801	ACATCTTAGGAGAGTGCACCC
NM_002340	LSS	10802	ACCCTGTATGAGCACCACCAC
NM_002412	MGMT	10803	ACTGCCTATTTCCACCAGCCC
NM_002412	MGMT	10804	ACTGAGAGGCAATCCTGTCCC
NM_002541	OGDH	10805	ACCTATGTGGAGGAGATGTAC
NM_002660	PLCG1	10806	ACCAACCGGCTCTTCGTCTTC
NM_002662	PLD1	10807	ACTCGTTGGAGGTTGGACTGC
NM_002662	PLD1	10808	ACGTACCATGAAGAGTCCATC
NM_002686	PNMT	10809	ACTGCTGGCAGGATAAGGAGC
NM_002905	RDH5	10810	ACTGCCTTTGTCTTCATCACC
NM_002905	RDH5	10811	ACTGTGAACACAATGGGTCCC
NM_002905	RDH5	10812	ACCCTGATCTGTGACCCGGAC
NM_002970	SAT	10813	ACAGAAGAGGTGCTTCTGATC
NM_003001	SDHC	10814	ACTGCTGTTCTTGGGAACC
NM_003032	SIAT1	10815	ACTCCTAATTGTATGGGACCC
NM_003032	SIAT1	10816	ACGTTCTTCGATAGTGCCTGC
NM_003033	SIAT4A	10817	ACGCAGATGGTCCTGGAGCTC
NM_003033	SIAT4A	10818	ACAGGGAACCTGGCACCCTAC
NM_003034	SIAT8A	10819	ACACAAATGGAAGACTGCTGC
NM_003034	SIAT8A	10820	ACTATGCATGAGCAGCCCATC
NM_003101	SOAT1	10821	ACGAGTTCTCATCCGCTGATC
NM_003101	SOAT1	10822	ACGAATGGTATGCACGTCGGC
NM_003104	SORD	10823	ACGTGGGATCATCGGTAAAGC
NM_003104	SORD	10824	ACGGAGAGCCCTCAGGAAATC
NM_003124	SPR	10825	ACCCGTGGTTAACATCTCGTC
NM_003167	SULT2A1	10826	ACCTGGTTGGCTGAGATTCTC
NM_003167	SULT2A1	10827	ACACAGGACACAGGAAGAACC
NM_003359	UGDH	10828	ACGGACCTAAAGAACCCAGAC
NM_003359	UGDH	10829	ACGTAGCTCGTTATTGGCAGC
NM_003359	UGDH	10830	ACCTACAAACCATTTGGCTTCC

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NM_003360	UGT8	10831	ACTCATTACAGCCTCCAGCGC
NM_003360	UGT8	10832	ACCTCACTCCTCACAGACCGC
NM_003360	UGT8	10833	ACCTATGTATCATGGTGTGCC
NM_003477	PDX1	10834	ACCACATACCCGGGACACTAC
NM_003491	ARD1	10835	ACGAGGACCCAGATGATGTGC
NM_003491	ARD1	10836	ACAGGCAATTACCTCCGAGC
NM_003561	PLA2G10	10837	ACCTGTGGGTTGTGTTGGTCC
NM_003561	PLA2G10	10838	ACCTGTTGTGCAAGTGTGACC
NM_003578	SOAT2	10839	ACACACTGAGACGCACAGAGC
NM_003595	TPST2	10840	ACCAAGGACCCATTTACGCTC
NM_003595	TPST2	10841	ACGGCCATCGAGGTGATGTAC
NM_003596	TPST1	10842	ACGTGCTGGATTCTGCCATGC
NM_003596	TPST1	10843	ACGACATGGCAGTGATTGCTC
NM_003635	NDST2	10844	ACGTATGTCAACCTGGATGCC
NM_003635	NDST2	10845	ACCTTCACCTTCAACTTGGGC
NM_003706	PLA2G4C	10846	ACCCATCCAAGCAGCGAGGTC
NM_003708	RODH-4	10847	ACGTATGTGTTTCATCACGGGC
NM_003708	RODH-4	10848	ACCGTCTTCAGTGTTCATGGGC
NM_003748	ALDH4A1	10849	ACCGAGCCCGTCTTAGCCTTC
NM_003748	ALDH4A1	10850	ACCTTCACTGCAATCGGCGGC
NM_003748	ALDH4A1	10851	ACGTGTGATGACTCCGTGGGC
NM_003774	GALNT4	10852	ACCTGAAGCAGCAAGAAGAAC
NM_003778	B4GALT4	10853	ACGTGTCCAGAGGCCCGGTATC
NM_003778	B4GALT4	10854	ACCGGATGAAGCTCTTACACC
NM_003779	B4GALT3	10855	ACGCCTTCCGTCAAGAGATGC
NM_003782	B3GALT4	10856	ACCCTGAACCAGAGAAACGCC
NM_003782	B3GALT4	10857	ACATTCCTGCTGACGTCCAC
NM_003859	DPM1	10858	ACTCATAGATGATGGAAGCCC
NM_003859	DPM1	10859	ACACATGCCACAGGAACTAC
NM_003859	DPM1	10860	ACCTCAGATCTTGCTGAGACC
NM_003883	HDAC3	10861	ACGAAGTTTGAGGCCCTCTGGC
NM_003888	ALDH1A2	10862	ACACAACGAGTGCCAGAACTC
NM_003896	SIAT9	10863	ACGTCTTGCAGAAGGAATGTC
NM_003935	TOP3B	10864	ACCCAGAGACCTACTGGGTGC
NM_003935	TOP3B	10865	ACCAACATCTGCCAGCGCAAC
NM_004036	ADCY3	10866	ACCCTACCTCATCATTTGCCCTC
NM_004036	ADCY3	10867	ACCTTCATGCTGCGCATAGGC
NM_004043	ASMT	10868	ACGGAATGCATGTCTCTGTAC
NM_004044	ATIC	10869	ACACTTTGCATCCTGCAGTCC
NM_004044	ATIC	10870	ACCTTGTCGATGCTTTGAAC
NM_004051	BDH	10871	ACTGCCGGCATCTCAACGTTT
NM_004051	BDH	10872	ACCTTCATCGCTGCCACCAGC
NM_004059	CCBL1	10873	ACTGGAGAACTGGGTTCCAGC
NM_004059	CCBL1	10874	ACCCAGCAGCTACTTTGTGC
NM_004088	DNTT	10875	ACTGAGCTCAGTGATTCTGTCT
NM_004088	DNTT	10876	ACGGACACAGAAGGAATTCCTC

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NM_004088	DNTT	10877	ACGACCAAGAGGATATTCCTC
NM_004129	GUCY1B2	10878	ACTGCCACAGAGGATGAGATC
NM_004135	IDH3G	10879	ACCATCGTCAACAATGTCTGC
NM_004168	SDHA	10880	ACGAAGCCCTTTGAGGAGCAC
NM_004169	SHMT1	10881	ACGCTGATCATCGCAGGAACC
NM_004190	LIPF	10882	ACGCAGCTACACTATGTTGGC
NM_004192	ASMTL	10883	ACAGAGAAGCTGGACAAAGCC
NM_004192	ASMTL	10884	ACGAAGGCGGAAGATCTGTTC
NM_004267	CHST2	10885	ACGACACTACGGAGAGTGTAC
NM_004314	ART1	10886	ACTTCAGCCATGGGTCAGAGC
NM_004377	CPT1B	10887	ACGAAACGCCTGATCCGCATC
NM_004377	CPT1B	10888	ACTTCCAGGACAAGACTGCC
NM_004377	CPT1B	10889	ACGAATGGCCAGTTGGGTCTC
NM_004462	FDFT1	10890	ACGATGGACCAGGACTCGCTC
NM_004479	FUT7	10891	ACCTCTCAGCACCGCGACTAC
NM_004481	GALNT2	10892	ACGAAAGACCTTCATCACAGC
NM_004481	GALNT2	10893	ACGCCAAGGTCTTGACCTTCC
NM_004481	GALNT2	10894	ACATGGGAACAGATCGAGGGC
NM_004482	GALNT3	10895	ACGGAAAGATGAAACCTACCC
NM_004482	GALNT3	10896	ACAGGTCAACAAGACAGTTGTC
NM_004493	HADH2	10897	ACTAGTGGGCATGACACTGCC
NM_004550	NDUFS2	10898	ACGTTGTATACTGAGGGCTAC
NM_004581	RABGGTA	10899	ACGGAGACCCTGCAGTACTTC
NM_004605	SULT2B1	10900	ACGCCTTCGATCGTGCCTACC
NM_004618	TOP3A	10901	ACGGACATGGTCCTTAAGACC
NM_004737	LARGE	10902	ACGATGGAAAGCCCGTGTCTC
NM_133642	LARGE	10902	ACGATGGAAAGCCCGTGTCTC
NM_004737	LARGE	10903	ACGCAATACCGCATCTGTCTC
NM_133642	LARGE	10903	ACGCAATACCGCATCTGTCTC
NM_004751	GCNT3	10904	ACGAGCAATGCAGAGATGGTC
NM_004751	GCNT3	10905	ACCCATCACCTGTTGGCCAAC
NM_004753	SDR1	10906	ACGGTGGGTGACATCACCATC
NM_004753	SDR1	10907	ACAGCGTCAGCCTTCGCCTTC
NM_004753	SDR1	10908	ACGCATACTTCCACAGGCTGC
NM_004775	B4GALT6	10909	ACTGTGGGCTTCAAAGAGGCC
NM_004776	B4GALT5	10910	ACTGCAGGCTATTCTGTGAGC
NM_004784	NDST3	10911	ACGACCCTCTCTGGCAGAATC
NM_004792	PPIG	10912	ACCTCCTTCCAGATCCAGATC
NM_004792	PPIG	10913	ACGAACACCACCAGGAAGATC
NM_004808	NMT2	10914	ACACCAAATTCCGGAGGCACC
NM_004808	NMT2	10915	ACAGACTTCAGGTTTGAGACC
NM_004832	GSTTLp28	10916	ACGGGAATCAGGCATGAAGTC
NM_004832	GSTTLp28	10917	ACGCATACCCAGGGGAAGAAGC
NM_004863	SPTLC2	10918	ACTGCTGGTGTGTGTGCTCAC
NM_004881	PIG3	10919	ACTTCTGCCTCACTTCTCCAC
NM_004905	AOP2	10920	ACAGGGCATGCCTGTGACAGC

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NM_004905	AOP2	10921	ACGCTGAAGCTGTCTATCCTC
NM_004911	ERP70	10922	ACTTCCAGTCCAAGTATGAGC
NM_004911	ERP70	10923	ACGATGGACGCCACTGCCAAC
NM_004964	HDAC1	10924	ACGGCCACCCAATGAAGCCTC
NM_004964	HDAC1	10925	ACTAAGCAGCAGACGGACATC
NM_005003	NDUFAB1	10926	ACTGTCTGGCAGTGAGGACAC
NM_005006	NDUFS1	10927	ACTTGCTGGTGTGGAAGAGGC
NM_005023	PGGT1B	10928	ACAGAAGCTTGCTTAGCGGGC
NM_005038	PPID	10929	ACTGCAGGCCGCAACACAAAC
NM_005038	PPID	10930	ACGCATTGTACCGCAGAGCTC
NM_005084	PLA2G7	10931	ACTGTTCCCAAGCTCTCAGTC
NM_005084	PLA2G7	10932	ACTCTTATTCCAGGGACCAAC
NM_005276	GPD1	10933	ACGGGCCATCTGAAGGCAAAC
NM_005276	GPD1	10934	ACCCATTGGCTGCAAGGACCC
NM_005276	GPD1	10935	ACCACCAAGGCGGCAGTGATC
NM_005309	GPT	10936	ACCCCTGATCTTCTGAGCAGC
NM_005309	GPT	10937	ACGCTCACCGAGCAGGTCTTC
NM_005327	HADHSC	10938	ACTGCCACCACCAGACAAGAC
NM_005357	LIPE	10939	ACGGACAGGACAGTGAGGAGC
NM_005412	SHMT2	10940	ACGAACACCTGTCCTGGAGAC
NM_005420	STE	10941	ACTTCATGCAAGGACAGGTTC
NM_005420	STE	10942	ACAGGAAGCCATCAGAGGAGC
NM_005484	ADPRTL2	10943	ACTTCTACACCAGGATTCCGC
NM_005525	HSD11B1	10944	ACTTCAGACCAGAGATGCTCC
NM_005525	HSD11B1	10945	ACGACATGACCTTCGCAGAGC
NM_005525	HSD11B1	10946	ACTGGTTGCTGCCTATTCTGC
NM_005530	IDH3A	10947	ACCAACCACCGGAGCAACGTC
NM_005566	LDHA	10948	ACCTCCAAGCTGGTCATTATC
XM_065943	LOC130896	10948	ACCTCCAAGCTGGTCATTATC
NM_005566	LDHA	10949	ACGTGGTTGCAATCTGGATTCT
NM_005668	SIAT8D	10950	ACTTGTCTTTGAGTCGGTCAC
NM_005668	SIAT8D	10951	ACAGAGCATTGAGGCTTTTC
NM_005771	RDHL	10952	ACCCTCAGAGAGACTTCGTAC
NM_005794	DHRS2	10953	ACTGAGTCTCTCTGGAAGAAC
NM_005891	ACAT2	10954	ACTTCCCTACTCTGTTCCAGC
NM_005891	ACAT2	10955	ACGGCTCCTCACTTGGCTTAC
NM_005896	IDH1	10956	ACGAAGCATAATGTTGGCGTC
NM_005896	IDH1	10957	ACATCAGAGGGAGGCTTCATC
NM_005911	MAT2A	10958	ACCAGTCACCAGATATTGCTC
NM_005917	MDH1	10959	ACCTGCAAGACTGTGCCCTTC
NM_005918	MDH2	10960	ACTGCCACGATTGTGGCCACC
NM_005918	MDH2	10961	ACCGTCCCTGTCATTGGTGGC
NM_005956	MTHFD1	10962	ACATGTGAAGCTGAAGGCTGC
NM_005956	MTHFD1	10963	ACTTCCTCCATCATTGCAGAC
NM_005957	MTHFR	10964	ACGGTTTGACCGGATGGCAGC
NM_005957	MTHFR	10965	ACGACAACGATGCTGCCATCC

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NM_005989	AKR1D1	10966	ACGGTACAATAAGACAGCAGC
NM_006033	LIPG	10967	ACCCGTTGTAATAGCATTGGC
NM_006037	HDAC4	10968	ACGAATGGCTTTGCTGTGGTC
NM_006037	HDAC4	10969	ACAGAGACCAGATGAGGAGCC
NM_006041	HS3ST3B1	10970	ACGACGCCCAGTTACTTCGTC
NM_006042	HS3ST3A1	10970	ACGACGCCCAGTTACTTCGTC
NM_006043	HS3ST2	10971	ACGACGCCCAGCTACTTTGTGTC
NM_006066	AKR1A1	10972	ACGCAGCTGTTAAGTATGCCC
NM_006066	AKR1A1	10973	ACTGAGCTAATTGCCCCACTGC
NM_006100	ST3GALVI	10974	ACACTGCAGAGTTGTGATCTC
NM_006111	ACAA2	10975	ACCCGAAAGCATGAGCCAAGC
NM_006111	ACAA2	10976	ACTGCAGGTAGACGAGCATGC
NM_006112	PPIE	10977	ACGAGGAAGAAGGGTCAGAGC
NM_006117	PECI	10978	ACCTCTACGCGCTATATAAGC
NM_006117	PECI	10979	ACAGCTGCCAGCAAGGATGAC
NM_006117	PECI	10980	ACTGAGCCCAGCCAAGGCAAC
NM_006169	NNMT	10981	ACGTGTGATGTGACTCAGAGC
NM_006169	NNMT	10982	ACGTTATTCTTCCACCATGGC
NM_006223	PIN4	10983	ACTGCAGTAAAGGTCAGACAC
NM_006223	PIN4	10984	ACGAAGCAGCATTTGCCCTTGC
NM_006223	PIN4	10985	ACGAGAAGTCAAGCAGACTCC
NM_006226	PLCL1	10986	ACAGCCCAAGGGAGCTTGTGC
NM_006226	PLCL1	10987	ACGCAGATCCAGCTGGCATGC
NM_006278	SIAT4C	10988	ACCAAGTACGATGTGGTCATC
NM_006278	SIAT4C	10989	ACCAAGAAGCAGACCATTAC
NM_006279	SIAT6	10990	ACAGCCATCTTGTCAGTCACC
NG_001063	NG_001063	10991	ACTATATCTGCCCGCATGCGC
NM_006330	LYPLA1	10991	ACTATATCTGCCCGCATGCGC
NG_001063	NG_001063	10992	ACCTGGCAGGTGTCACTGCAC
NM_006330	LYPLA1	10992	ACCTGGCAGGTGTCACTGCAC
NM_006347	PPIH	10993	ACTGGAGATGGTACTGGAGTC
NM_006347	PPIH	10994	ACGACTGAATCAGGCCTTCCC
NM_006412	AGPAT2	10995	ACCCACCAGAGCATCCTGGAC
NM_006437	ADPRTL1	10996	ACCTATGATCCACAAGCTGGC
NM_006437	ADPRTL1	10997	ACCACTGGCAGGATGCTGTGC
NM_006456	STHM	10998	ACTGGAGCTGTGATCAAAGGC
NM_006581	FUT9	10999	ACCTGGAACCCCTGAGCATGCC
NM_006581	FUT9	11000	ACGTATCTGAAGGAAGTCGAC
NM_006636	MTHFD2	11001	ACCTGGCCCAGCAGATCAAGC
XM_093758	LOC166268	11001	ACCTGGCCCAGCAGATCAAGC
NM_006636	MTHFD2	11002	ACTATCTGCTGCAGGTATTCC
XM_093758	LOC166268	11002	ACTATCTGCTGCAGGTATTCC
NM_006774	INMT	11003	ACAGTGGCTGAAGAAGGAGCC
NM_006798	UGT2A1	11004	ACTGTGACTGTCCTAGTTGCC
NM_006798	UGT2A1	11005	ACTGATCTTCTGGACATCCC
NM_006810	PDIR	11006	ACTGTACTGGTGCTTTACTCC

NM_006810	PDIR	11007	ACGAAGGAAGAGAAGCCGCTC
NM_006810	PDIR	11008	ACGCGGATAGCTCTGGTGTCC
NM_006877	GMPR	11009	ACTGTAGCCGTGAGTTCAGGC
NM_006892	DNMT3B	11010	ACGCTGTACCCTGCCATTCCC
NM_006895	HNMT	11011	ACGACATCGAACCTCGAGAAC
NM_006895	HNMT	11012	ACGTACGGATCACGCTTTCCC
NM_006899	IDH3B	11013	ACGGAGGTGTTCAAGGCTGCC
NM_006899	IDH3B	11014	ACTCTTGAGTATCACTCCAGC
NM_006907	PYCR1	11015	ACGATGGGACTTCCAAGGCGC
NM_006927	SIAT4B	11016	ACCATGGATCTTCCACCGGAC
NM_007210	GALNT6	11017	ACGGAGAAGCTGGAGCAGTAC
NM_007210	GALNT6	11018	ACATGTCCTTCCGGGTGTGGC
NM_007255	B4GALT7	11019	ACTGGGATGTCCAACCGCTTC
NM_007255	B4GALT7	11020	ACGACATTTTCGCCACCTGCAC
NM_007255	B4GALT7	11021	ACCATCATGTTGGACTGTGAC
NM_007260	LYPLA2	11022	ACCATGAAGATGGTGATGCCC
NM_007260	LYPLA2	11023	ACGAAGGCAGCAGAGAACATC
NM_007260	LYPLA2	11024	ACTCGAATCGTCTGGGAGGC
NM_007283	MGLL	11025	ACGTGCTCAACCTTGTGCTGC
NM_007283	MGLL	11026	ACCTGCTGAATGCCGTCTCAC
NM_012079	DGAT1	11027	ACGCCCTTCAAGGACATGGAC
NM_012190	FTHFD	11028	ACCCGCAACCTGACCTTGACC
NM_144776	FTHFD	11028	ACCCGCAACCTGACCTTGACC
NM_012190	FTHFD	11029	ACGGCCCTGTATGTCAGTGAC
NM_144776	FTHFD	11029	ACGGCCCTGTATGTCAGTGAC
NM_012203	GRHPR	11030	ACCTCGCAGTCTCCCTGCTAC
NM_012203	GRHPR	11031	ACGAAGTGTGTGATTCTGCCC
NM_012320	LYPLA3	11032	ACGCCGACAGTGGTGCACCTAC
NM_012320	LYPLA3	11033	ACCTACACACTGCGGGACTAC
NM_012320	LYPLA3	11034	ACGTGTTGCTGCAGGAGCTGC
NM_012331	MSRA	11035	ACCTTTTCCCAGAGGGAACAC
NM_012331	MSRA	11036	ACGGTCTTCTGGGAGAATCAC
NM_012400	PLA2G2D	11037	ACAGATGCCACGGACTGGTGC
NM_012400	PLA2G2D	11038	ACGCGCAACCTGGACACCTAC
NM_013240	N6AMT1	11039	ACTATGCCTGGAAGTAGGGTC
NM_013240	N6AMT1	11040	ACTGGTCGGGAAGTCATGGAC
NM_013305	SIAT8E	11041	ACGAAGTGTGCTGTAGTGGGC
NM_013305	SIAT8E	11042	ACGTACGTGCTGGACGACTTC
NM_013391	DMGDH	11043	ACCATCAAAGGCCAAGATTCC
NM_013391	DMGDH	11044	ACCTAAGTGAAGTGGGACAGC
NM_013443	VI	11045	ACCAGTGCCAATGAGGTCTTC
NM_013443	VI	11046	ACTCCGCATGAATGATGCACC
NM_014234	HSD17B8	11047	ACAGTCATAGCTGTCAACCTC
NM_014234	HSD17B8	11048	ACACTATGCAGCATCCAAGGC
NM_014236	GNPAT	11049	ACATGCTACACACCTCTTGTC
NM_014236	GNPAT	11050	ACTGCTTGGTTGTAAGACACC

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NM_014256	B3GNT3	11051	ACCACCTCTATGGTCACCCAC
NM_014291	GCAT	11052	ACATAGCCCGCTTCCACCAGC
XM_090836	LOC161282	11052	ACATAGCCCGCTTCCACCAGC
NM_014291	GCAT	11053	ACTGCCATGCCACTGGCTTCC
NM_014317	TPT	11054	ACCTCCCGACATGTGCAAGCC
NM_014317	TPT	11055	ACCAAACAACCTACCTCGCCC
NM_014337	PPIL2	11056	ACGGCCAAGAACTTCCGGGAC
NM_014337	PPIL2	11057	ACGTACATCAACCCAGCAGCC
NM_014351	SULT4A1	11058	ACTGATAAGCTGGGCTACGGC
NM_014351	SULT4A1	11059	ACGGACATCTTCACCGTCTCC
NM_014384	ACAD8	11060	ACGCATCCACAACATGTGTGC
NM_014434	NR1	11061	ACGTTACCCCTGCTGTTCCTC
NM_014434	NR1	11062	ACGCCCTGATGTCCATCTTCC
NM_014465	SULT1B1	11063	ACTGTTGGAAATGACTCTCCC
NM_014465	SULT1B1	11064	ACTGCCAAGGATGTTTCAGTC
NM_014473	HSA9761	11065	ACCCTAAGAATCCACCACCAC
NM_014475	DHDH	11066	ACGGAGTTTGACAGAAACAC
NM_014475	DHDH	11067	ACGAATCTCATCCACGTTCCC
NM_014589	PLA2G2E	11068	ACGATGACAGGCAAGTCCGCC
NM_014589	PLA2G2E	11069	ACCGACTATGGCTGTTACTGC
NM_015192	PLCB1	11070	ACCACCTACCTCACAGCTGGC
NM_015715	PLA2G3	11071	ACCATCTCACCCCTTGAGTAC
NM_015715	PLA2G3	11072	ACAGCCAACACCACAGCCCTC
NM_015715	PLA2G3	11073	ACGGCACAGATGAGAGGCAGC
NM_015725	PRRDH	11074	ACCGATGTCTATGCAGCTTCC
NM_015879	SIAT8C	11075	ACAGGAGAACATCTTCACCAC
NM_015900	PS-PLA1	11076	ACGTGCGCTGACTTCCAGAGC
NM_015900	PS-PLA1	11077	ACGTTGAGCCTCGAGATCTCC
NM_015917	LOC51064	11078	ACGAACCAGCTCAAGGAGACC
NM_015922	H105E3	11079	ACGGTTAACCAGAATCAGGCC
NM_016026	ARSDR1	11080	ACCCACTTGGGTCACTTCCTC
NM_016059	PPIL1	11081	ACTTCTCGCAATGGCCAATGC
NM_016059	PPIL1	11082	ACACAACTCCCAGGACCGCC
NM_016142	HSD17B12	11083	ACGCATGGAATGAAGGTTGTC
NM_016142	HSD17B12	11084	ACTCCCGAACCAATGGATACC
NM_016229	LOC51700	11085	ACCCAGACAGAGGAGGATATC
NM_016243	LOC51706	11086	ACGCGGGTTGCTCACTTACAC
NM_016243	LOC51706	11087	ACGATCCAACCCAGTGCTTTC
NM_016245	LOC51170	11088	ACATCAGTCACCGGCGAAATC
NM_016246	LOC51171	11089	ACGACCCTGGTTTCTGAGACC
NM_016286	DCXR	11090	ACGGTGATGGCCCTAGAGCTC
NM_016341	PLCE1	11091	ACATGTGGCAGTTCATGGACC
NM_016341	PLCE1	11092	ACTGGCACTGGGATTGAGAGC
NM_016576	LOC51292	11093	ACAGTGGGAATTGGGCCAGGC
NM_016576	LOC51292	11094	ACCATACCATCCGAGACATCC
NM_016591	LOC51301	11095	ACATGTGAGACGACTCTTTC

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NM_016591	LOC51301	11096	ACGCGTGTGTATTTATGGAGC
NM_017421	COQ3	11097	ACCAATTCCTAATCACCAGCC
NM_017421	COQ3	11098	ACGGGAGAAACAGAAGAGCTC
NM_017423	GALNT7	11099	ACTGAAGGATGGTCAACCCTC
NM_018137	PRMT6	11100	ACGCAGCACTATGGTGTGGAC
NM_018396	METL	11101	ACGAGAAGAGTTACCCAGTGC
NM_018396	METL	11102	ACGTTCAGAACCTGGTGGACC
NM_018441	HSA250303	11103	ACGCAGGCACGAGTCATTCCC
NM_018441	HSA250303	11104	ACTGGGCCTGCAGTGAATAC
NM_018446	AD-017	11105	ACGTCTTGGAAGATAGCATGC
NM_018486	HDAC8	11106	ACGAGGGCGATGATGATCATC
NM_018486	HDAC8	11107	ACGTCTATGACCGTGTCCCTGC
NM_018486	HDAC8	11108	ACCACTATCCTCTGAGATCCC
NM_018960	GNMT	11109	ACGTGGGTCTATCGAAGAAGCC
NM_018960	GNMT	11110	ACGAGTGACTTGACCAAGGAC
NM_019854	HRMT1L3	11111	ACATGCTGAAGGATGAGGTGC
NM_019854	HRMT1L3	11112	ACTGTGCGAGACCTCGATTTC
NM_020121	UGCGL2	11113	ACGCTGCTGCCAGAATTGTCC
NM_020121	UGCGL2	11114	ACAGCATGACAGGAAACCTGC
NM_020132	LPAAT-gamma1	11115	ACCCACAACCTTCGAGATCGAC
NM_020139	LOC56898	11116	ACCTCGTGTCTTGTATGTCAC
NM_020139	LOC56898	11117	ACTACAAGCCAGAGGAAATCC
NM_020139	LOC56898	11118	ACAGACGGGAAGATTCGCAAC
NM_020156	C1GALT1	11119	ACAGGCCAAACACGTCAAAGC
NM_020156	C1GALT1	11120	ACGCCTTATGTAAAGCAGGGC
NM_020244	CHPT1	11121	ACTGTGGGACTATACGATTCC
NM_020299	AKR1B10	11122	ACAGAAGCAGTGAAGGTGGCC
NM_020299	AKR1B10	11123	ACGCTGAGCTATCTGGACGTC
XM_069833	LOC136330	11123	ACGCTGAGCTATCTGGACGTC
NM_020474	GALNT1	11124	ACAGGAGAGAGGACTTCCTGC
NM_020474	GALNT1	11125	ACAGGCCAAGTGATCACCTTC
NM_020664	DECR2	11126	ACGGAGTTTGGCAGAATCGAC
NM_020664	DECR2	11127	ACCAAGACCGAGATCGCCAC
NM_020664	DECR2	11128	ACACGGTGTCAAAGGGCTGCC
NM_020981	B3GALT1	11129	ACGATAGCCACCCTGTTCTCTC
ENSG00000169066	ENSG00000169066	11130	ACTGCTGCTGTCAACCCTTTC
NM_021004	humNRDR	11130	ACTGCTGCTGTCAACCCTTTC
ENSG00000169066	ENSG00000169066	11131	ACAGCATGAAAGAAACCCTGC
NM_021004	humNRDR	11131	ACAGCATGAAAGAAACCCTGC
NM_021071	ART4	11132	ACAGCTTCCAGCAAGAAATGC
NG_001161	NG_001161	11133	ACAGGCAGAATGGGTGGTTGC
NM_021074	NDUFV2	11133	ACAGGCAGAATGGGTGGTTGC
NG_001161	NG_001161	11134	ACGTATCACATTTCAGGTCTGC
NM_021074	NDUFV2	11134	ACGTATCACATTTCAGGTCTGC
NM_021079	NMT1	11135	ACGCTACCAGTTCTGGGATAC
NG_000914	NG_000914	11136	ACGACCAGCAAGAAGATCACC

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NG_001014	NG_001014	11136	ACGACCAGCAAGAAGATCACC
NG_001048	NG_001048	11136	ACGACCAGCAAGAAGATCACC
NM_021130	PPIA	11136	ACGACCAGCAAGAAGATCACC
XM_060625	LOC127711	11136	ACGACCAGCAAGAAGATCACC
XM_064968	LOC126170	11136	ACGACCAGCAAGAAGATCACC
XM_066074	LOC128430	11136	ACGACCAGCAAGAAGATCACC
XM_067531	LOC131748	11136	ACGACCAGCAAGAAGATCACC
XM_070771	LOC138130	11136	ACGACCAGCAAGAAGATCACC
XM_071167	LOC138924	11136	ACGACCAGCAAGAAGATCACC
XM_089309	LOC164022	11136	ACGACCAGCAAGAAGATCACC
XM_116396	LOC202227	11136	ACGACCAGCAAGAAGATCACC
XM_172314	LOC257232	11136	ACGACCAGCAAGAAGATCACC
NG_000914	NG_000914	11137	ACGAAGATCACCATTGCTGAC
NG_001014	NG_001014	11137	ACGAAGATCACCATTGCTGAC
NG_001048	NG_001048	11137	ACGAAGATCACCATTGCTGAC
NM_021130	PPIA	11137	ACGAAGATCACCATTGCTGAC
XM_060625	LOC127711	11137	ACGAAGATCACCATTGCTGAC
XM_064968	LOC126170	11137	ACGAAGATCACCATTGCTGAC
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XM_070771	LOC138130	11137	ACGAAGATCACCATTGCTGAC
XM_071167	LOC138924	11137	ACGAAGATCACCATTGCTGAC
XM_089309	LOC164022	11137	ACGAAGATCACCATTGCTGAC
XM_091100	LOC161751	11137	ACGAAGATCACCATTGCTGAC
XM_092514	LOC165317	11137	ACGAAGATCACCATTGCTGAC
XM_172314	LOC257232	11137	ACGAAGATCACCATTGCTGAC
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NM_021139	UGT2B4	11139	ACTCCCTATGGTGGGCGTTCC
NM_021199	SQRDL	11140	ACGCGATCCAAGGCCAATATC
NM_021232	PRODH2	11141	ACTGCTGAGCAGAACCAGCAC
NM_021232	PRODH2	11142	ACGTCCATTCCCTATGGCTCC
NM_021808	GALNT9	11143	ACGTATGAGGAGTACGGCTAC
NM_021808	GALNT9	11144	ACGTCCACGTGTACATGGCC
NM_021808	GALNT9	11145	ACGATGCCAACTTTGGGCTCC
NG_001331	NG_001331	11146	ACCGTGGTCTTCAGGAGAAGC
NM_022120	OXCT2	11146	ACCGTGGTCTTCAGGAGAAGC
NG_001331	NG_001331	11147	ACTGCAGGCAAGCAGACGGTC
NM_022120	OXCT2	11147	ACTGCAGGCAAGCAGACGGTC
NM_022167	XT2	11148	ACCCGGGACAAGAATTTCTC
NM_022819	PLA2G2F	11149	ACGAACATGGTTCTGTGCC
NM_024827	HDAC11	11150	ACGCTGCATCCCTTTGATGCC
NM_025193	C(27)-3BETA-HSD	11151	ACCACGGTTCCTGGTCTACAC
NM_025193	C(27)-3BETA-HSD	11152	ACCACCACCTTCACCGTCAGC
NM_030821	PLA2G12	11153	ACTGCAGTGACGGATCTAAGC
NM_030821	PLA2G12	11154	ACGTGTTGCAACCAACACGAC
NM_030965	MGC3184	11155	ACTGCACTGCAGGGACTGTGC
NM_030965	MGC3184	11156	ACGCAGGAGACTGGCAAAGAC

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NM_030965	MGC3184	11157	ACGAACTGGGCACGGACATTC
NM_031279	AGXT2L1	11158	ACTGTGCACGGATACACATTC
NM_031302	LOC83468	11159	ACTGACGCAGATGATGAATCC
NM_031463	LOC83693	11160	ACGCAGTATGGAAGATGGGCC
NM_031900	AGXT2	11161	ACCAGTCAAGAAGTTGGGACC
NM_032019	HDAC10	11162	ACCGGGTTCTGTGTGTTCAAC
NM_032019	HDAC10	11163	ACTGGCGCCATGTCAGAGTGC
NM_032019	HDAC10	11164	ACTGGAGAGGCACCTCCTAGC
NM_032047	B3GNT5	11165	ACTCTCCGGTGATGTAGCTGC
NM_032664	FUT10	11166	ACCTGGCAAGTTACATCAGAC
NM_006411	AGPAT1	11167	ACCGTCGAGAACATGAAGATC
NM_032741	AGPAT1	11167	ACCGTCGAGAACATGAAGATC
NM_003781	B3GALT3	11168	ACGGTGTTCCCTCCATACTGC
NM_033167	B3GALT3	11168	ACGGTGTTCCCTCCATACTGC
NM_033168	B3GALT3	11168	ACGGTGTTCCCTCCATACTGC
NM_033169	B3GALT3	11168	ACGGTGTTCCCTCCATACTGC
NM_033195	LDHL	11169	ACACGCGCCTTAATTTAGTCC
NM_033195	LDHL	11170	ACGCGGCTGTAATCTGGATAC
NM_033195	LDHL	11171	ACAGGTTATACTTCTTGGGCC
NM_006577	B3GNT1	11172	ACGCTGAACCGGCAGTACAAC
NM_033252	B3GNT1	11172	ACGCTGAACCGGCAGTACAAC
NM_006577	B3GNT1	11173	ACGGCAAGCAATCCGGGAATC
NM_033252	B3GNT1	11173	ACGGCAAGCAATCCGGGAATC
NM_052968	APOA5	11174	ACAGGCAGGGTGGAGCAGATC
NM_052968	APOA5	11175	ACGACACCAAGGCCAGTTGC
NM_053017	ART5	11176	ACAGCCCAGAATGGAATAGCC
NM_080605	B3GALT6	11177	ACCTCTGCGACTACTACCTGC
NM_080605	B3GALT6	11178	ACCCAGTACCTGGTGACGCAC
NM_133373	LOC113026	11179	ACTGGGCAGTGTGGCTACGTC
NM_133491	SSAT2	11180	ACGTTGGCAGGAAAGTGACGC
NM_138706	IMAGE:4907098	11181	ACGCACCTGCACTTGCTCGAC
NM_138969	RDH-E2	11182	ACAGCCACGGAAGAACGTTGC
NM_138969	RDH-E2	11183	ACTGCCGGAATCGTAACAGGC
NM_139126	PPIL4	11184	ACCTGGCGATCCTACAGGGAC
NM_139126	PPIL4	11185	ACGAAGATGAGGACTACATGC
NM_000348	SRD5A2	11186	ACCATACAGAGCCCACATTTTC
XM_002471	SRD5A2	11186	ACCATACAGAGCCCACATTTTC
XM_036383	ADCY2	11187	ACAGAAAGTGAGGGATGCTAC
XM_036392	PRMT3	11188	ACGGACATCCATGTGCACGGC
XM_036392	PRMT3	11189	ACGAATTGCCACAACAGGGTC
XM_036392	PRMT3	11190	ACAGGAAAGGTCACAGTTTAC
XM_042836	PLCL2	11191	ACTTCCTTGATACCAAGGACC
XM_042836	PLCL2	11192	ACATGCTGATGTCCAGAAGCC
XM_050509	GALNT5	11193	ACAGTTCGGATTCTTCGCCTC
XM_051264	TR2	11194	ACTTGATGCATCAGGCTGCCC
XM_051264	TR2	11195	ACACAGCTACTTGATGACACC

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XM_051896	PLA2G4A	11196	ACGCTCTGGACAACCTGTCAC
XM_055342	LOC115154	11197	ACAGAAGATTGCCAACGGCAC
XM_055342	LOC115154	11198	ACAGAGGCCTTGAAATGTCAC
XM_056254	HS3ST4	11199	ACACTGGCTCCAGTATTCC
XM_058404	LOC119548	11200	ACGGTTGCCCAACAATGGGTC
XM_058404	LOC119548	11201	ACGCGAAGTCACTCAAGGAAC
XM_058856	LOC124872	11202	ACCCTGGCCATATCTCAGGTC
XM_058856	LOC124872	11203	ACTACATACCGGTCCAACACC
XM_058991	LOC126133	11204	ACCCTTGGTCTCCAACCTGCC
XM_058991	LOC126133	11205	ACCTATGACACCTTTGGCCTC
XM_058991	LOC126133	11206	ACACCTCAAACCGGTGTGGGC
XM_058992	LOC126129	11207	ACAGACTACATCCGCCACCTC
XM_058992	LOC126129	11208	ACGGCCTCAATGACATCCACC
XM_059366	LOC129644	11209	ACGGAAACAGTTTGGACATCC
XM_059366	LOC129644	11210	ACGATGAGAATCCCAAGCAGC
XM_059665	LOC133688	11211	ACCAGCGTAATGGAGGCCATC
XM_059933	LOC137964	11212	ACGCCCTACACCAACGGAATC
XM_059933	LOC137964	11213	ACCTGTGGTGGGATACTTGCC
XM_059933	LOC137964	11214	ACGCTGCCTATCCTCATCTTC
XM_090901	LOC145538	11214	ACGCTGCCTATCCTCATCTTC
XM_171187	LOC253897	11214	ACGCTGCCTATCCTCATCTTC
XM_060166	LOC126766	11215	ACCTATCTGGCCATTGACCTC
NM_016022	APH-1A	11216	ACGAAGGCAGATGAGGGGTTA
NM_016022	APH-1A	11217	ACGATCACCCATCTCCATCCG
XM_060331	LOC127107	11218	ACACTGCAGCAGGAAGATGGC
NM_031301	DKFZP564D0372	11219	ACTACCCTATCTGACTCCTTG
NM_031301	DKFZP564D0372	11220	ACCAAAGATGGACCAACACAG
NM_015331	NCSTN	11221	ACGGGCAAGTTTCCCGTGCAG
NM_172341	PEN-2	11222	ACAGGCTATGTCTGGCGCTCA
XM_060822	LOC128096	11223	ACGCTGAGCATTCCCGACTGC
NM_172341	PEN-2	11224	ACATCAAAGGCTATGTCTGGC
XM_060828	LOC128103	11225	ACCAGTGTTTCTGTACCACC
XM_060828	LOC128103	11226	ACACTGTGGCATGACAGCTGC
NM_001168	BIRC5	11227	ACAGCATTCGTCCGGTTGCGC
NM_001168	BIRC5	11228	ACACTGGACAGAGAAAGAGCC
NM_001168	BIRC5	11229	ACACTGCGAAGAAAGTGCGCC
NM_001168	BIRC5	11230	ACGTGGCACCAGAGGTGCTTC
NM_000888	ITGB6	11231	ACGACTGCCTGCTTATTGGAC
NM_000888	ITGB6	11232	ACCTAGCAGGCATCGTCATTC
NM_000888	ITGB6	11233	ACCTGCGGTCTGAGGTGGAAC
XM_060863	LOC128183	11234	ACGGCTGGTATACAGGAACAC
XM_060863	LOC128183	11235	ACAGAAAGGGCAGCCTGAAGC
XM_060871	LOC128189	11236	ACTAGGAGGGCTATTCAAGAC
XM_061222	LOC118934	11237	ACCCTGGAGCTGATGAATGTC
XM_061440	LOC119376	11238	ACAGTGGATACTGTCACCATC
XM_061440	LOC119376	11239	ACGCTTAAGACCCTGGATGGC

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XM_061440	LOC119376	11240	ACGGTGGTTGTCTCCTCTGAC
XM_062367	LOC120943	11241	ACCGGAAAGCCTTGGACCGTC
XM_062519	LOC121214	11242	ACGTGACCCTTCACATGCTGC
XM_062519	LOC121214	11243	ACCTATCGGACAGCCATTCTC
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NG_001025	NG_001025	11244	ACGCATACAGGTCCTGGCATC
XM_060398	LOC127257	11244	ACGCATACAGGTCCTGGCATC
XM_062758	LOC121734	11244	ACGCATACAGGTCCTGGCATC
XM_066074	LOC128430	11244	ACGCATACAGGTCCTGGCATC
XM_066617	LOC139318	11244	ACGCATACAGGTCCTGGCATC
XM_068341	LOC133419	11244	ACGCATACAGGTCCTGGCATC
XM_071167	LOC138924	11244	ACGCATACAGGTCCTGGCATC
XM_116396	LOC202227	11244	ACGCATACAGGTCCTGGCATC
XM_171632	LOC253521	11244	ACGCATACAGGTCCTGGCATC
XM_171826	LOC253104	11244	ACGCATACAGGTCCTGGCATC
XM_172314	LOC257232	11244	ACGCATACAGGTCCTGGCATC
XM_062758	LOC121734	11245	ACTGGTTCCAGTTTGTCTATC
XM_062786	LOC121789	11246	ACACCCTGAAGAAGCAGCTCC
XM_062786	LOC121789	11247	ACTGACCTGAAGGAGATGCTC
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XM_062787	LOC121790	11249	ACGGTCTTCAGTGCCACCCCTC
XM_062787	LOC121790	11250	ACGCCGACAGTAAATCCTGGC
XM_062787	LOC121790	11251	ACCTGACATTAAAGGAAGACCC
XM_062862	LOC121927	11252	ACAGGGTCATCATCACTGCCC
XM_063084	LOC122335	11253	ACCAGCACTGGTGGCAAGTCC
XM_063084	LOC122335	11254	ACGAAGATCGCTGTTGCTGAC
XM_063325	LOC122842	11255	ACCAGCCTCCAATTGAAAGGC
XM_063325	LOC122842	11256	ACGGAGGAGTTCTATTCAAGC
XM_063325	LOC122842	11257	ACGAAGATCGCCATTGCTAAC
XM_063491	LOC123137	11258	ACTTTGCCTGAGCTCTCTAGC
XM_063491	LOC123137	11259	ACGCAGGCTTGGAGATAGTTC
XM_063491	LOC123137	11260	ACGAGTACTGGAGTACTCTGC
XM_063593	LOC123326	11261	ACGAACAGGTAGAAGTGGGCC
XM_063593	LOC123326	11262	ACGGAAGTGGAGCATTACCCC
XM_063826	LOC123745	11263	ACCCTGCTGGATGCCTGGAAC
XM_063826	LOC123745	11264	ACGGTAACCCTACCTGGCTAC
XM_064449	LOC125110	11265	ACACTTTGGTGCTCTGAGCAC
XM_068341	LOC133419	11265	ACACTTTGGTGCTCTGAGCAC
XM_062890	LOC121981	11266	ACTGGCAAGACCAGCAAGATC
XM_064449	LOC125110	11266	ACTGGCAAGACCAGCAAGATC
NM_002631	PGD	11267	ACTATAGGGACACCACAAGAC
XM_064597	LOC125399	11267	ACTATAGGGACACCACAAGAC
XM_064597	LOC125399	11268	ACGTTCCAAGGTGCTGATGGC
XM_064597	LOC125399	11269	ACCCAGAACCTCAGAACCTC
XM_064826	LOC125850	11270	ACAGGGTCATCACCTCTGCCC
XM_064826	LOC125850	11271	ACTCGTGGAAGGACTCATGGC

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XM_064826	LOC125850	11272	ACGGCTGTAGGCAAAGTCATC
XM_065242	LOC129440	11273	ACCAGAGACTACCCCTCTGGCC
XM_067688	LOC131961	11273	ACCAGAGACTACCCCTCTGGCC
XM_065242	LOC129440	11274	ACCTCGGTGTATCAGATTGCC
XM_065721	LOC130422	11275	ACTGCACATTGAGAGGCCACC
XM_065721	LOC130422	11276	ACTAGGCATTGAGAGGGCTCC
XM_065721	LOC130422	11277	ACCAGGGAACCACTTTGCTGC
XM_065756	LOC130516	11278	ACCCCAATGACCAACTATACC
XM_065756	LOC130516	11279	ACGAAGATGGCAGGAAGCACC
XM_065757	LOC130517	11280	ACCTTACCCAAAGTCAGGTAC
XM_065757	LOC130517	11281	ACGGATTGCCTGGTGTCTTAC
XM_065757	LOC130517	11282	ACCAAGATTGTCCACCATACC
XM_065789	LOC130585	11283	ACCGGAAATCTCATCACCATC
XM_065789	LOC130585	11284	ACGCTGTAGGCAAGGTCATCC
XM_065943	LOC130896	11285	ACGGCTTTCTCTCCAGGAGC
XM_065961	LOC130946	11286	ACCATGTGGACAAACATGAGC
XM_065961	LOC130946	11287	ACCAAGTTCACGGATATGTCC
XM_066634	LOC139334	11288	ACGCTGGTGGGTATCATCGCC
XM_066634	LOC139334	11289	ACATTCTGCCTGGACCTGCTC
XM_066753	LOC139543	11290	ACTGGCAACTCCAAGCAGATC
XM_066916	LOC139835	11291	ACTGAACTGCAAGACTGTGC
XM_066916	LOC139835	11292	ACGACTTGGATGTGGCCATTC
NG_001025	NG_001025	11293	ACGCATGAATATTGTGGAGGC
NM_021130	PPIA	11293	ACGCATGAATATTGTGGAGGC
XM_060398	LOC127257	11293	ACGCATGAATATTGTGGAGGC
XM_062758	LOC121734	11293	ACGCATGAATATTGTGGAGGC
XM_063182	LOC122552	11293	ACGCATGAATATTGTGGAGGC
XM_064968	LOC126170	11293	ACGCATGAATATTGTGGAGGC
XM_065541	LOC130040	11293	ACGCATGAATATTGTGGAGGC
XM_067531	LOC131748	11293	ACGCATGAATATTGTGGAGGC
XM_067765	LOC132281	11293	ACGCATGAATATTGTGGAGGC
XM_091100	LOC161751	11293	ACGCATGAATATTGTGGAGGC
XM_172784	LOC253265	11293	ACGCATGAATATTGTGGAGGC
XM_067584	LOC131872	11294	ACGACAACCTTCTTTGGTGGC
XM_067680	LOC131998	11295	ACAGAACCTGTGTGAGGAGAC
XM_067680	LOC131998	11296	ACAGTACCTGGAGGAACCTCC
XM_067680	LOC131998	11297	ACGTTGGATGCAGGACCATGC
XM_067765	LOC132281	11298	ACTATGTAGTGCTCTGAGCAC
XM_068039	LOC132795	11299	ACCATCACAGAAGAAAGGGCC
XM_068039	LOC132795	11300	ACGTGGATATCCAGAAATGAC
XM_068039	LOC132795	11301	ACGGCCCTCAATGTGGACATC
XM_068041	LOC132797	11302	ACTGGCATCTACGAGGTGACC
XM_068041	LOC132797	11303	ACCATTTCTCACATGAAGGCC
XM_068041	LOC132797	11304	ACACACCTTCAGGTTGCAGCC
XM_068075	LOC132869	11305	ACTCAGGTGCTCAATGGGATC
XM_068075	LOC132869	11306	ACACCAACAGCTCATGATCCC

XM_068131	LOC132990	11307	ACTGACCGCTTCATTGACCTC
XM_068188	LOC133105	11308	ACGTACCAGATATGGAAAGGC
XM_068188	LOC133105	11309	ACTCATCGGCCCATAACCAAC
XM_068188	LOC133105	11310	ACTCCATGGGCAAGGTGCTTC
XM_068341	LOC133419	11311	ACTGCTGGACCTGGCACAAAC
XM_068376	LOC133486	11312	ACTGGGTACATTGCGGAGTCC
XM_068588	LOC133883	11313	ACGGGATGCAAGGTCAGATAC
XM_068588	LOC133883	11314	ACACTCCTGCAAGTCTCTGCC
XM_068609	LOC133937	11315	ACTATCGTCAGCTATGCCTCC
XM_068609	LOC133937	11316	ACGAAGCTCACTGACATGGGC
XM_068926	LOC134602	11317	ACATCATCGCGTTTCAGCGACC
XM_069334	LOC135399	11318	ACGTGGTGTTGGATTTCATGGC
XM_069334	LOC135399	11319	ACGAGTCTCCATGCTGAGTTC
XM_069825	LOC136307	11320	ACAGGGTCCATTTCAGAAGTTC
XM_089729	LOC159648	11320	ACAGGGTCCATTTCAGAAGTTC
XM_095828	LOC169633	11320	ACAGGGTCCATTTCAGAAGTTC
XM_070277	LOC137202	11321	ACCCTTCTGGACACCTCCTTC
XM_070277	LOC137202	11322	ACGTTGCTCTGTGCCTGTGAC
XM_070717	LOC138031	11323	ACCCAGGAGTAGGAGGCAATC
XM_070717	LOC138031	11324	ACTATAGCGCTGACATGGTTC
XM_070771	LOC138130	11325	ACCTGCCATCTTCATGCCCTC
XM_085058	LOC145226	11326	ACGCAGCTCCATATTCTGATC
XM_085674	LOC147011	11327	ACGGAGCCTGACAAGTGCTGC
XM_085674	LOC147011	11328	ACAGCCCGGTTAAATTGGAGC
XM_085674	LOC147011	11329	ACGACAGCTGGCCAGGATGTC
XM_087088	LOC151056	11330	ACTATGCTGGAGCCTGTTGGC
XM_087136	LOC151234	11331	ACAGCAGGCGCGCTTCCATTC
XM_088569	LTB4DH	11332	ACAGCTGCTGACAGAGTGGCC
XM_088569	LTB4DH	11333	ACCCTTGAAGAAAGCGTCTCC
XM_088569	LTB4DH	11334	ACGGATTGCCATATGTGGAGC
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XM_089555	LOC159373	11336	ACCTGGATTTCCAACCTGCCC
XM_089729	LOC159648	11337	ACTGAGATCCTGCAGCGTAAC
XM_089729	LOC159648	11338	ACGAAGTACCAGGGCATGGGC
XM_090320	LOC160469	11339	ACGTTTGCTGACAGTGACCAC
XM_090836	LOC161282	11340	ACCTTAACCTCGGTCCGCTTC
XM_090836	LOC161282	11341	ACCTGTGCCTCCATCATCCAC
XM_090901	LOC145538	11342	ACGCATGAGTTGAGCAGCTTC
XM_091291	LOC162024	11343	ACCCCTGGATGGGCAGATCAC
XM_091291	LOC162024	11344	ACGCACTTCTACTTCAACGCC
XM_091633	LOC147116	11345	ACCACCCTCATAACCCTAAAC
XM_092514	LOC165317	11346	ACGCATACAGGCCCTGGCATC
XM_093062	LOC170027	11347	ACCTGGGAACAGCCAACAACC
XM_093615	LOC166039	11348	ACTACAGCATGTGGTCTTGGC
XM_093615	LOC166039	11349	ACGACCAGCAAGAATATCACC
XM_093758	LOC166268	11350	ACGCGAAGTGACATTCCAACC

XM_093980	LOC166624	11351	ACTGGCACCTATGAGAGGATC
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XM_094098	LOC166794	11353	ACGGTTGGACTTCACTCCTGC
XM_094098	LOC166794	11354	ACGAGGGCCTAATGGCATGAC
XM_094300	LOC167127	11355	ACACATGGTCCGAGTAGAAGC
XM_095705	LOC169445	11356	ACGAAGTACCCATGATGGTGC
XM_095705	LOC169445	11357	ACACTTCTGACGTACCTTGAC
XM_095828	LOC169633	11358	ACGTGATGGCTTGTGGTCAGC
XM_095861	LOC169681	11359	ACTAACTTCCGCCCACCTCCC
XM_095884	LOC158284	11360	ACCTGCCCAGTGGTGCTTACC
XM_095921	LOC169760	11361	ACAGTCATCAAGACAGAGGGC
XM_108641	LOC169330	11362	ACCATGGCTTCATCACGGACC
XM_108641	LOC169330	11363	ACGCTGCCTATCGTCAATGAC
XM_108641	LOC169330	11364	ACCCTGATTGATGCTGGGCAC
XM_114786	LOC199971	11365	ACCTCAGTGGCATGGCATTCC
XM_114786	LOC199971	11366	ACGCCAGTGAGTCCATCCTAC
XM_114787	LOC199972	11367	ACTGAGATCCATGGGCTGAAC
XM_114787	LOC199972	11368	ACGCAGACATCAGAGGATCCC
XM_115401	LOC204474	11369	ACAGTGCAAGATGCTGTTCCC
XM_115847	LOC205089	11370	ACCCTGCCATGCCACATCCTC
XM_115847	LOC205089	11371	ACTGCCGTCTTTCAGCTGGAC
XM_115847	LOC205089	11372	ACGTGAGTGGCAAGGTTCTGC
XM_115853	LOC205093	11373	ACGGACCTCCGTAATATGGCC
XM_115853	LOC205093	11374	ACGGTGCTGGTGATCAGCCTC
XM_116186	LOC205858	11375	ACCTCACTGGGCATTCTCTTC
XM_116186	LOC205858	11376	ACACTGGCACCGGAATTTGCC
XM_116186	LOC205858	11377	ACGAAGCCGAAGCTGTCTATC
XM_116260	LOC205983	11378	ACCGACAGAGCATATTGGTTC
XM_116285	LOC206030	11379	ACGGAACGAGAATGGAAGAGC
XM_116285	LOC206030	11380	ACCTTTGTCAACAGGCTGTGC
XM_116493	LOC202432	11381	ACTGACCCATTTCATTGACCTC
XM_116529	LOC206469	11382	ACTGACCTCTTCATTGACCTC
XM_116529	LOC206469	11383	ACCAGTGACATCGACCTTCC
XM_166248	LOC220027	11384	ACTACCAGGAGGCTGGCATT
XM_166504	LOC221893	11385	ACGATGAATTTGCTGCTGCCC
XM_166504	LOC221893	11386	ACTCCTTCTTGGCAGTCTGGC
XM_166593	ADCY1	11387	ACTGTCATGGAAGCCGCTGGC
XM_166652	LOC220201	11388	ACAGAAGTGGTGAAGGTGGCC
XM_166652	LOC220201	11389	ACGCGGGAGGACCTCTTCATC
XM_166652	LOC220201	11390	ACGGGCATCACCATTATGGCC
XM_166722	LOC222360	11391	ACGGACCCAACATTGTAGGTC
XM_166722	LOC222360	11392	ACACCTGACCCTTTCTATCGC
XM_167023	LOC221270	11393	ACGATACCCAGAGCAAGGCC
XM_167035	LOC222537	11394	ACGGACTGAAGTAGGTTCTC
XM_167035	LOC222537	11395	ACCCTACATCCGGCAGTAGTC
XM_167035	LOC222537	11396	ACCCTCTGCCAGAACTTCAGC

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XM_167096	LOC222591	11397	ACTGGATGGAATGGTGCTGAC
XM_167096	LOC222591	11398	ACGTCAGAGGCAACCACTATC
XM_167096	LOC222591	11399	ACTTCAGCTGGGCAGACATAC
XM_167098	LOC221355	11400	ACGCTGGTTTCAGACCAGAGCC
XM_167098	LOC221355	11401	ACCTACGTTGCCAGCAAATAC
XM_167098	LOC221355	11402	ACGACATAAAGGAGAGAGTCC
XM_167104	LOC222593	11403	ACACCAGAATCAGCAACCTCC
XM_167104	LOC222593	11404	ACGCTCTTGATAGGACTCTCC
XM_167105	LOC222594	11405	ACCCTGGAAGCCAAAGGAAGC
XM_167188	LOC221654	11406	ACGGATCACAACACCCTCCTC
XM_167201	LOC222789	11407	ACTATCAAGCCCTTTCCCGAC
XM_167308	LOC222980	11408	ACCTGTTGATCCTACAGGGAC
XM_167308	LOC222980	11409	ACCGTCCCAAGAATTAAGCAC
XM_167308	LOC222980	11410	ACAGAGTGGTAGAGTTGACAC
XM_168454	POR	11411	ACTTCAGACATTGACCTCCTC
XM_169007	ST8SIA-VI	11412	ACAGCCCTATTTCTGGAGGAC
XM_169007	ST8SIA-VI	11413	ACAGGTGTGACTGCATACCGC
XM_171048	LOC255218	11414	ACCATCGTGGGTGTCTGCACC
XM_171048	LOC255218	11415	ACGCAGACATCAACGCCAAGC
XM_171276	LOC254817	11416	ACTGATGCCTTCAATGACCTC
XM_171289	LOC254592	11417	ACAGTCATCCCTCAGCTGAAC
XM_171347	LOC254558	11418	ACGCCTACAGGTCCTGGCATC
XM_171347	LOC254558	11419	ACGACTGAGTGGCTGGATGGC
XM_171347	LOC254558	11420	ACGGAGGTCACTATTGCTGAC
XM_171406	LOC254142	11421	ACATGTGTTGTGGAGTCCGCC
XM_171406	LOC254142	11422	ACTGAGGGCAATGACATTGCC
XM_171437	LOC253659	11423	ACGGATCATAATCTCTGCTCC
XM_171437	LOC253659	11424	ACCTGCTTAGCACCTCTGGCC
XM_171635	LOC254885	11425	ACTGGATTTGGCCATAAGGGC
XM_171659	LOC256896	11426	ACGGAGCCTGTGAGAAGATGC
XM_171659	LOC256896	11427	ACGGGCTGCTACAACAAGAAC
NM_001618	ADPRT	11428	ACGTTACCCAAGGGCAAGCAC
XM_062787	LOC121790	11428	ACGTTACCCAAGGGCAAGCAC
XM_171663	LOC254927	11428	ACGTTACCCAAGGGCAAGCAC
XM_172177	LOC255139	11429	ACGCTCAAGGATTCTTCTGTC
XM_172177	LOC255139	11430	ACGCAGCAAGGATATGACCAC
XM_172181	LOC255782	11431	ACACACTGACACCACCAAGGC
XM_172235	LOC255412	11432	ACAGGCCCTGGATTCTTCTAC
XM_172235	LOC255412	11433	ACGGCTGTAGGCAAGGTCATC
XM_172242	LOC254652	11434	ACCTCCTCTCACAATATGGGC
XM_172242	LOC254652	11435	ACCGGCACCTATGAGAGGATC
XM_172244	LOC253533	11436	ACCAGATAGCCACATCTTCTC
XM_172244	LOC253533	11437	ACCGATAGTGACAGTGAAGGC
XM_172281	LOC257047	11438	ACAGCCAGCAAAGGCAATTGC
XM_172281	LOC257047	11439	ACCATCAGCCATCGTCAACCC
XM_172308	LOC257210	11440	ACGTATACAGGTTCTGGCATC

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XM_172308	LOC257210	11441	ACGACTGAGTGGTTGGTAGGC
XM_172308	LOC257210	11442	ACGGTGGAAGCCATGGAATGC
XM_172380	LOC254420	11443	ACGAGGATGAACAAGGCACCC
XM_172516	LOC255961	11444	ACCAAGGGTGCTGGAAAGGCC
XM_172516	LOC255961	11445	ACCCATACCTAGCATTCCTAC
XM_172573	LOC254613	11446	ACTCATCAAATGGCAGGGTGC
XM_172573	LOC254613	11447	ACTATCAACTGCCTGACTGCC
XM_172573	LOC254613	11448	ACACTTGGTGTGACTGCTGAC
XM_172596	LOC256726	11449	ACTTCGCTGTGGCCCTTATCC
XM_172597	LOC256727	11450	ACGCACACCTAGCATTCCTAC
XM_172777	LOC253554	11451	ACATGATGATTGTGCTTGCCC
NM_000043	TNFRSF6	11452	ACGGCCTGCATCATGATGGCC
NM_000043	TNFRSF6	11453	ACCTGCTTCGTAATTGGCATC
NM_000074	TNFSF5	11454	ACCGATACAGAGATGCAACAC
NM_000074	TNFSF5	11455	ACCATCTGTGTTACAGTGGGC
NM_000074	TNFSF5	11456	ACGCTCCATTTATAGCCAGCC
NM_000210	ITGA6	11457	ACGGTCGTGACATGTGCTCAC
NM_000213	ITGB4	11458	ACCCTGATGGCCTCTGACCAC
NM_000213	ITGB4	11459	ACCCTGTACCCGTATTGCGAC
NM_000230	LEP	11460	ACCCTCCGGGATCTTCTTCAC
NM_000315	PTH	11461	ACGAAGCTGCAGGATGTGCAC
NM_000419	ITGA2B	11462	ACCACCCTGAGCCGCATTTAC
NM_000419	ITGA2B	11463	ACGAACAGCCAGAATCCAAAC
NM_000419	ITGA2B	11464	ACGCTCAGGTGTGGACACAGC
NM_000460	THPO	11465	ACTGCCATCTTCCTGAGCTTC
NM_000479	AMH	11466	ACGTGACCTGGGAGCCAACAC
NM_000479	AMH	11467	ACCAATTGCCAGGGCGTGTGC
NM_000546	TP53	11468	ACGGGCCTGACTCAGACTGAC
NM_000549	TSHB	11469	ACTGGCAAACGTGTTTCTTCCC
NM_000549	TSHB	11470	ACATACCAGGATGCCCCACTCC
NM_000572	IL10	11471	ACGGAGTCCTTGCTGGAGGAC
NM_000572	IL10	11472	ACGCTCCAAGAGAAAGGCATC
NM_000575	IL1A	11473	ACGCTTACCTTCAAGGAGAGC
NM_000575	IL1A	11474	ACGCAAGACTACTGGGTGTGC
NM_000576	IL1B	11475	ACCAGATGAAGTGCTCCTTCC
NM_000576	IL1B	11476	ACATACCTGTGGCCTTGGGCC
NM_000588	IL3	11477	ACGACAAGCTGGGTAACTGC
NM_000588	IL3	11478	ACTAACCTTCGAAGGCCAAAC
NM_000588	IL3	11479	ACTCTCCTGCCATGTCTGCCC
NM_000590	IL9	11480	ACCCAAACCACGGCAGGCAAC
NM_000595	LTA	11481	ACGATGCATCTTGCCACAGC
NM_000595	LTA	11482	ACAGCCTACTCTCCCAAGGCC
NM_000597	IGFBP2	11483	ACCAGGAACCTGGACCAGGTCC
NM_000597	IGFBP2	11484	ACGCATGGCCTGTACAACCTC
NM_000597	IGFBP2	11485	ACTGAGCAGCAGGAGGCTTGC
NM_000598	IGFBP3	11486	ACAGGGCATGCTAAAGACAGC

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NM_000599	IGFBP5	11487	ACGAGCTACCGCGAGCAAGTC
NM_000599	IGFBP5	11488	ACGATCTTCCGGCCCAACAC
NM_000605	IFNA2	11489	ACGGCTGAAACCATCCCTGTC
NM_000609	SDF1	11490	ACCAGACAAGTGTGCATTGAC
NM_000614	CNTF	11491	ACCAAGAACATCAACCTGGAC
NM_000639	TNFSF6	11492	ACCTCCGAGAGTCTACCAGCC
NM_000639	TNFSF6	11493	ACGAAGGGTGGCCTTGTGATC
NM_000660	TGFB1	11494	ACGGTCCTGGCCCTGTACAAC
NM_000735	CGA	11495	ACACCCATTCTTCTCCAGCC
NM_000735	CGA	11496	ACGAACGTCACCTCAGAGTCC
NM_000758	CSF2	11497	ACTGTTTGACCTCCAGGAGCC
NM_000758	CSF2	11498	ACGGACTTTCTGCTTGTGCATC
NM_000759	CSF3	11499	ACGCTGGTGAGTGAGTGTGCC
NM_000759	CSF3	11500	ACAGACAGGGAAGAGCAGAAC
NM_000759	CSF3	11501	ACAGCTCCTGTCTCTCCATCC
NM_000800	FGF1	11502	ACACTCCTCTACTGTAGCAAC
NM_033136	FGF1	11502	ACACTCCTCTACTGTAGCAAC
NM_033137	FGF1	11502	ACACTCCTCTACTGTAGCAAC
NM_000800	FGF1	11503	ACGAATGGGAGCTGCAAACGC
NM_033136	FGF1	11503	ACGAATGGGAGCTGCAAACGC
NM_033137	FGF1	11503	ACGAATGGGAGCTGCAAACGC
NM_000825	GNRH1	11504	ACCCCAACGCTTCGAATGCAC
NM_000825	GNRH1	11505	ACTCCTTACACCAAGTTGCAC
NM_000879	IL5	11506	ACGTGCATTGGTGAAAGAGAC
NM_000879	IL5	11507	ACTCTTTCAGGGAATAGGCAC
NM_000880	IL7	11508	ACACTGAATGCTCCAGTCAAC
NM_000882	IL12A	11509	ACCTAATGGGAGTTGCCTGGC
NM_000882	IL12A	11510	ACGATGTACCAGGTGGAGTTC
NM_000885	ITGA4	11511	ACATGGATGAGACTTCAGCAC
NM_000887	ITGAX	11512	ACCTGTGGAGCCGACCATATC
NM_000887	ITGAX	11513	ACGTTGGCTTCTTCAAGCGTC
NM_000939	POMC	11514	ACACGCCATCATCAAGAACGC
NM_000939	POMC	11515	ACGAACGCCTACAAGAAGGGC
NM_001173	ARHGAP5	11516	ACGAGGTATATGGTAGGCATC
NM_001173	ARHGAP5	11517	ACGGAGGCGAATACAGATCAC
NM_001173	ARHGAP5	11518	ACCCTCAGCTGATACAACCAC
XM_170205	LOC223006	11518	ACCCTCAGCTGATACAACCAC
NM_001200	BMP2	11519	ACCAGCCAACTCGAAATTCCC
NM_001201	BMP3	11520	ACCATTACGTCCAAGGGACGC
NM_001201	BMP3	11521	ACTTGCGCCAGGAGATACCTC
NM_001242	TNFRSF7	11522	ACAGGCTGCTCAGTGTGATCC
NM_001242	TNFRSF7	11523	ACTGCTGAGTGTGCCTGTGCG
NM_001243	TNFRSF8	11524	ACGCAGTGTGAGCCTGACTAC
NM_001243	TNFRSF8	11525	ACGCAGTGTGAGCCCGACTAC
NM_001243	TNFRSF8	11526	ACGCGAATTCGGCAGAAGCTC
NM_001244	TNFSF8	11527	ACGAAGTCATGGGCCTACCTC

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NM_001244	TNFSF8	11528	ACGTTGGAGCTTCTCATCAAC
NM_001250	TNFRSF5	11529	ACATGTCACCCTTGGACAAGC
NM_001250	TNFRSF5	11530	ACGAAGCCAACCAATAAGGCC
NG_001334	NG_001334	11531	ACACCGTTCCGTTATCCAGGC
NM_001317	CSH1	11531	ACACCGTTCCGTTATCCAGGC
NM_020991	CSH2	11531	ACACCGTTCCGTTATCCAGGC
NM_022640	CSH1	11531	ACACCGTTCCGTTATCCAGGC
NM_022641	CSH1	11531	ACACCGTTCCGTTATCCAGGC
NM_022644	CSH2	11531	ACACCGTTCCGTTATCCAGGC
NM_022645	CSH2	11531	ACACCGTTCCGTTATCCAGGC
NG_001334	NG_001334	11532	ACGAACCTACGGGCTGCTCCAC
NM_001318	CSHL1	11532	ACGAACCTACGGGCTGCTCCAC
NM_022578	CSHL1	11532	ACGAACCTACGGGCTGCTCCAC
NM_022579	CSHL1	11532	ACGAACCTACGGGCTGCTCCAC
NM_022580	CSHL1	11532	ACGAACCTACGGGCTGCTCCAC
NM_022581	CSHL1	11532	ACGAACCTACGGGCTGCTCCAC
NM_001561	TNFRSF9	11533	ACCTGCCAGCTGGTACATTC
NM_001666	ARHGAP4	11534	ACGGAGCTCTTGGGAAAGACC
NM_001709	BDNF	11535	ACGTGCCTTTGGAGCCTCCTC
NM_001709	BDNF	11536	ACAGACTGCAGTGGACATGTC
NM_001709	BDNF	11537	ACGAGAATTGGCTGGCGATTTC
NM_001719	BMP7	11538	ACCGAGGTGCACTCGAGCTTC
NM_001719	BMP7	11539	ACGAAGCACGAGCTGTATGTC
NM_001719	BMP7	11540	ACTACAGAAACATGGTGGTCC
NM_001901	CTGF	11541	ACGGGCCTCTTCTGTGACTTC
NM_001901	CTGF	11542	ACGTTTGAGCTTTCTGGCTGC
NM_002006	FGF2	11543	ACCGAACCTGGGCAGTATAAAC
NM_002007	FGF4	11544	ACGCTCTATGGCTCGCCCTTC
NM_002053	GBP1	11545	ACAGGGCTTCTCTCTGGGCTC
XM_032826	FLJ10961	11545	ACAGGGCTTCTCTCTGGGCTC
NM_002053	GBP1	11546	ACCCTGCCCAGACTCTGTATC
NM_002059	GH2	11547	ACTCTAACCTAGAGCTGCTCC
NM_022556	GH2	11547	ACTCTAACCTAGAGCTGCTCC
NM_022557	GH2	11547	ACTCTAACCTAGAGCTGCTCC
NM_022558	GH2	11547	ACTCTAACCTAGAGCTGCTCC
NG_001334	NG_001334	11548	ACTCGCACAACGATGACGCAC
NM_002059	GH2	11548	ACTCGCACAACGATGACGCAC
NM_022556	GH2	11548	ACTCGCACAACGATGACGCAC
NM_022557	GH2	11548	ACTCGCACAACGATGACGCAC
NM_022558	GH2	11548	ACTCGCACAACGATGACGCAC
NM_002170	IFNA8	11549	ACCAGGAGGGCCTTGATACTC
NM_002170	IFNA8	11550	ACCCTCTTCAGCACAAAGGAC
NM_002176	IFNB1	11551	ACTGGGAGGCTTGAATATTGC
NM_002176	IFNB1	11552	ACCTCATGAGCAGTCTGCACC
NM_002177	IFNW1	11553	ACCACCTTGGTGCTTCTGCAC
NM_002178	IGFBP6	11554	ACTCCTAAGGAGAGTAAACCC

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NM_002188	IL13	11555	ACTGGCAGCATGGTATGGAGC
NM_002188	IL13	11556	ACCCTGACAGCTGGCATGTAC
NM_002188	IL13	11557	ACGACCCAGAGGATGCTGAGC
NM_002203	ITGA2	11558	ACGACACCATTACAGACGTGC
NM_002203	ITGA2	11559	ACGGGAAAGTGCATACAACAC
NM_002205	ITGA5	11560	ACTTTGACAGCAAAGGCTCTC
NM_002206	ITGA7	11561	ACACTTTGGACCCTGCTGACC
NM_002206	ITGA7	11562	ACGCAAGGCTGTGGTGAAGAC
NM_002208	ITGAE	11563	ACTCAGCTCTGTAACCACAGC
NM_002209	ITGAL	11564	ACTGGAATCCCTGCAGAAGAC
NM_002309	LIF	11565	ACCAACCTCATGAACCAGATC
NM_002342	LTBR	11566	ACTGTTCTGTGCTGCCTGGGC
NM_002416	MIG	11567	ACGGGTCGCTGTTCCCTGCATC
NM_002416	MIG	11568	ACGTGGGAGAAACAGGTCAGC
NM_002507	NGFR	11569	ACCCCTCATCCCTGTCTATTGC
NM_002820	PTHLH	11570	ACAGAGCTGTGTCTGAACATC
NM_002820	PTHLH	11571	ACCTCCAAGCCCTCTCCAAC
NM_002891	RASGRF1	11572	ACGAGTTCGTCCGCAACCACC
NM_002891	RASGRF1	11573	ACTGCAAGGTGATCGGCTTCC
NM_003238	TGFB2	11574	ACTGTGCAGGATAATTGCTGC
NM_003243	TGFBR3	11575	ACGTCTGTCAACTGGGTGATC
NM_003326	TNFSF4	11576	ACGGTGCAGAACAACCTCAGTC
NM_003326	TNFSF4	11577	ACGAAGGTCAAGTCTGTCAAC
NM_003326	TNFSF4	11578	ACTACCTCCCTGGATGACTTC
NM_003327	TNFRSF4	11579	ACGCCTGGAGTTGACTGTGCC
NM_003327	TNFRSF4	11580	ACTCTGTGAGGACAGGGACCC
NM_003376	VEGF	11581	ACGGAGGAGGGCAGAATCATC
NM_003376	VEGF	11582	ACATCCCTGTGGGCCTTGCTC
NM_003377	VEGFB	11583	ACAGGACAGTGCTGTGAAGCC
NM_003637	ITGA10	11584	ACCATCACCCACGCCTATTCC
NM_003790	TNFRSF12	11585	ACCTGTTTCAGCAGTGGCCGAC
NM_003808	TNFSF13	11586	ACCAAACAGAGCTGCAGAGCC
NM_003808	TNFSF13	11587	ACCGCCACCTCCAAGGATGAC
NM_003808	TNFSF13	11588	ACGAAGTATGCCCTCCCAACC
NM_003809	TNFSF12	11589	ACGAAAGCCAGGATCCTGCGC
NM_003810	TNFSF10	11590	ACGATGACAGTTATTGGGACC
NM_003811	TNFSF9	11591	ACGGCTGGAGTCTACTATGTC
NM_003820	TNFRSF14	11592	ACACCACTGACCCACAGACTC
NM_003839	TNFRSF11A	11593	ACATGCAGACCCTGGACCAAC
NM_003839	TNFRSF11A	11594	ACGGTGTCTTACTGCTGACTC
NM_003839	TNFRSF11A	11595	ACAGCTGCAACTGCACTGAGC
NM_003840	TNFRSF10D	11596	ACTATACTGGAGCCTGTAACC
NM_003840	TNFRSF10D	11597	ACTGAATCAGCTGCCAGTTCC
NM_003840	TNFRSF10D	11598	ACCACTGGAAGAAGGACATGC
NM_003841	TNFRSF10C	11599	ACCATACTGGAGCCTGTAACC
NM_003841	TNFRSF10C	11600	ACGAGACAATGAACACCAGCC

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NM_003842	TNFRSF10B	11601	ACTGGAAGTCCAGGAGCCAGC
NM_003842	TNFRSF10B	11602	ACGCAGAAGATTGAGGACCAC
NM_003844	TNFRSF10A	11603	ACAGAGAAGATTTCAGGACCTC
NM_003862	FGF18	11604	ACCGTGGACTTCCGCATCCAC
NM_033649	FGF18	11604	ACCGTGGACTTCCGCATCCAC
NM_003862	FGF18	11605	ACGGGCAAGGAGACGGAATTC
NM_033649	FGF18	11605	ACGGGCAAGGAGACGGAATTC
NM_003862	FGF18	11606	ACCCAGCAGGACGTGCATTTTC
NM_033649	FGF18	11606	ACCCAGCAGGACGTGCATTTTC
NM_003867	FGF17	11607	ACGCTCATAGTGAGACGGAC
NM_003868	FGF16	11608	ACCTCTATGGGTCGAAGAAAC
NM_003868	FGF16	11609	ACACTGGTACAACACCTATGC
NM_003868	FGF16	11610	ACCGACACCAGAAATTCACCTC
NM_004112	FGF11	11611	ACGCTGGGTCACTACATGGCC
NM_004112	FGF11	11612	ACTTACTACGTCTGTACGCC
NM_004112	FGF11	11613	ACGAAGACCAAGGCAGCTGCC
NM_004115	FGF14	11614	ACAGTGCGCATCTTCGGCCTC
NM_004120	GBP2	11615	ACGTCTCACACCAAGGGAATC
NM_004120	GBP2	11616	ACAGGAGGAAGAGCTGAACCC
NM_004195	TNFRSF18	11617	ACACCTTGGACAGACTGCACC
NM_004195	TNFRSF18	11618	ACGACCCACAACGCTGTGTGC
NM_004469	FIGF	11619	ACCTCTGTCTTATGACATGC
NM_004490	GRB14	11620	ACGTATGGCATGCAGCTGTAC
NM_004658	RASAL1	11621	ACCACCTCTTCCGTTCTAAC
NM_004658	RASAL1	11622	ACGAAGCGCTACGTCTGGCTC
NM_004706	ARHGEF1	11623	ACAGCCAAGCAACGCAAGGAC
NM_004761	RAB2L	11624	ACTGTGCTGGCTATAACCTCC
NM_004761	RAB2L	11625	ACGGTCTCTACTGCTACACC
NM_004815	PARG1	11626	ACCAATTGCAGCTCTCCAGGC
NM_004962	GDF10	11627	ACCCATGCCACCATCCAGAGC
NM_005117	FGF19	11628	ACCAGAGGCTTTCTTCCACTC
NM_005117	FGF19	11629	ACTCTGACATGTTCTCTTCGC
NM_005118	TNFSF15	11630	ACTCAGTTCCCAGCTCTGCAC
NM_005167	ARHC	11631	ACTTCACCCACCTTGAGTTCC
NM_005167	ARHC	11632	ACGCCCTTCTCTCTCTGCTTC
NM_005247	FGF3	11633	ACGTACCACCTCCAGCTGCAC
NM_005247	FGF3	11634	ACATCAGGGTCCAGTGGGAAC
NM_005259	GDF8	11635	ACTCCTGAGACTCATCAAACC
NM_005259	GDF8	11636	ACTCACGATGCTGTCTGTTACC
NM_005260	GDF9	11637	ACGTCTTCTAGCAGGACTCTC
NM_005310	GRB7	11638	ACCTTCGAGAGGAGGAGAGGC
NM_005310	GRB7	11639	ACGACCTCATCCAGAACTTCC
NM_005310	GRB7	11640	ACTACCCTGGTGGCCATGGAC
NM_005311	GRB10	11641	ACGACCATGAGCTGGTGGTCC
NM_005429	VEGFC	11642	ACGATCTGGAGGAGCAGTTAC
NM_005429	VEGFC	11643	ACACATGCAGCTGTTACAGAC

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NM_005435	ARHGEF5	11644	ACGCTTCGGTGGATCTCAGCC
NM_005435	ARHGEF5	11645	ACCTACAGCTGGTGGAAACAGC
NM_005614	RHEB2	11646	ACTTTGTGGACTCCTACGATC
NM_005618	DLL1	11647	ACGCTGCAGGAGTTCGTCAAC
NM_005618	DLL1	11648	ACCACCAACAAGAAGGCGGAC
NM_005733	RAB6KIFL	11649	ACGAACCTGCTATCAGACTGC
NM_005733	RAB6KIFL	11650	ACGAACCAGAGCTTTGCCAGC
NM_005733	RAB6KIFL	11651	ACCTGCAGAACAAACATGGTGC
NM_005739	RASGRP1	11652	ACGGAGACAAAGTTCGCATGTC
NM_005739	RASGRP1	11653	ACGAGACCACCTACCTGAAGC
NM_005739	RASGRP1	11654	ACTCAAAGGAGGAGCTCCGTC
NM_005766	FARP1	11655	ACGGAGGACATAAGAAGGTGC
NM_005766	FARP1	11656	ACGGTGTGTTACCTACCGCTC
NM_005766	FARP1	11657	ACGACTACGTGTTCAAGCTGC
NM_005811	GDF11	11658	ACGTGCTACACAGCTGGTTCC
NM_006116	MAP3K7IP1	11659	ACGTTTCAGGAGTGAGAACAAC
NM_006116	MAP3K7IP1	11660	ACTTGCCAGAGGGAGTCCCTC
NM_006270	RRAS	11661	ACCGAGGTGGGCAAGCTCTTC
NM_006270	RRAS	11662	ACTACCAGGAACAAGAGCTCC
NM_006325	RAN	11663	ACTGTATGGGACACAGCCGGC
NM_006325	RAN	11664	ACTTTGTTGCCATGCCTGCTC
NM_006506	RASA2	11665	ACATAGTGGGAGGGCACTACC
NM_006573	TNFSF13B	11666	ACTTCCTGCTATTTCAGCTGGC
NM_006850	IL24	11667	ACTGCAGATGGTTGTGCTCCC
NM_006850	IL24	11668	ACCGTCTCGGATGCTGAGAGC
NM_006989	CAPRI	11669	ACTGAGCCCATCATCAGGTAC
NM_006989	CAPRI	11670	ACCACCCTGTTCCGGAGCAAC
NM_006989	CAPRI	11671	ACGGACTTCATCACCAGCTC
NM_007182	RASSF1	11672	ACCAGCAACCTCTTCATGAGC
NM_007182	RASSF1	11673	ACGTCATTGAGGCCCTGCTGC
NM_007368	GAP1IP4BP	11674	ACATTCCTCGGAGCTTTCGTC
NM_007368	GAP1IP4BP	11675	ACCGTGGTATACACGGAAGAC
NM_012211	ITGA11	11676	ACCATCTTCCACAGAGACTGC
NM_012211	ITGA11	11677	ACATACGAGGCTGACGTCCCTC
NM_012219	MRAS	11678	ACTCAATGGGCCATCTTGGAC
NM_012219	MRAS	11679	ACAGAAATGGCGACCAACAC
NM_012452	TNFRSF13B	11680	ACGAGCAGTACTGGGATCCTC
NM_012452	TNFRSF13B	11681	ACGGCAAGTTCTATGACCATC
NM_013371	IL19	11682	ACGGACACCTTCCCAATGTC
NM_013371	IL19	11683	ACTCAGCAGCATTGCCAACTC
NM_014438	IL1F8	11684	ACCATAGGGAAGGACACTTGC
NM_014438	IL1F8	11685	ACCCTGGATGTGAGAGAGAGC
NM_014440	IL1F6	11686	ACGTCCTTTCTCTTCTACCAC
NM_014440	IL1F6	11687	ACGGAGGCTGTCTCTCATCC
NM_014448	ARHGEF16	11688	ACGCAGACGAGGTACACTGC
NM_014452	TNFRSF21	11689	ACGGCCTCGAATCTCATTGGC

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NM_014452	TNFRSF21	11690	ACTGCCATGACTGTAGTCAGC
NM_014482	BMP10	11691	ACCCAACAGTGAGTGGGAGAC
NM_014482	BMP10	11692	ACGGAGATTGGGTGGGACTCC
NM_014737	RASSF2	11693	ACTCAGACGCCACCGCTTCTC
NM_014737	RASSF2	11694	ACGCTGATGCGCAAGTACACC
NM_014784	ARHGEF11	11695	ACGCTCAATGCTGTGCTCATC
NM_014958	ARHGEF15	11696	ACGCTCCTCAGAATACTCCTC
NM_014958	ARHGEF15	11697	ACGATCATCGAGCGTTGCAGC
NM_015313	ARHGEF12	11698	ACGAAGATGGAGCAGCCATGC
NM_015318	P114-RHO-GEF	11699	ACGATATCCTGGCTATCCTGC
NM_015318	P114-RHO-GEF	11700	ACGCAGCAGCTGCTGCTCAAC
NM_015647	TNFRSF6B	11701	ACGCAGGAGTTGAGCCAAGCC
NM_016434	TNFRSF6B	11701	ACGCAGGAGTTGAGCCAAGCC
NM_032957	TNFRSF6B	11701	ACGCAGGAGTTGAGCCAAGCC
NM_016084	RASD1	11702	ACGAAGAACAGCAGCCTGGAC
NM_016204	GDF2	11703	ACCATTGTGCGGAGCTTCAGC
NM_016205	PDGFC	11704	ACGCTGTGAGTCCTTCAGTGC
NM_018402	IL26	11705	ACGCAACGATTCCAGAAGACC
NM_018402	IL26	11706	ACGCAGTCAGTAAACCAAAGC
NM_018724	IL20	11707	ACGACACTCAATTTGGGAAGC
NM_018724	IL20	11708	ACTCTTAAGGAGGACTGAGTC
NM_018724	IL20	11709	ACAGCTGGAACCTCAGGCAGC
NM_018993	RIN2	11710	ACCTGAAACAGGAGATGGTGC
NM_018993	RIN2	11711	ACCTCAAGGAGAACCTGCAGC
NM_018993	RIN2	11712	ACGAACGATCCTTATGGCATC
NM_019074	DLL4	11713	ACGATCTCAACTACTGCACCC
NM_019074	DLL4	11714	ACGAAGGAGCTGGAAGTGGAC
NM_019113	FGF21	11715	ACGACATCCAGGTTCTCTGTGC
NM_019113	FGF21	11716	ACTGTTTACCAGTCCGAAGCC
NM_019555	ARHGEF3	11717	ACGTAGCCGCCAAAGCTCTGC
NM_019555	ARHGEF3	11718	ACAGACCTCCTGCTGGAAGAC
NM_019851	FGF20	11719	ACACATGGAGACACTGGCCGC
NM_020525	IL22	11720	ACGGTGATGACCTGCATATCC
NM_020634	GDF3	11721	ACCTGGCTCTGTTCTCTGGTTC
NM_020637	FGF22	11722	ACAGCAGTGTCTCAGGCTTC
NM_020638	FGF23	11723	ACCAGCTACCACCTGCAGATC
NM_020638	FGF23	11724	ACGAATGGCCATGTGGATGGC
NM_020996	FGF6	11725	ACCGTGGGCATCGGCTTTCAC
NM_020996	FGF6	11726	ACTGCAAGTTCAGAGAAACCC
NM_021073	BMP5	11727	ACGGAGGTTTGGGAGACAATC
NM_021073	BMP5	11728	ACGAAAGGGATACCCAGCCTC
NM_021073	BMP5	11729	ACGCTTTAGATGTGGGTTGGC
NM_022481	ARAP3	11730	ACCGCATCTACGCCTGCTAC
NM_022481	ARAP3	11731	ACTGATCGTGCCAACCGCTTC
NM_022481	ARAP3	11732	ACGATGTGATTGGCTGCCTGC
NM_000515	GH1	11733	ACTCCAACCTAGAGCTGCTCC

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NM_022559	GH1	11733	ACTCCAACCTAGAGCTGCTCC
NG_001334	NG_001334	11734	ACGCAGACCTACAGCAAGTTC
NM_000515	GH1	11734	ACGCAGACCTACAGCAAGTTC
NM_022559	GH1	11734	ACGCAGACCTACAGCAAGTTC
NM_022560	GH1	11734	ACGCAGACCTACAGCAAGTTC
NM_022561	GH1	11734	ACGCAGACCTACAGCAAGTTC
NM_022562	GH1	11734	ACGCAGACCTACAGCAAGTTC
NM_032496	ARHGAP9	11735	ACCAAACCTAAAGCGGCTCATC
NM_052851	GT650	11736	ACTTGGAGGACCGGTAGCATC
NM_052851	GT650	11737	ACCAGTTCTTCCGGGACCTCC
NM_052949	RASGRP4	11738	ACTCAGCAAGGTCATGGCTTC
NM_052949	RASGRP4	11739	ACGGTCATGGCTTCCATGAAC
NM_130769	GPHA2	11740	ACTGTGACAGTGCGAAGTGAC
NM_001202	BMP4	11741	ACAGTCGCCGAGATTTCAGGGC
NM_130850	BMP4	11741	ACAGTCGCCGAGATTTCAGGGC
NM_130851	BMP4	11741	ACAGTCGCCGAGATTTCAGGGC
NM_001202	BMP4	11742	ACCTGAGTGCCATCTCCATGC
NM_130850	BMP4	11742	ACCTGAGTGCCATCTCCATGC
NM_130851	BMP4	11742	ACCTGAGTGCCATCTCCATGC
NM_133639	ARHV	11743	ACGAGCAGCCTCATCGTCAGC
NM_133639	ARHV	11744	ACGTCCTGGTGGATGGAGCTC
XM_027943	RASGRF2	11745	ACGAGTGGATGGAGGCCATTC
XM_027943	RASGRF2	11746	ACTTGAACCTCGACTCCCTGC
XM_030185	LOC90230	11747	ACTGCCGTGTCCAACGCAGAC
XM_030185	LOC90230	11748	ACGCTGCAGCTTCTGTCAAC
XM_032902	ITGA1	11749	ACCGTGACCCATGAGTTCAAC
XM_035950	LOC56832	11750	ACGAGGGACATCAAGAAGGCC
XM_035950	LOC56832	11751	ACCCAATGCTTGGAGGAAGAC
XM_051143	SRGAP1	11752	ACGACCAGAACCTGTTGTCTC
XM_051143	SRGAP1	11753	ACTCCTACCATAGGACCTGCC
XM_054745	LOC257478	11754	ACGTTGACTAATCCTCCTTCC
XM_054745	LOC257478	11755	ACGCCGTCTCCAGATAGAGTC
XM_059095	SRGAP2	11756	ACATCGGTAAAGCAGGAGGAC
XM_059095	SRGAP2	11757	ACGCCAAGCATGACCTTCTGC
XM_059095	SRGAP2	11758	ACTGGCATCGACGGACTCATC
XM_059230	LOC128272	11759	ACGAGGACAGAGGAACATC
XM_063142	LOC122460	11760	ACGAATGTGACTGTGGCTCCC
XM_065455	LOC129896	11761	ACGGAGCTCATTAAGGAGGGC
XM_067344	LOC131363	11762	ACAGGAACAAGAGAGCACCTC
XM_067344	LOC131363	11763	ACATGCCTGTGGGCAGAGCAC
XM_067344	LOC131363	11764	ACCTCACGCAGTGTCTGTAC
XM_071038	LOC138685	11765	ACGCCTTATTCTAGTGCCAGC
XM_071048	LOC138684	11766	ACGGACACACTCTGGCCATTC
XM_084665	LOC143872	11767	ACGCCTTGGTCTGTGGACAAC
XM_090404	LOC160629	11768	ACAGGAGGGACCCATGAACCTC
XM_092722	LOC164209	11769	ACGCTGAATCCCAGTGGCTGC

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XM_092722	LOC164209	11770	ACGCTGACCACAAAGTCCTCC
XM_094119	LOC166824	11771	ACATTAGCAGTGATGTGGCTC
XM_094119	LOC166824	11772	ACTTAGGGTTACAGTTGGAC
XM_095759	LOC158011	11773	ACCGACTCTCCAGACTTGATC
XM_113880	LOC197414	11774	ACCCTCCTGAAGATCCACTTC
XM_113880	LOC197414	11775	ACGGCTGGCATCATCCGCTAC
XM_167711	ITGA8	11776	ACCCATCAGGCTCATCGCGTC
XM_167711	ITGA8	11777	ACTAAGAGGAGTGTACACCC
XM_167936	LOC221178	11778	ACGATAAGGAAGCCTGGTTCC
XM_167936	LOC221178	11779	ACGAAGACAAGGCGAGGTGGC
XM_170205	LOC223006	11780	ACCTTGATCTTCGGCCAGTTC
XM_170205	LOC223006	11781	ACCGGTACTACTTCAGTTGCC
AF182273	AF182273	11813	ACGGTTGAGTCAAGGGATGGC
NG_000004	NG_000004	11813	ACGGTTGAGTCAAGGGATGGC
NM_000776	CYP3A3	11813	ACGGTTGAGTCAAGGGATGGC
NM_017460	CYP3A4	11813	ACGGTTGAGTCAAGGGATGGC
J02906	HUMCYPIIF	11814	ACGGGCAATGGCATCGCCTTC
NM_000774	CYP2F1	11814	ACGGGCAATGGCATCGCCTTC
J02906	HUMCYPIIF	11815	ACGAGTCCAGCCTTCATGCCC
NG_000008	NG_000008	11815	ACGAGTCCAGCCTTCATGCCC
NM_000774	CYP2F1	11815	ACGAGTCCAGCCTTCATGCCC
M33189	HUMCYP2DG	11816	ACGGACTCTGTACCTCCTATC
NM_000102	CYP17	11817	ACGACTACAGTGATTGTCCGC
NM_000102	CYP17	11818	ACGGCCAACGTTGACTCCAGC
NM_000103	CYP19	11819	ACACTTGGGCTGCAGTGCATC
NM_031226	CYP19	11819	ACACTTGGGCTGCAGTGCATC
NM_000104	CYP1B1	11820	ACCACCTCTGTCTTGGGCTAC
NM_000104	CYP1B1	11821	ACGTGGCCTAACCCGAGAAC
NM_000104	CYP1B1	11822	ACTAAGAAGCAAGAGGCAAGC
M33189	HUMCYP2DG	11823	ACGGGAACGACACTCATCACC
NG_000853	NG_000853	11823	ACGGGAACGACACTCATCACC
NM_000106	CYP2D6	11823	ACGGGAACGACACTCATCACC
NM_000497	CYP11B1	11824	ACGCTGCAACAGGTGGACAGC
NM_000498	CYP11B2	11824	ACGCTGCAACAGGTGGACAGC
NM_000499	CYP1A1	11825	ACTGGTCAGAGCATGTCTTTC
NM_000761	CYP1A2	11826	ACCGTCATTGGTGCCATGTGC
NM_000761	CYP1A2	11827	ACGATCCAGAAGGAGCTGGAC
NM_000762	CYP2A6	11828	ACAGGCTATGGCGTGGTATTC
NG_000008	NG_000008	11829	ACGAGTTCCTGTCACTGTTGC
NM_000762	CYP2A6	11829	ACGAGTTCCTGTCACTGTTGC
NM_000766	CYP2A13	11829	ACGAGTTCCTGTCACTGTTGC
U22027	HSU22027	11829	ACGAGTTCCTGTCACTGTTGC
U22028	HSU22028	11829	ACGAGTTCCTGTCACTGTTGC
NG_000008	NG_000008	11830	ACCTTCCGCCTCAAGTCCCTCC
NM_000762	CYP2A6	11830	ACCTTCCGCCTCAAGTCCCTCC
NM_000764	CYP2A7	11830	ACCTTCCGCCTCAAGTCCCTCC

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NM_030589	CYP2A7	11830	ACCTTCCGCCTCAAGTCCTCC
U22027	HSU22027	11830	ACCTTCCGCCTCAAGTCCTCC
U22029	HSU22029	11830	ACCTTCCGCCTCAAGTCCTCC
NG_000008	NG_000008	11831	ACGTTTCAGTGAGTGCTATGGC
NM_000764	CYP2A7	11831	ACGTTTCAGTGAGTGCTATGGC
U22029	HSU22029	11831	ACGTTTCAGTGAGTGCTATGGC
NM_000765	CYP3A7	11832	ACGCCTGTACCTTGAAACAC
NG_000008	NG_000008	11833	ACCATCATCTGCTCCATCGTC
NM_000767	CYP2B6	11833	ACCATCATCTGCTCCATCGTC
NM_000767	CYP2B6	11834	ACAGAGAAATCCAACGCACAC
NM_000769	CYP2C19	11835	ACGGCTTCACCCTGTGATCCC
NM_000770	CYP2C8	11835	ACGGCTTCACCCTGTGATCCC
NM_030878	CYP2C8	11835	ACGGCTTCACCCTGTGATCCC
NM_000770	CYP2C8	11836	ACCAGAGACAACAAGCACCAC
NM_030878	CYP2C8	11836	ACCAGAGACAACAAGCACCAC
NM_000772	CYP2C18	11837	ACGGAGATCCGGCGTTTCTGC
NM_000772	CYP2C18	11838	ACCAGAGACAACGAGCACCAC
NM_000773	CYP2E	11839	ACTATTCCCAAGTCCTTCACC
NM_000773	CYP2E	11840	ACCGTCATAGCCGACATCCTC
NM_000775	CYP2J2	11841	ACGCCCTTATCCACATGGACC
NM_000775	CYP2J2	11842	ACAGCACACAGGCAATCCTAC
NM_000777	CYP3A5	11843	ACATCGAAGGTCTTTAGGCCC
NM_000778	CYP4A11	11844	ACCAGGACCAGGAGCTACAAC
AF208532	AF208532	11845	ACGGAGGCACTGAGGCTCTAC
NM_000778	CYP4A11	11845	ACGGAGGCACTGAGGCTCTAC
NM_000780	CYP7A1	11846	ACTTCCATACCTGGGCTGTGC
NM_000780	CYP7A1	11847	ACGTCAGCTTGGAAGGCAATC
NM_000780	CYP7A1	11848	ACTCTACCCAGACCCCTTGAC
NM_000781	CYP11A	11849	ACGGCGGGCTCCGGAAATTAC
NM_000782	CYP24	11850	ACACCGTGGAAGGCCTATCGC
NM_000783	CYP26A1	11851	ACTGACCCGCAATCTCTTCTC
NM_057157	CYP26A1	11851	ACTGACCCGCAATCTCTTCTC
NM_000784	CYP27A1	11852	ACCTGCACCAGTTACAGGTGC
NM_000786	CYP51	11853	ACAGTGGCCTTAACATAGCCC
NM_000786	CYP51	11854	ACGACTCATGGGTAGAACGCC
NM_000896	CYP4F3	11855	ACCGGAATTGGTTCTTGGGTC
NM_000896	CYP4F3	11856	ACGAAGTTGTCCGATGAGGAC
NM_001061	TBXAS1	11857	ACGCAGGTGTTGGTTGAGAAC
NM_030984	TBXAS1	11857	ACGCAGGTGTTGGTTGAGAAC
NM_001061	TBXAS1	11858	ACGAGAGGCGGAGAGACTTCC
NM_030984	TBXAS1	11858	ACGAGAGGCGGAGAGACTTCC
NM_001061	TBXAS1	11859	ACGTTCCGGTTCCAAGCCTGC
NM_001082	CYP4F2	11860	ACCTGCATCGGGCAGACGTTT
NM_004391	CYP8B1	11861	ACTGAGACCATGCTGGACAGC
NM_004820	CYP7B1	11862	ACGCAACATGGTGACACTTTC
NM_007253	CYP4F8	11863	ACTACCAAGAACGCTGCCGGC

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NM_016593	CYP39A1	11864	ACCTCACCCAATTATGGGCTC
NM_020674	CYP-M	11865	ACTTCCAGGGATTACTCCAAC
NM_020674	CYP-M	11866	ACACTGACTCCAGTTTCTGCC
NM_021187	CYP4F11	11867	ACCCAGCAGATTCTCTTGAC
NG_000004	NG_000004	11868	ACCTTGCTGTGATTAGAGCAC
NM_022820	CYP3A43	11868	ACCTTGCTGTGATTAGAGCAC
NM_057095	CYP3A43	11868	ACCTTGCTGTGATTAGAGCAC
NM_030622	CYP2S1	11869	ACGAACATGCTGATGACAGTC
NM_057096	CYP3A43	11870	ACGTTCTGCCCTGAAAGATCC
XM_058459	LOC120227	11871	ACTGCCTTTCCATGGATTGGC
XM_058459	LOC120227	11872	ACTGGGAAGCCTTCTTGGGAC
XM_059042	LOC126410	11873	ACTTGATCGGACAGAGCTTC
XM_059135	LOC127352	11874	ACACCCTCAGGTCTTTAACCC
XM_114074	LOC199974	11874	ACACCCTCAGGTCTTTAACCC
XM_059135	LOC127352	11875	ACGTGGCAGTGGCATTAACTC
XM_114074	LOC199974	11875	ACGTGGCAGTGGCATTAACTC
XM_065069	LOC126408	11876	ACCACTTGACCATCAGCATC
XM_065151	LOC126537	11877	ACTGCCAGTGACAAGTGGAGC
XM_065151	LOC126537	11878	ACGCTATCATCCAGGAGCAGC
XM_069332	LOC135397	11879	ACGAGAGAAGCGTTCTGCCC
XM_069332	LOC135397	11880	ACGTTCACCTTCCAGCCACTC
XM_069332	LOC135397	11881	ACGCCTGGACGTTGGCTTCAC
XM_071222	LOC138967	11882	ACTTGCTGCTATGTCAGATCC
XM_089093	LOC163720	11883	ACACCTGGCTTCAACATCAGC
XM_103864	LOC165245	11884	ACCATCTTCTCAGACCAATGC
XM_104192	LOC164193	11885	ACTTGATGTCAAGGCGGGTGC
XM_114074	LOC199974	11886	ACGACCCTCAGGTCTTTAACC
XM_171967	LOC256991	11887	ACCCAGCAGATCCTCCTGCAC
XM_172333	LOC255434	11888	ACCAGTAACACGAGGCGTCCC

Claims

1. Polynucleotide comprising an RNA sequence comprising a first stretch of 21 consecutive nucleotides and a second
5 stretch of 21 consecutive nucleotides, complementary to the first stretch of 21 consecutive nucleotides, wherein in first stretch of 21 consecutive nucleotides:

a. in the 5' -> 3' direction, the first nucleotide is an A-nucleotide, the second nucleotide is a C-nucleotide
10 and the last nucleotide is a C-nucleotide; and

b. no stretches of four or more consecutive identical nucleotides are present;

c. the total number of G- and C-nucleotides is between 33-71% of the total number of nucleotides

15 d. in the 5' -> 3' direction, consecutive nucleotides 3-21 are homologous to a RNA-molecule.

2. Polynucleotide according to claim 1, wherein the RNA-molecule is a human RNA molecule.

3. Polynucleotide according to claims 1-2, wherein in
20 the first stretch of 21 consecutive nucleotides no stretches of three or more consecutive A- nucleotides are present

4. Polynucleotide according to claims 1-3 wherein in the first stretch of 21 consecutive nucleotides no stretches of three or more consecutive U-nucleotides are present

25 5. Polynucleotide according to claims 1-4, wherein, in the 5' -> 3' direction, consecutive nucleotides 3-21 of the first stretch of 21 consecutive nucleotides are unique.

6. Polynucleotide according to claims 1-5, wherein, in the 5' -> 3' direction, consecutive nucleotides 3-21 of the
30 first stretch of 21 consecutive nucleotides are homologous to a sequence positioned at least 75 nucleotides downstream of the translation initiation site of the transcribed RNA molecule encoding a polypeptide.

7. Polynucleotide according to claims 1-6, wherein, in the 5' -> 3' direction, consecutive nucleotides 3-21 of the first stretch of 21 consecutive nucleotides are homologous to a sequence positioned at least upstream of the translation
5 termination site of the transcribed RNA molecule encoding a polypeptide.

8. Polynucleotide according to claims 1-7 wherein the RNA sequence also comprises a linker sequence linking the first stretch of 21 consecutive nucleotides with the second
10 stretch of 21 consecutive nucleotides.

9. Polynucleotide according to claim 8, wherein the linker sequence is 4-30 nucleotides long, preferably 5-15 nucleotides long and most preferably 8 nucleotides long

10. Polynucleotide according to claims 8-9, wherein the
15 linker sequence is SEQ ID NO: 1

11. Polynucleotide according to claims 1-10, wherein the first stretch of 21 consecutive nucleotides is selected from a group consisting of SEQ ID NO: 2-11888

12. Polynucleotide according to claims 1-11, wherein the
20 first stretch of 21 consecutive nucleotides is selected from a group consisting of SEQ ID NO: 1342, 1338, 1343, 633, 635

13. Vector capable of transfecting a host cell and comprising a sequence encoding the polynucleotide according to claims 1-12 and a promoter sequence operatively linked to
25 the sequence encoding the polynucleotide.

14. Vector according to claim 13, wherein the promoter is a microRNA promoter, preferably a let-7 promoter.

15. Vector according to claim 14, wherein the promoter is a promoter recognized by RNA Polymerase III, preferably U6
30 small nuclear RNA.

16. The vector according to claims 13-15, wherein the vector is an adenoviral vector, preferably the adenoviral vector is replication defective.

17. Library of polynucleotide sequences according to claims 1-12.

18. Library of vectors according to claims 13-16.

19. Library according to claim 18 wherein the vectors
5 are viral vectors preferably selected from a group consisting of AAV, Lentivirus or Retrovirus.

20. Library according to claim 18 wherein the vectors are adenoviral vectors, preferably the adenoviral vectors are replication defective.

10 21. Method of making a vector according to claim 16 comprising the steps:

a. synthesizing a forward primer with the following sequence in the 5' -> 3' direction:

i. the nucleotides ACC

15 ii. a DNA sequence corresponding to the antisense sequence of a sequence selected from the group consisting of SEQ ID NO: 2-11888

iii. the nucleotides TTGCTATA

20 iv. the antisense sequence corresponding to the DNA sequence from step a-ii

v. the nucleotides TTT

b. synthesizing a reverse primer with the following sequence in the 5' -> 3' direction

i. the nucleotides TAAAAA

25 ii. a DNA sequence corresponding the antisense sequence of a sequence selected from the group consisting of SEQ ID NO: 2-11888

iii. the nucleotides TATAGCAA

30 iv. the antisense sequence corresponding to the DNA sequence from step b-ii

c. annealing the primers from step (a) and (b)

d. exchanging the ccdB sequences in plasmid pKD122 for the annealed primers from step (c)

22. Method of preparing a vector according to claim 15 comprising the steps:

a. synthesizing a forward primer with the following sequence in the 5' -> 3' direction:

- 5 i. the nucleotides ACC
- ii. a DNA sequence corresponding to a sequence selected from the group consisting of SEQ ID NO: 2-11888
- iii. the nucleotides TTGCTATA
- iv the antisense sequence corresponding to the DNA
- 10 sequence from step a-ii
- v. the nucleotides TTT

b. synthesizing a reverse primer with the following sequence in the 5' -> 3' direction

- i. the nucleotides TAAAAA
- 15 ii. a DNA sequence corresponding to a sequence selected from the group consisting of SEQ ID NO: 2-11888
- iii. the nucleotides TATAGCAA
- iv. the antisense sequence corresponding to the DNA sequence from step b-ii

- 20 c. annealing the primers from step (a) and (b)
- d. exchanging the ccdB sequences in plasmid pKD122 for the annealed primers from step (c).

23. Method of determining the function of a naturally occurring polynucleotide sequence comprising transfecting a
25 host cell with a vector according to claims 13-16, the vector transcribing a polynucleotide sequence according to claims 1-12 and detecting a change in cellular phenotype.

24. Method of determining the function of a naturally occurring polynucleotide sequence in a high throughput
30 setting,

a. providing a library of vectors according to claims
17-20

b. transducing a host cell with the vectors of step (a),

c. expressing in the host cell the product(s) of the vectors of step (a),

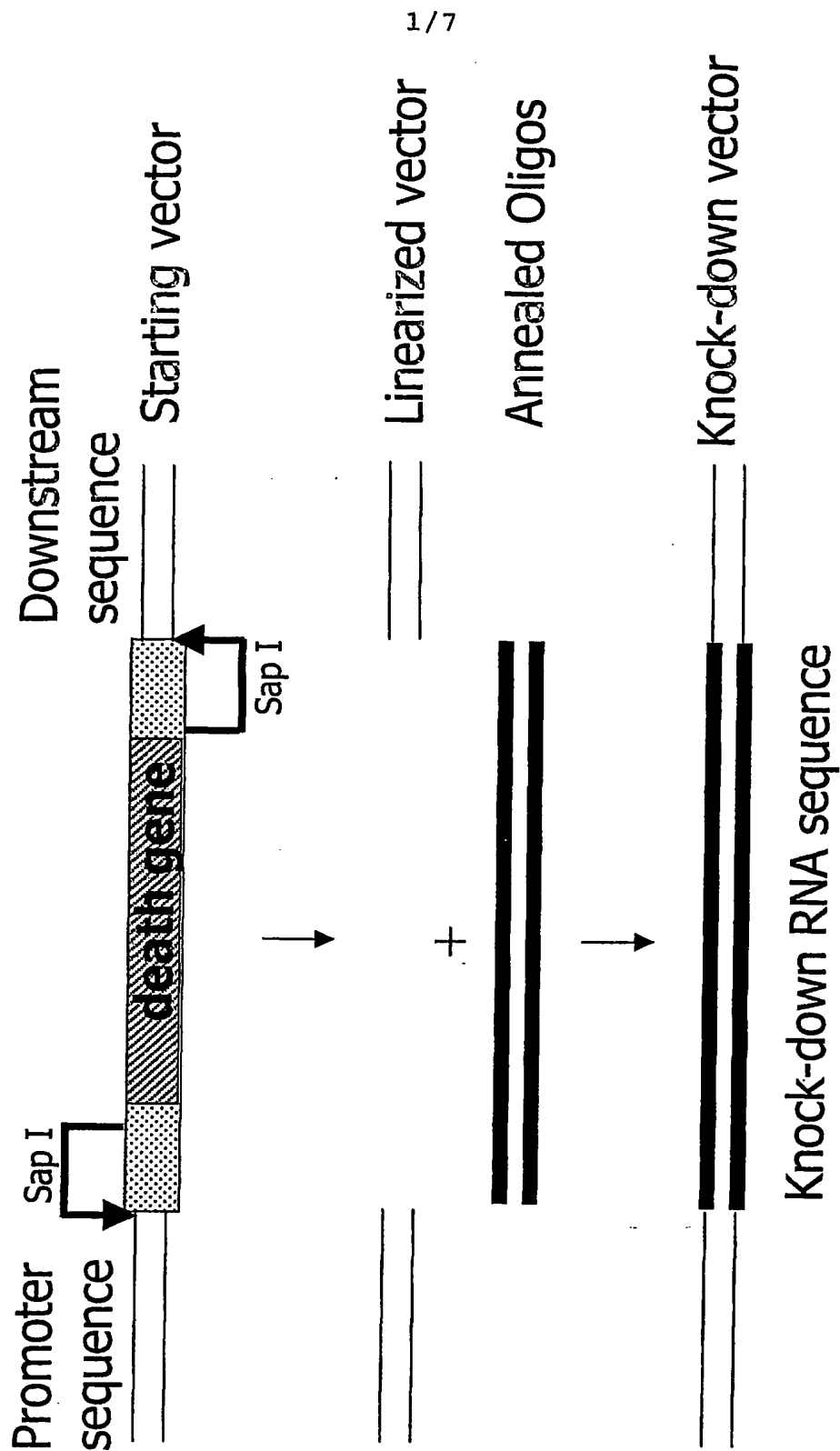
d. thereby altering a phenotype of the host,

e. identifying the altered phenotype and,

5 f. assigning a function to the naturally occurring polynucleotide sequence (s).

Vector development

Figure 1



Adenovirus vector development

Knock-down cloning vector

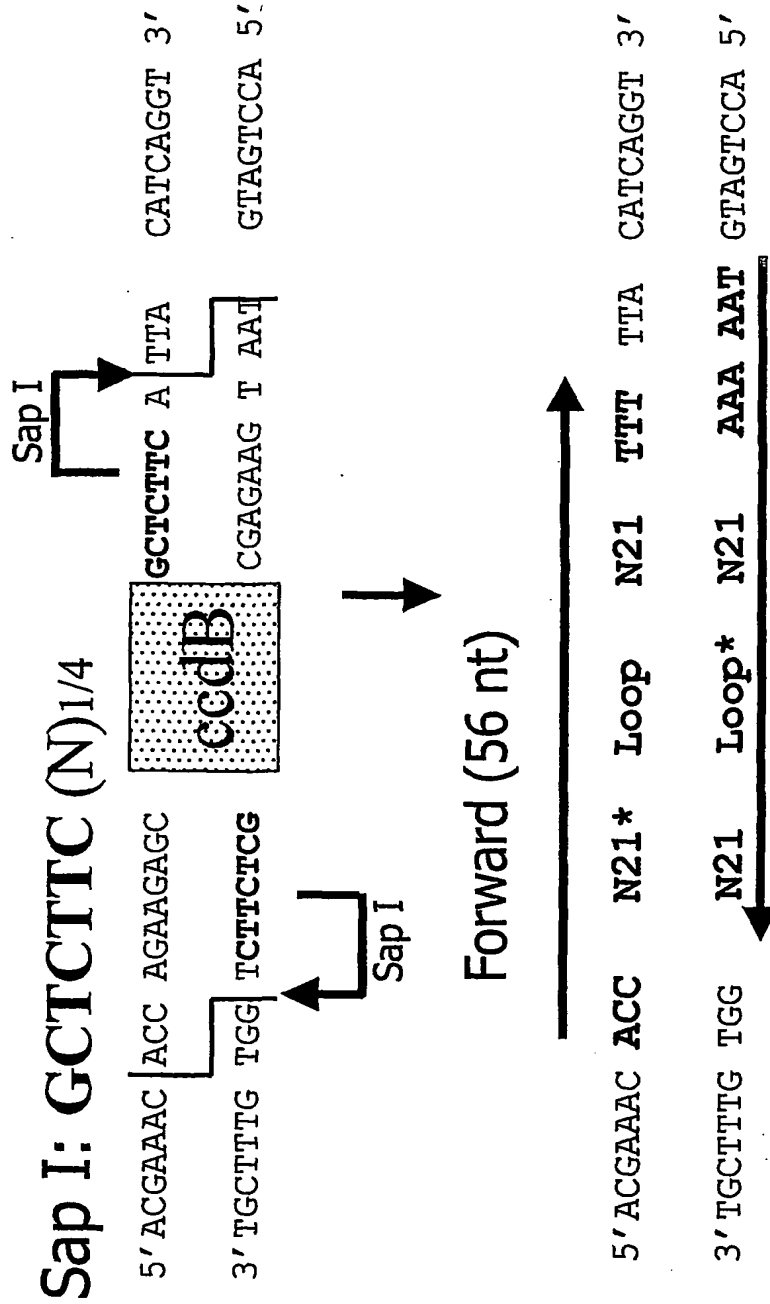
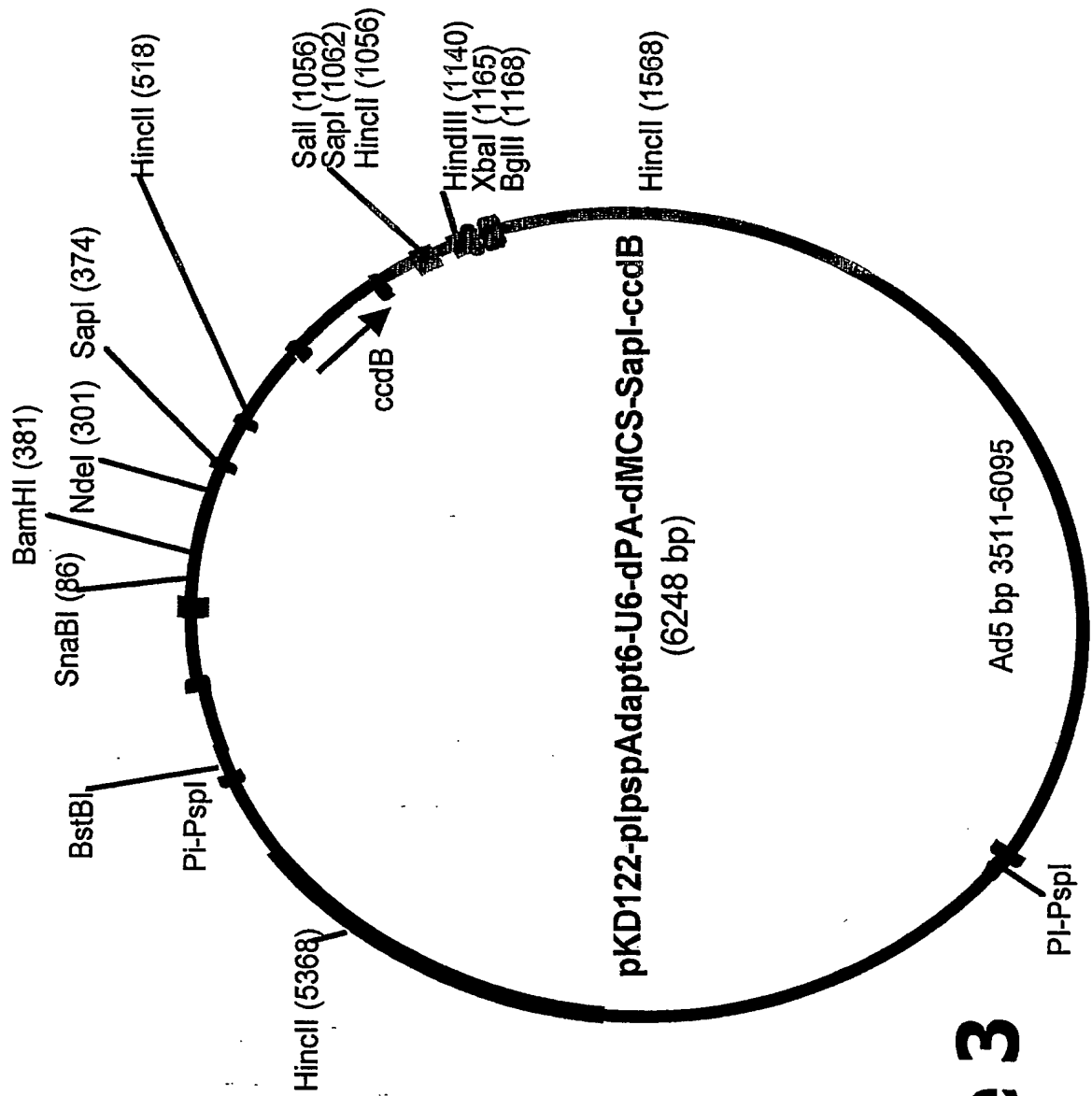


Figure 2

3/7

**Figure 3**

Knock-down of GNAS

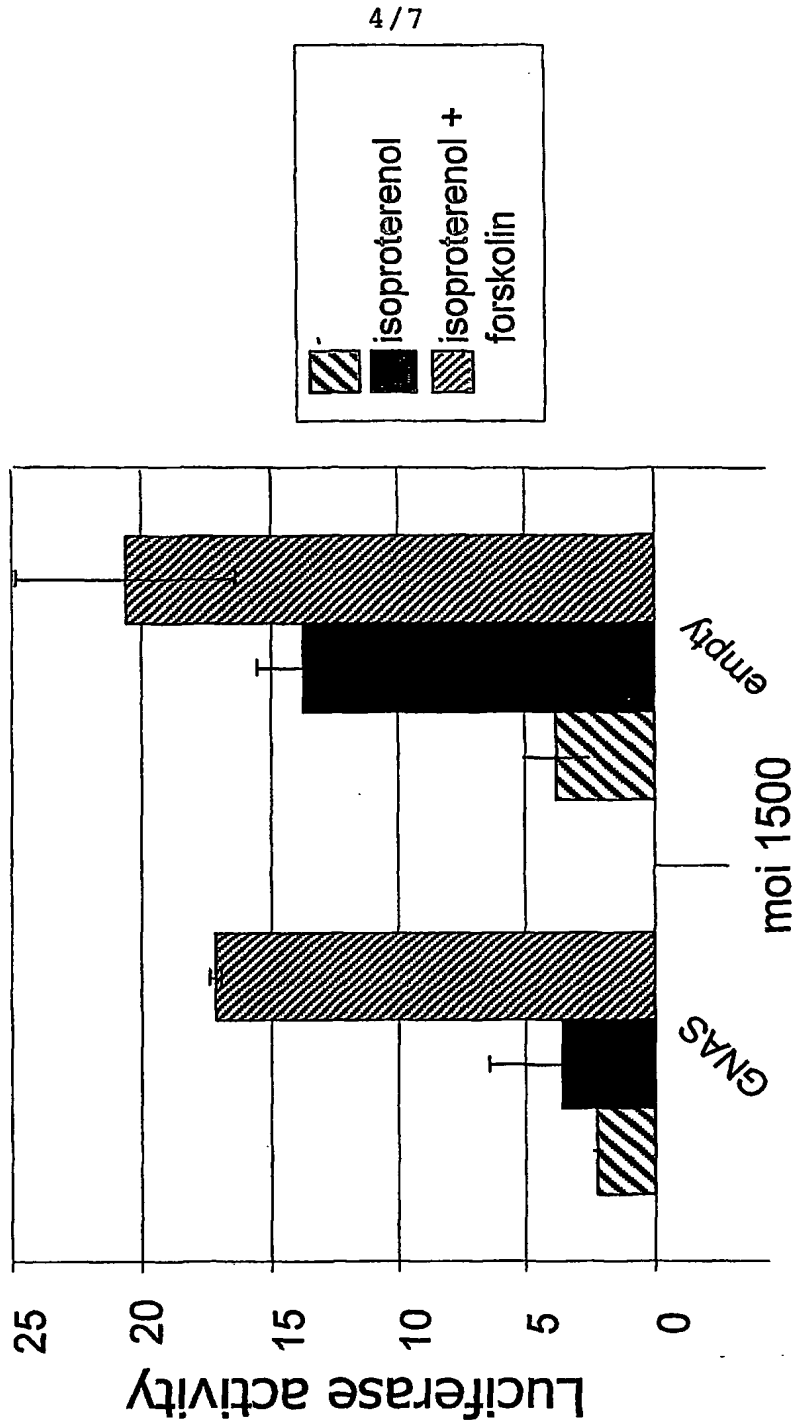
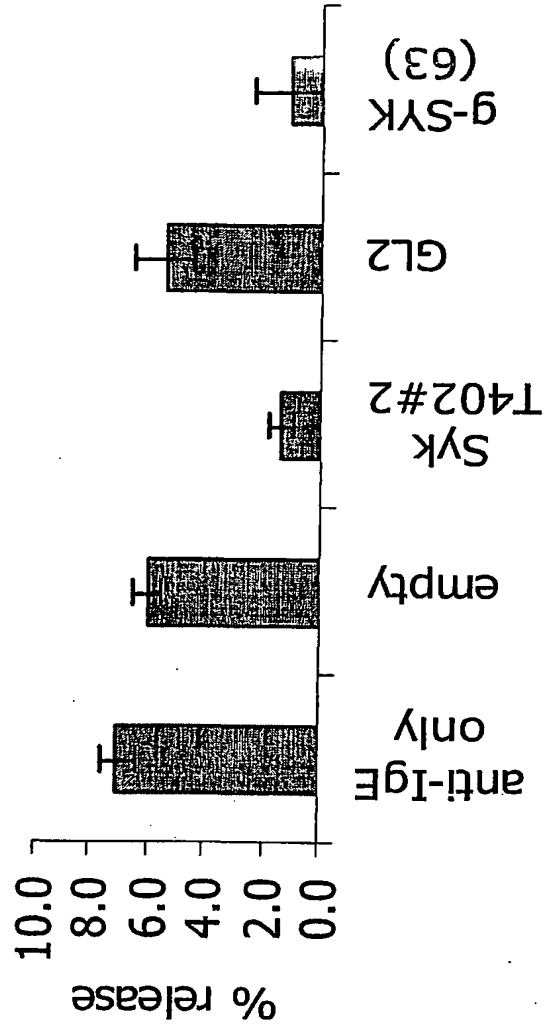


Figure 4

Knock-down of SYK Released Beta-hexosaminidase

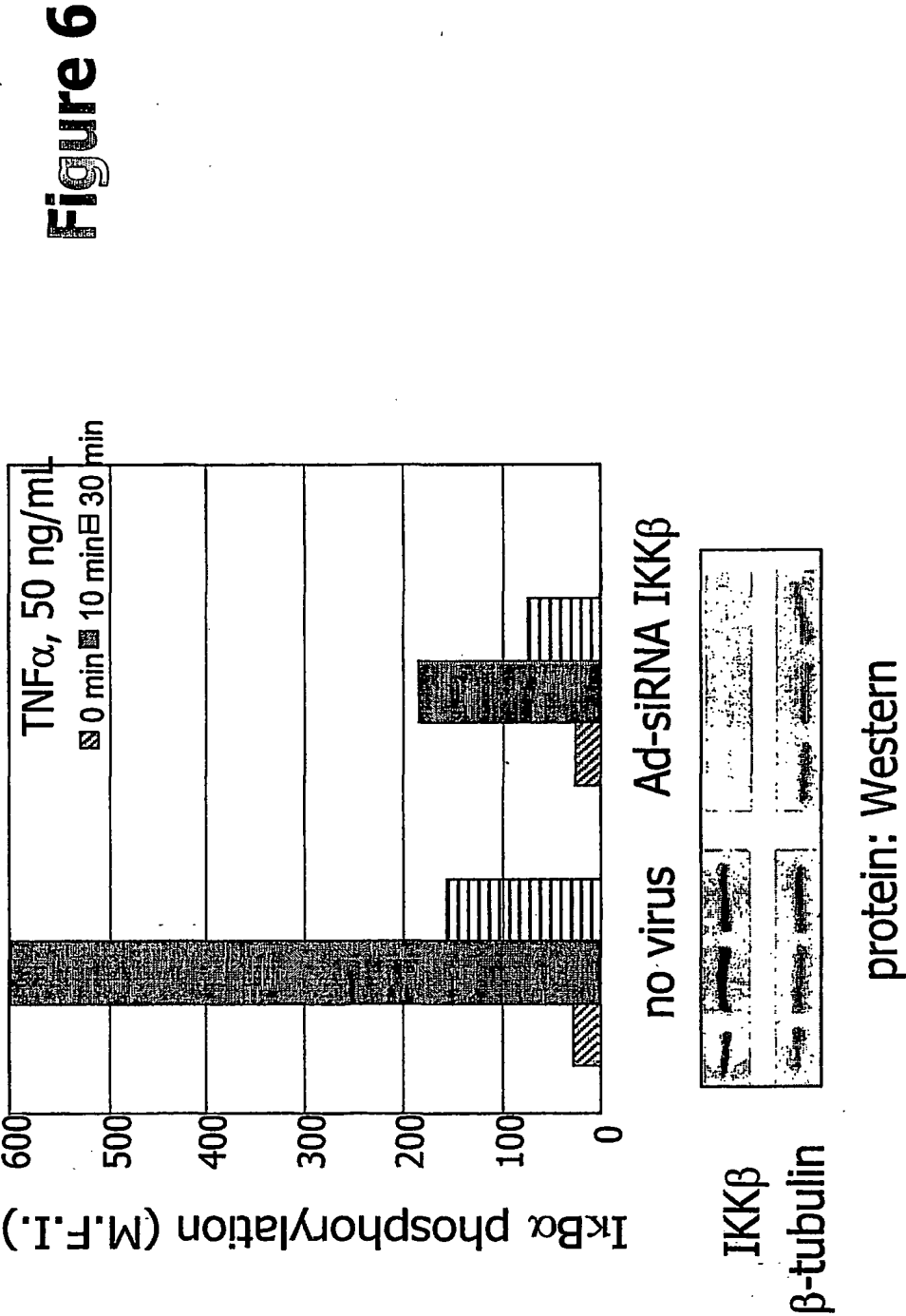
Released beta-hexosaminidase Human Mast Cells
triplo, (background subtracted)



MOI 1000
anti-IgE 1500 ng/ml
3dpi
1E+05 c/w

Figure 5

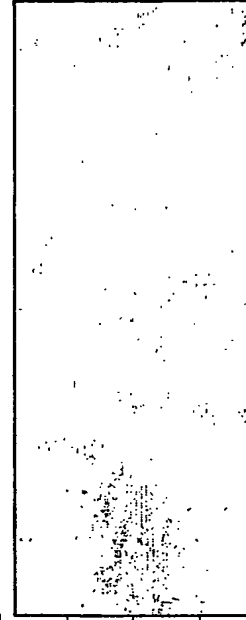
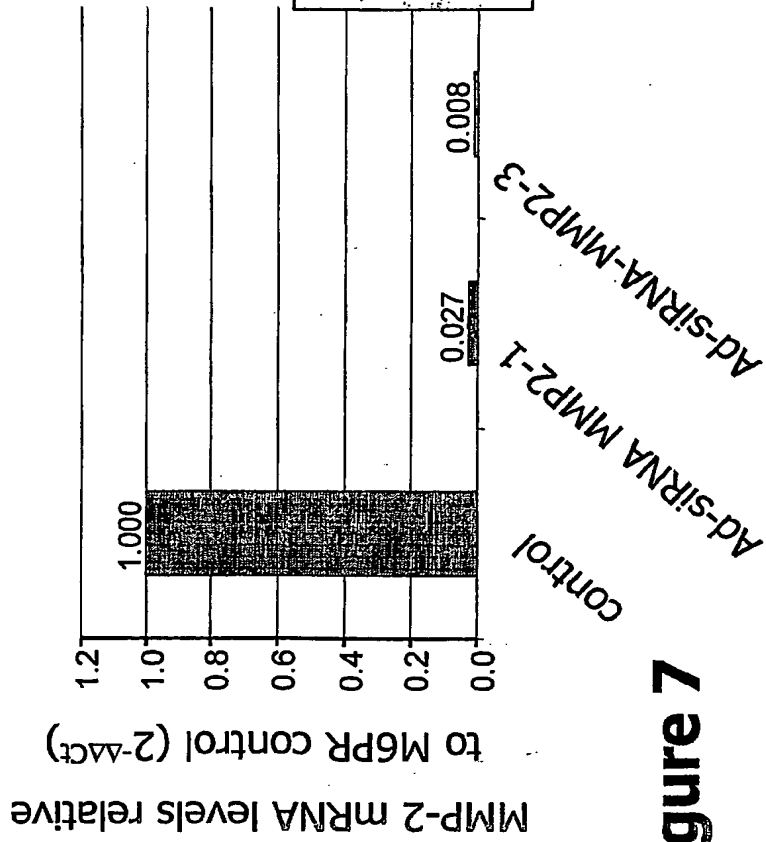
TNF α induced phospho-I κ B α
Effect of Ad-IKK β knock-down on phospho-I κ B α



MMP-2 knock-down

Reduction of MMP-2 mRNA and activity levels

mRNA: RT-PCR activity: zymogram



30 μl SN loaded on 7.5% gelatin
zymogram (inverted picture)

Figure 7

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/EP 03/04362

A. CLASSIFICATION OF SUBJECT MATTER

IPC 7 C12N15/11 A01K67/027 C12N15/861 C12Q1/68 C12N15/10
C12N5/10

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

IPC 7 C12N

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practical, search terms used)

CHEM ABS Data, EPO-Internal, WPI Data, PAJ, BIOSIS, MEDLINE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	WO 03 020931 A (GALAPAGOS GENOMICS N V ;ARTS GERT-JAN (NL); PIEST IVO (NL); LANGEM) 13 March 2003 (2003-03-13) cited in the application example 6	1-10, 13, 15, 16
Y	example 6	11, 14, 17-24
Y	figures 25A, 25B, 26-28; examples 3, 4, 9, 11, 12	11, 14, 17-24
X	WO 03 012052 A (ALTON ERIC WFW ;GRIESENBACH UTA (GB); IMP COLLEGE INNOVATUIONS LTD) 13 February 2003 (2003-02-13) SEQ ID NO's: 264 & 265 example 6; table 8	1-7
	--- -/-	

☒ Further documents are listed in the continuation of box C.

☒ Patent family members are listed in annex.

* Special categories of cited documents:

- *A* document defining the general state of the art which is not considered to be of particular relevance
- *E* earlier document but published on or after the international filing date
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- *O* document referring to an oral disclosure, use, exhibition or other means
- *P* document published prior to the international filing date but later than the priority date claimed

- *T* later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
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- *Y* document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
- *&* document member of the same patent family

Date of the actual completion of the international search

12 August 2003

Date of mailing of the international search report

04.12.03

Name and mailing address of the ISA

European Patent Office, P.B. 5818 Patentlaan 2
NL - 2280 HV Rijswijk
Tel. (+31-70) 340-2040, Tx. 31 651 epo nl,
Fax (+31-70) 340-3016

Authorized officer

Steffen, P

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 03/04362

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X	<p>KAPADIA SHAROOKH B ET AL: "Interference of hepatitis C virus RNA replication by short interfering RNAs."</p> <p>PROCEEDINGS OF THE NATIONAL ACADEMY OF SCIENCES OF THE UNITED STATES OF AMERICA. UNITED STATES 18 FEB 2003, vol. 100, no. 4, 18 February 2003 (2003-02-18), pages 2014-2018, XP002251050</p> <p>ISSN: 0027-8424</p> <p>page 2014, right-hand column, paragraph 3 -page 2015, left-hand column, paragraph 1; figure 1</p>	1,4,6,7
Y	<p>PASCALL J C ET AL: "Characterization of a mammalian cDNA encoding a protein with high sequence similarity to the Drosophila regulatory protein Rhomboid"</p> <p>FEBS LETTERS, ELSEVIER SCIENCE PUBLISHERS, AMSTERDAM, NL, vol. 429, no. 3, 16 June 1998 (1998-06-16), pages 337-340, XP004258029</p> <p>ISSN: 0014-5793</p> <p>figure 1</p>	11
Y	<p>WO 02 05843 A (ROBERTSON STEPHANIE A ;BELVIN MARCIA (US); CHEN CHANGYOU (US); FRI) 24 January 2002 (2002-01-24)</p> <p>SEQ ID NO's: 1 & 2</p> <p>page 3, line 17 -page 5, line 11</p> <p style="text-align: center;">-/--</p>	11

INTERNATIONAL SEARCH REPORT

International Application No.

PCT/EP 03/04362

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	BRIDGE ALAN J ET AL: "Induction of an interferon response by RNAi vectors in mammalian cells." NATURE GENETICS. UNITED STATES JUL 2003, vol. 34, no. 3, 8 June 2003 (2003-06-08) - July 2003 (2003-07), pages 263-264, XP002251051 ISSN: 1061-4036 figure 1A	19
A	-& "Supplementary table 1. Bridge et al." NATURE GENETICS, 'Online! 8 June 2003 (2003-06-08), pages 1-3, XP002251052 Retrieved from the Internet: <URL:http://www.nature.com/ng/journal/v34/n3/extref/ng1173-S1.pdf> 'retrieved on 2003-08-12! the whole document	
A	-& "Supplementary Note 1, Bridge et al." NATURE GENETICS, 'Online! 8 June 2003 (2003-06-08), pages 1-6, XP002251053 Retrieved from the Internet: <URL:http://www.nature.com/ng/journal/v34/n3/extref/ng1173-S2.pdf> 'retrieved on 2003-08-12! the whole document	
Y	XIA HAIBIN ET AL: "siRNA-mediated gene silencing in vitro and in vivo." NATURE BIOTECHNOLOGY. UNITED STATES OCT 2002, vol. 20, no. 10, October 2002 (2002-10), pages 1006-1010, XP002251054 ISSN: 1087-0156 page 1009, right-hand column, paragraph 4 -page 1010, left-hand column, paragraph 1; figures 1,2	19,20
A	ELBASHIR SAYDA M ET AL: "Analysis of gene function in somatic mammalian cells using small interfering RNAs." METHODS (SAN DIEGO, CALIF.) UNITED STATES FEB 2002, vol. 26, no. 2, February 2002 (2002-02), pages 199-213, XP002251055 ISSN: 1046-2023 cited in the application page 200, right-hand column, paragraph 3 -page 202, right-hand column, paragraph 1; figure 2	

-/-

INTERNATIONAL SEARCH REPORT

International Application No

PCT/EP 03/04362

C.(Continuation) DOCUMENTS CONSIDERED TO BE RELEVANT

Category *	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
A	<p>SHI Y: "Mammalian RNAi for the masses" TRENDS IN GENETICS, ELSEVIER, AMSTERDAM, NL, vol. 19, no. 1, January 2003 (2003-01), pages 9-12, XP004398851 ISSN: 0168-9525 page 9, right-hand column, paragraph 2 -page 11, right-hand column, paragraph 1; figure 1</p> <p style="text-align: center;">-----</p>	

Form PCT/ISA/210 (continuation of second sheet) (July 1992)

INTERNATIONAL SEARCH REPORT

Information on patent family members

International Application No

PCT/EP 03/04362

Patent document cited in search report		Publication date	Patent family member(s)	Publication date
WO 03020931	A	13-03-2003	WO 03020931 A2	13-03-2003
			US 2003198627 A1	23-10-2003
WO 03012052	A	13-02-2003	WO 03012052 A2	13-02-2003
WO 0205843	A	24-01-2002	AU 7696701 A	30-01-2002
			CA 2416445 A1	24-01-2002
			EP 1301611 A2	16-04-2003
			WO 0205843 A2	24-01-2002
			US 2003165497 A1	04-09-2003
			US 2002022029 A1	21-02-2002

INTERNATIONAL SEARCH REPORT

International application No.
PCT/EP 03/04362

Box I Observations where certain claims were found unsearchable (Continuation of item 1 of first sheet)

This International Search Report has not been established in respect of certain claims under Article 17(2)(a) for the following reasons:

1. ☐ Claims Nos.:
because they relate to subject matter not required to be searched by this Authority, namely:
2. ☐ Claims Nos.:
because they relate to parts of the International Application that do not comply with the prescribed requirements to such an extent that no meaningful International Search can be carried out, specifically:
3. ☐ Claims Nos.:
because they are dependent claims and are not drafted in accordance with the second and third sentences of Rule 6.4(a).

Box II Observations where unity of invention is lacking (Continuation of item 2 of first sheet)

This International Searching Authority found multiple inventions in this international application, as follows:

see additional sheet

1. ☐ As all required additional search fees were timely paid by the applicant, this International Search Report covers all searchable claims.
2. ☐ As all searchable claims could be searched without effort justifying an additional fee, this Authority did not invite payment of any additional fee.
3. ☐ As only some of the required additional search fees were timely paid by the applicant, this International Search Report covers only those claims for which fees were paid, specifically claims Nos.:
4. ☒ No required additional search fees were timely paid by the applicant. Consequently, this International Search Report is restricted to the invention first mentioned in the claims; it is covered by claims Nos.:

1-11, 13-24 (all partially)

Remark on Protest

☐ The additional search fees were accompanied by the applicant's protest.

☐ No protest accompanied the payment of additional search fees.

FURTHER INFORMATION CONTINUED FROM PCT/ISA/ 210

This International Searching Authority found multiple (groups of) inventions in this international application, as follows:

Invention 1: claims 1-11, 13-24 (all partially)

A polynucleotide comprising an RNA sequence as set out in claim 1, with the said sequence being selected from SEQ ID NO: 2 and various embodiments thereof. Furthermore vectors encoding the said polynucleotide, methods for making the said vector and methods of determining polynucleotide function comprising using the said vector.

Inventions 2-11887: claims 1-24 (all partially)

A polynucleotide comprising an RNA sequence as set out in claim 1, with the said sequence being selected from SEQ ID NO's: 3-11888 each respectively and various embodiments thereof. Furthermore vectors encoding the said polynucleotide, methods for making the said vector and methods of determining polynucleotide function comprising using the said vector.